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CARINE MARMENTINI

PROLACTINA AUMENTA A EXPRESSÃO DE ENZIMAS ANTIOXIDANTES E ATIVA O RECEPTOR ATIVADO POR PROLIFERADOR DE PEROXISSOMA (PPAR) EM CÉLULAS INS-1E

CASCAVEL- PR Fevereiro/2019

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Dissertação apresentada ao Programa de Pós-Graduação em Biociências e Saúde – Mestrado, do Centro de Ciências Biológicas e da Saúde, da Universidade Estadual do Oeste do Paraná, como requisito parcial para a obtenção do título de Mestre em Biociências e Saúde.

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Prolactina aumenta a expressão de enzimas antioxidantes e ativa o receptor ativado por proliferadores de peroxissoma PPAR em células INS-1E

Dissertação apresentada ao Programa de Pós-Graduação em Biociências e Saúde em cumprimento parcial aos requisitos para obtenção do título de Mestra em Biociências e Saúde, área de concentração Biologia, Processo Saúde-doença e Políticas de Saúde, linha de pesquisa Fatores Que Influenciam A Morfofisiologia Orgânica, APROVADO(A) pela seguinte banca examinadora:

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RESUMO

MARMENTINI, C. Prolactina aumenta a expressão de enzimas antioxidantes e ativa o receptor ativado por proliferador de peroxissoma (ppar) em células INS-1E. 101 páginas. Dissertação (Mestrado). Programa de Pós-Graduação em Biociências e Saúde, Centro de Ciências Biológicas e da Saúde, Campus Cascavel, UNIOESTE, 2019.

O diabetes mellitus (tipos 1 e 2) é caracterizado pela morte de células beta pancreáticas, a qual é induzida, entre outros fatores, pelo estresse oxidativo (EO). Sabe-se que a prolactina (PRL) melhora a sobrevivência de células beta frente a essa condição; entretanto, o mecanismo pelo qual isso ocorre ainda é desconhecido. Uma vez que a PRL modula a expressão gênica de enzimas antioxidantes em diferentes tipos celulares, nesta pesquisa investigamos se a PRL protege as células beta pancreáticas do estresse oxidativo por aumentar a produção de enzimas antioxidantes e quais vias de sinalização estariam envolvidas nesse efeito. Para isso, utilizamos células de insulinoma de rato da linhagem INS-1E. As células foram pré-tratadas por 24h com veículo (0,3 mmol/L de NaHCO₃ + 0,3% de BSA) ou PRL (0,5 μ g/mL), seguido da indução do estresse oxidativo com peróxido de hidrogênio (H₂O₂) para avaliação da viabilidade celular, produção mitocondrial de espécies reativas de oxigênio (EROs) e conteúdo proteico das enzimas antioxidantes catalase (CAT), glutationa peroxidase 1 (GPx1), superóxido dismutase 1 (SOD1) e superóxido dismutase 2 (SOD2). O conteúdo proteico dessas enzimas também foi avaliado no experimento de timecourse, no qual as células foram tratadas com PRL (0,5 µg/mL) em diferentes tempos. Fisiologicamente, durante a prenhes/gravidez ocorre acentuada secreção hipofisária de PRL. Por isso, com o objetivo de elencarmos possíveis vias de sinalização a serem investigadas, nosso próximo passo foi realizar análises de bioinformática com os genes upregulated em ilhotas de ratas prenhas, identificados previamente por nosso grupo de pesquisa a partir de macroarray. Os achados dessas análises levaram-nos à realização do ensaio de promotor repórter utilizando diferentes concentrações de PRL por 24h. Por fim, para testar se os efeitos da PRL são mediados pela via de sinalização sugerida pelas análises de bioinformática, avaliamos novamente a viabilidade celular na presença de siRNA para knockdown do gene alvo. As análises estatísticas foram feitas por teste t ou ANOVA seguida do pós-teste de Bonferroni. A PRL aumentou a sobrevivência das células beta pancreáticas expostas a H_2O_2 , assim como o conteúdo proteico da SOD2 e da CAT. Também observamos a diminuição da concentração mitocondrial de H_2O_2 em células pré-tratadas com o hormônio. As análises de bioinformática revelaram enriquecimento da via do receptor ativado por proliferadores de peroxissoma (PPAR), o qual está envolvido na transcrição de enzimas antioxidantes. Com o ensaio de promotor repórter observamos que PRL ativa PPAR. Dentre as isoformas de PPAR existentes, avaliamos se PRL seria dependente de PPARy para evitar a morte celular causada pelo EO, uma vez que a expressão de PPARy é aumentada pela PRL em linhagem celular de pré-adipócitos e no tecido adiposo de ratos. No entanto, o knockdown desse fator de transcrição não alterou a eficiência da PRL em proteger as células beta da morte causada pelo H₂O₂. Concluímos que a PRL aumenta a expressão de enzimas antioxidantes e essa ação parece ser independente de PPARy. Investigações futuras são necessárias para identificar a via de sinalização que medeia esse efeito.

Palavras-chaves: células beta pancreáticas; estresse oxidativo; morte celular; prolactina; diabetes; PPAR

ABSTRACT

MARMENTINI, C. Prolactin increases the expression of antioxidant enzymes and activates peroxisome proliferator-activated receptor (PPAR) in INS-1E cells. 101 páginas. Dissertação (Mestrado). Programa de Pós-Graduação em Biociências e Saúde, Centro de Ciências Biológicas e da Saúde, Campus Cascavel, UNIOESTE, 2019.

Diabetes mellitus (types 1 and 2) is characterized by pancreatic beta cells death induced, among other factors, by oxidative stress (OE). It is known that prolactin (PRL) improves the survival of beta cells against this condition, however the mechanism by which this occurs is still unknown. Since PRL modulates the gene expression of antioxidant enzymes in different cell types, our objective was to investigate whether PRL protects pancreatic beta cells from oxidative stress by increasing the production of antioxidant enzymes and what signaling pathways would be involved in this effect. For this, we used beta cell line from rats insulinoma, INS-1E. Cells were pretreated for 24 h with vehicle (0.3 mmol/L NaHCO₃ + 0.3% BSA) or PRL (0.5 µg/mL), followed by induction of oxidative stress with hydrogen peroxide (H₂O₂) for evaluation of cell viability, mitochondrial production of reactive oxygen species (ROS) and protein content of antioxidant enzymes catalase (CAT), glutathione peroxidase 1 (GPx1), superoxide dismutase 1 (SOD1) and superoxide dismutase 2 (SOD2). The protein content of these enzymes was also evaluated in the time-course experiment, in which the cells were treated with PRL (0.5 µg/mL) at different times. Physiologically, during pregnancy there is marked pituitary secretion of PRL. Therefore, in order to indicate possible signaling pathways to be investigated, our next step was to perform bioinformatics analyzes with the genes upregulated in islets of pregnant rats previously identified by our research group from macroarray. The findings of these analyzes led us to carry out the reporter promoter assay using different concentrations of PRL for 24h. Finally, to test whether the effects of PRL are mediated by the signaling pathway suggested by bioinformatics analyzes, we again evaluate cell viability in the presence of siRNA for target gene knockdown. Statistical analyzes were performed by t-test or ANOVA followed by the Bonferroni posttest. PRL increased the survival of pancreatic beta cells exposed to H₂O₂, as well as the protein content of SOD2 and CAT. We also observed decrease in mitochondrial H₂O₂ concentration in cells pretreated with the hormone. Bioinformatics analyzes revealed enrichment of the peroxisome proliferator-activated receptor (PPAR) pathway, which is involved in the transcription of antioxidant enzymes. Using the reporter promoter assay we observed that PRL activates PPAR. Among the existing PPAR isoforms, we evaluated whether PRL would be dependent on PPARy to prevent cell death caused by EO, since PPARy expression is increased by PRL in preadipocyte cell line and in adipose tissue of rats. However, the knockdown of this transcription factor did not alter the efficiency of PRL in protecting beta cells from death caused by H₂O₂. We conclude that PRL increases the expression of antioxidant enzymes and this action seems to be independent of PPARy. Future investigations are needed to identify the signaling pathway that mediates this effect.

Keywords: pancreatic beta cells; cell death; oxidative stress; prolactin; diabetes; PPAR

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LISTA DE ABREVIATURAS

ADP: adenosina difosfato **ARE**: elementos de resposta antioxidante ATP: adenosina trifosfato cAMP: monofosfato cíclico de adenosina **CAT**: catalase CCK: colecistocinina **DAG**: diacilglicerol DM: diabetes mellitus DM1: diabetes mellitus do tipo 1 DM2: diabetes mellitus do tipo 2 DNA: ácido desoxirribonucleico EO: estresse oxidativo EROs: espécies reativas de oxigênio FAD: flavina adenina dinucleotídeo **GLUT:** Transportador de glicose GLP-1: peptídeo semelhante ao glucagon 1 GLP1R: receptor de GLP-1 GPx: glutationa peroxidase **IKKβ**: I-kappa-B-quinase beta **IFN-**γ: Interferon gama **IL-1**β: Interleucina 1 beta IP₃: inositol trifosfato IR: receptor de insulina **IRS**: substrato do receptor de insulina JAK2: janus quinase 2 JNK: c-jun-N-terminal quinase LAFEM: Laboratório de Fisiologia Endócrina e Metabolismo

LAPEM: Laboratório de Pâncreas Endócrino e Metabolismo **MAPK**: proteíno-quinase ativada por mitógenos mRNA: RNA (ácido ribonucleico) mensageiro **NAD**: nicotinamida adenina dinucleotídeo NF-Kb: fator nuclear kappa B PCK: proteinoquinase C PDX-1: fator promotor de insulina 1 **PI3K**: fosfatidilinositol 3-quinase PKA: proteinoquinase A PLC: fosfolipase C PPARs: receptores ativados por proliferadores de peroxissoma **PPRE**: elementos responsivos aos proliferadores de peroxissoma **PRL**: prolactina **Prir:** receptor PRL **RXR**: receptor x retinoide **SOD**: superóxido dismutase **STAT**: transdutor de sinal e ativador de transcrição **TNF-** α : fator de necrose tumoral alfa **TSP-1**: Trombospondina 1 **UCP**: proteínas de desacoplamento

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1. INTRODUÇÃO

O diabetes mellitus (DM) é uma doença crônica multifatorial, caracterizada por elevada concentração sanguínea de glicose, denominada "hiperglicemia". Essa hiperglicemia pode ser decorrente da produção insuficiente de insulina ou da resistência na sua ação (WHO, 2018).

Nas últimas décadas, a prevalência do DM aumentou de forma muito expressiva, tornando essa doença uma das maiores preocupações globais em saúde do século XXI (IDF, 2015). Atualmente, cerca de 422 milhões de adultos em todo o mundo têm DM e 1,6 milhões de mortes por ano vêm sendo atribuídas às suas complicações (WHO, 2018). No Brasil, os dados não são menos alarmantes. De acordo com a Federação Internacional do Diabetes (IDF, 2015), em âmbito mundial, o país ocupa o 3º lugar no número de crianças de 0 a 14 anos com diabetes do tipo 1 (DM1) e o 4º lugar no número de adultos com diabetes do tipo 2 (DM2).

Dentre os tipos de DM, o DM1 e o DM2 são os mais recorrentes. O DM1 representa de 5 a 10% dos casos (DANEMAN, 2006; SBD, 2018), e é caracterizado pela destruição seletiva das células beta do pâncreas pelo sistema imune, o que resulta na deficiência de insulina (THOMAS et al., 2009). A causa exata do DM1 é desconhecida, mas o que se sabe é que advém de uma complexa interação entre os fatores genéticos e ambientais (WHO, 2016). Já o DM2, diagnosticado em 90 a 95% dos casos, pode ser decorrente da resistência à insulina e/ou da deficiência na sua secreção (SALSALI; NATHAN, 2006), e está associado principalmente ao sedentarismo, à dieta rica em carboidratos e aos lipídeos e envelhecimento. Pode ocorrer em qualquer idade, mas geralmente é diagnosticado após os 40 anos (SBD, 2018).

O estresse oxidativo (EO), que é o aumento na relação entre a produção de espécies moleculares altamente reativas e as defesas antioxidantes (SIES; JONES, 2007), contribui para a ativação do ataque autoimune contra as células beta pancreáticas (CERIELLO, 2000; LICHTENBERG; PINCHUK, 2015; NEWSHOLME et al., 2007) e prejudica a via de sinalização da insulina, condições estritamente

associadas ao DM1 e DM2 (MATOUGH et al., 2012).

Dentre as espécies reativas, as de oxigênio (EROs) estão presente em maior quantidade nas células e são representadas principalmente pela hidroxila (OH⁻), pelo superóxido (O_2) , pelo hidroperóxido (HO_2) e pelo peróxido de hidrogênio (H₂O₂). Em concentrações fisiológicas, elas são necessárias para a expressão gênica, para a supressão de células tumorais, para a ativação de fatores de transcrição nuclear e de crescimento celular, além de atuarem como mecanismo de defesa contra infecções (LEE; KOO; MIN, 2004). Todavia, em excesso, esses compostos tornam-se nocivos por conta da sua ação deletéria sobre proteínas, lipídeos e DNA. Nas proteínas, as EROs provocam mudanças estruturais a partir da modificação dos resíduos de aminoácidos, resultando na diminuição da atividade proteica e na maior suscetibilidade à desnaturação e à hidrólise. Nos lipídeos, o processo mais frequente é o de oxidação, que diminui a fluidez das membranas e a seletividade no transporte iônico e promove a formação de produtos tóxicos para as células (GIROTTI, 1998; LEE; KOO; MIN, 2004). Quanto ao DNA, podem ocorrer mudanças na sequência das bases nitrogenadas, alterando a expressão gênica e favorecendo a patogenia de doenças crônicas (SINGH et al., 2009).

Para manter a concentração apropriada de EROs e evitar o EO, as células têm sistemas de defesa antioxidante que abrangem enzimas como a catalase (CAT), a glutationa peroxidase (GPx) e a superóxido dismutase (SOD) (VALKO et al., 2007). A SOD é responsável pela dismutação do O_2^- , formando o H_2O_2 . O H_2O_2 pode ser metabolizado pela CAT ou pela GPx. No primeiro caso, ocorre a produção de uma molécula de H_2O e O_2 e, no segundo, duas moléculas de H_2O (LEE; KOO; MIN, 2004).

A prolactina (PRL), hormônio proteico secretado predominantemente pela hipófise anterior (FRIESEN; GUYDA; HARDY, 1970; IGNACAK et al., 2012), tem efeitos sobre o pâncreas como o aumento da secreção de insulina estimulada pela glicose e da expressão de transportador de glicose tipo 2 (GLUT2) em ilhotas de ratos neonatos (BOSCHERO et al., 1992; CREPALDI; CARNEIRO; BOSCHERO, 1997); acréscimo da massa de ilhotas pancreáticas e da secreção de insulina em ratas prenhas (BRELJE et al., 1993; SORENSON; BRELJE, 1997; AMARAL et al., 2004); aumento da vascularização em ilhotas de ratos transplantadas (JOHANSSON et al., 2009); e melhora da viabilidade de células beta humanas expostas à citocinas pró-inflamatórias e H₂O₂ (YAMAMOTO et al., 2010). Recentemente, foram descritas vias envolvidas na proteção das células beta pela PRL frente ao insulto causado por citocinas pró-inflamatórias (NARDELLI et al., 2018). Entretanto, ainda são desconhecidos os mecanismos pelos quais esse hormônio protege as células beta do estresse oxidativo.

Nesse sentido, estudos já demostraram que a PRL aumenta a expressão gênica da SOD em ilhotas pancreáticas de ratas (BORDIN et al., 2004) e em linhagem de fibroblastos (ADACHI et al., 2004). Além disso, em células da retina de camundongos submetidos ao estresse oxidativo, a ausência do receptor de PRL diminuiu o mRNA de CAT (MELÉNDEZ GARCÍA et al., 2016). Dessa forma, investigamos se a proteção exercida pela PRL sobre as células beta pancreáticas contra o estresse oxidativo deve-se ao aumento da produção das enzimas antioxidantes e qual via de sinalização estaria envolvida nesse efeito.

2. OBJETIVOS

2.1 Objetivo Geral

Investigar mecanismos envolvidos na proteção das células beta pancreáticas pela PRL frente ao estresse oxidativo.

2.2. Objetivos específicos

Em linhagem de células beta pancreáticas (INS-1E), verificar se a PRL:

- Previne a morte celular induzida pelo H₂O₂;

- Aumenta a expressão de enzimas antioxidantes;

- Diminui a produção de EROs;

- Modula vias de sinalização envolvidas na expressão de enzimas antioxidantes.

3. REVISÃO DE LITERATURA

3.1 Produção, secreção e ação da insulina

O pâncreas é uma glândula dividida anatomicamente em três regiões: cabeça (proximal), corpo e cauda (distal). A primeira encontra-se em contato com o duodeno, enquanto a última com o hilo esplênico e flexura cólica esquerda. O pâncreas é constituído por uma porção exócrina e outra endócrina. A exócrina é formada pelos ácinos, responsáveis pela secreção de suco pancreático no duodeno, favorecendo a digestão (DOLENSEK; RUPNIK; STOZER, 2015). A endócrina é formada pelas ilhotas de Langerhans, descritas pela primeira vez em 1869, por Paul Langerhans (YAGIHASHI, 2015).

Para a manutenção de concentrações adequadas de nutrientes no sangue, as ilhotas pancreáticas secretam hormônios que agem em diversos tecidos, promovendo a captação de glicose, de aminoácidos e de ácidos graxos quando há excesso desses substratos, como é o caso da insulina, ou a liberação deles quando estão em concentrações insuficientes, ação que é induzida pelo glucagon, por exemplo. (HARDIE, 2012). Um pâncreas adulto normal contém cerca de 1 milhão de ilhotas, o que constitui até 2% da massa pancreática (ELIASCHEWITZ et al., 2009). As ilhotas de Langerhans de humanos são formadas principalmente pelas células beta (54%), pelas células alfa (34%) e pelas células delta (10%). Essas células secretam insulina, glucagon e somatostatina, respectivamente (BRISSOVA et al., 2005).

A fim de compreender acerca da fisiopatologia do diabetes, primeiramente é necessário entender como ocorre a produção e a secreção de insulina em condições fisiológicas normais, como fizemos nos parágrafos seguintes.

A insulina é um hormônio anabólico e, entre outras ações, é responsável pela captação de glicose principalmente pelas células musculares e adiposas, ou seja, pela redução da glicemia. Sua síntese é estimulada por nutrientes tais como glicose, aminoácidos e lipídeos (HABER et al., 2001), e tem início com a tradução do mRNA da insulina pelos ribossomos do retículo endoplasmático, formando um

pré-pró-hormônio da insulina. Essa molécula tem em torno de 11,5 kDa e é constituída por quatro domínios: peptídeo C, cadeias A e B e um peptídeo sinalizador. (DODSON; STEINER, 1998; SKELIN; RUPNIK; CENCIC, 2010). Nessa mesma organela, a pré-pró-insulina sofre clivagem de seu peptídeo sinalizador, dando origem à pró-insulina. A pró-insulina, com 9,0 kDa, é transportada até o complexo de Golgi, onde é armazenada em vesículas. Após a clivagem do peptídeo C dentro das vesículas, a insulina com 5,8 kDa, composta pelas cadeias A e B, está pronta para ser secretada (DODSON; STEINER, 1998).

A glicose é o principal estímulo para a secreção da insulina e a sua concentração no interstício varia em paralelo à concentração do substrato no sangue. A entrada de glicose nas células beta é facilitada pelo transportador de glicose (GLUT). Dentro da célula, a glicose é metabolizada, elevando a proporção de ATP/ADP, o que fecha os canais de K+ sensíveis a ATP e provoca a despolarização da membrana da célula beta. A despolarização promove a abertura dos canais de Ca²⁺ controlados por voltagem e a entrada desse íon. O aumento da concentração intracelular de Ca²⁺ ativa a exocitose das vesículas contendo a insulina e o peptídeo C, mediada pelos microtúbulos e proteínas de membrana. Outros substratos metabolizáveis pelas células e que geram ATP, tais como os aminoácidos arginina, lisina e leucina, também estimulam a secreção de insulina (ASHCROFT; RORSMAN, 1989; RUTTER et al., 2015).

A acetilcolina e hormônios como a colecistocinina (CCK) e o peptídeo semelhante ao glucagon 1 (GLP-1) atuam como potencializadores da secreção de insulina (RUTTER et al., 2015). A acetilcolina, por meio do seu receptor M3 (BOSCHERO et al., 1995), e a colecistocinina, pelo receptor GLP1R, ativam a fosfolipase C (PLC), culminando no aumento de inositol trifosfato (IP₃) e de diacilglicerol (DAG). O IP₃ promove a abertura dos canais de Ca²⁺ do retículo endoplasmático ao se ligar ao seu receptor (IP₃R), o que aumenta a concentração citoplasmática desse íon e ativa a maquinaria exocitótica (SHAWL; PARK; KIM, 2009). O DAG ativa a proteína quinase C (PKC), que aumenta a quantidade de vesículas contendo insulina (WAN et al., 2004) e ativa proteínas responsáveis pela translocação dessas vesículas para as proximidades da membrana plasmática (HABER et al., 2001). Já o GLP-1 ativa a adenilato ciclase, que promove a geração de monofosfato cíclico de adenosina (cAMP). O cAMP ativa a proteína quinase A (PKA), que, assim como a PKC, aumenta a quantidade e a mobilidade das

vesículas de insulina, além de permitir a entrada de Ca²⁺ extracelular por meio da fosforilação dos canais de Ca²⁺ sensíveis à voltagem (RORSMAN et al., 2000; TENGHOLM, 2012).

A meia-vida plasmática da insulina é de, aproximadamente, seis minutos; portanto, ela é, na sua maior parte, eliminada da circulação dentro de 10 a 15 minutos. Com exceção da porção da insulina que se liga aos receptores nas células-alvo, o restante é degradado pela enzima que degrada a insulina (IDE), encontrada principalmente no fígado (HULSE; RALAT; WEI-JEN, 2009).

A insulina regula a homeostase de glicose especialmente pela diminuição da sua produção hepática (inibindo enzimas gliconeogênicas e a secreção de glucagon) e aumento da captação desse carboidrato (conduzindo o transportador de glicose, GLUT, até a membrana plasmática), principalmente nos tecidos muscular e adiposo. A insulina também atua nesses tecidos estimulando a síntese proteica e a lipogênese, respectivamente (CARVALHEIRA; ZECCHIN; SAAD, 2002). Para que a insulina consiga desempenhar essas ações, é necessário que ocorra a interação do hormônio com o seu receptor e a ativação de uma série de cascatas de sinalização. A sinalização intracelular da insulina tem início com a sua ligação a um receptor específico de membrana, uma proteína heterotetramérica com atividade quinase, composta por duas subunidades α e duas subunidades β . A ligação da insulina à subunidade α extraceular permite que a subunidade β adquira atividade quinase, levando a alteração conformacional, autofosforilação e consequente ativação (PATTI; KAHN, 1998). Uma vez ativado, o receptor de insulina (IR) fosforila vários substratos proteicos em tirosina, entre eles, os substratos do receptor de insulina (IRS). A partir dos IRS, a sinalização de insulina ocorre por duas principais vias. A primeira envolve a fosfatidilinositol 3-quinase (PI3K), importante na captação de glicose, síntese de glicogênio e de proteínas, bem como na inibição da gliconeogênese e lipólise (FOLLI et al., 1992). A segunda via é a da proteíno-quinase ativada por mitógenos (MAPK), que medeia a expressão gênica e a síntese proteica (PAEZ-ESPINOSA et al., 1999).

Caso ocorra algum problema na síntese, na secreção e na ativação de vias de sinalização de insulina, a glicose não será metabolizada adequadamente, o que pode resultar em hiperglicemia e, caso persista esse quadro, no desenvolvimento do DM.

3.2 Diabetes Mellitus (DM)

O DM foi primeiramente relatado pelos egípcios por volta de 1500 a.C. A doença apresentava como principais aspectos a poliúria e a presença de açúcar na urina, o que foi constatado por se observar que as formigas eram atraídas pela urina dos doentes (MACCRACKEN; HOEL; JOVANOVIS, 1997). Por conta das suas características, a doença recebeu os nomes "diabetes", palavra de origem grega que significa "sifão", e "mellitus", que significa "mel" em latim (LAKHTAKIA, 2010).

A primeira descrição detalhada da doença foi feita pelo grego Aretaeus da Capadócia (150 d.C.). Segundo ele, o DM era uma aflição notável, não muito comum na época. Apesar de levar um período longo até se estabelecer, o enfermo morria rapidamente após a doença se instaurar. A sede era inextinguível e proporcional à quantidade de urina eliminada. Além disso, a emaciação era grande, como se os músculos fossem excretados com a urina (LAIOS et al., 2012).

Em 1798, John Rollo verificou que o açúcar não estava presente apenas na urina dos pacientes diabéticos, mas também no sangue, o que significou se tratar de uma condição sistêmica (MACCRACKEN; HOEL; JOVANOVIS, 1997). Outra descoberta de extrema importância foi feita na década seguinte por Joseph von Mering e Oscar Minkowski. Eles constataram que a remoção do pâncreas de um cachorro levou o animal ao desenvolvimento do DM (MEHRING; MINKOWSKI,1890).

No início do século XIX, Claude Bernard supôs que o glicogênio era armazenado no fígado e que a partir dele era secretado no sangue uma substância "doce". Foi a superprodução dessa substância, mais tarde chamada de glicose, que o pesquisador considerou como causa do DM (MACCRACKEN; HOEL; JOVANOVIS, 1997).

Atualmente, sabe-se que o DM é uma doença crônica multifatorial, caracterizada por elevadas concentrações sanguíneas de glicose, o que é denominado "hiperglicemia". Essa hiperglicemia pode ser decorrente da produção insuficiente de insulina ou pela deficiência na sua ação, em que não é possível utilizar efetivamente a insulina produzida (WHO, 2018).

De acordo com a Organização Mundial da Saúde – OMS - (WHO, 2018), cerca de 422 milhões de pessoas em todo o mundo convivem com DM. Além disso, há por volta de 318 milhões de adultos com tolerância à glicose diminuída, o que faz com que esses indivíduos tenham alto risco de desenvolver a doença no futuro (IDF, 2015). Outra informação que justifica a preocupação a respeito do DM é o fato de que em torno de 1,6 milhões de mortes por ano por ano vêm sendo atribuídas às suas complicações (WHO, 2018).

Dentre os tipos de DM, o DM1 e o DM2 são os mais recorrentes. O DM1 representa 5 a 10% dos casos de DM (DANEMAN, 2006; SBD, 2016) e é caracterizado pela deficiência de insulina como consequência da progressiva destruição das células beta pelo sistema imune. A causa exata do DM1 é desconhecida, mas há o consenso de que resulta de uma complexa interação entre os fatores genéticos e ambientais (WHO, 2018). Já o DM2, diagnosticado em 90 a 95% dos casos, pode ser decorrente da resistência à insulina e/ou da deficiência na sua secreção (SALSALI; NATHAN, 2006), e frequentemente está associado ao sedentarismo, à dieta rica em carboidratos e lipídeos e ao envelhecimento. Pode ocorrer em qualquer idade, mas geralmente é diagnosticado após os 40 anos (SBD, 2018).

Para confirmar o diagnóstico do DM, pode-se utilizar, no mínimo, um dos quatro critérios a seguir: glicemia casual $\geq 200 \text{ mg/dL}$, acrescida de poliúria, polidipsia, polifagia e fadiga; glicemia de jejum $\geq 126 \text{ mg/dL}$; glicemia $\geq 200 \text{ mg/dL}$ 2 horas após sobrecarga com 75g de glicose e hemoglobina glicada (A1C) $\geq 6,5\%$ (ADA, 2017; SBD, 2018).

O que torna o DM uma doença tão grave são as complicações que podem acometer diferentes locais do organismo, tais como: olhos (cegueira); cavidade oral (periodontite); coração (angina, infarto agudo do miocárdio, insuficiência cardíaca congestiva); cérebro (acidente vascular encefálico); rins (insuficiência renal); nervos (formigamento, perda da sensibilidade) e vasos (ulceração e amputação de membros) (GROSS et al., 2002; WHO, 2018).

Por conta desses agravos, o impacto econômico causado pela enfermidade é gigantesco, uma vez que são necessários recursos para custear tratamentos, internações prolongadas e recorrentes. De acordo com a Federação Internacional do Diabetes (IDF, 2015), o gasto mundial com o DM mais que triplicou no período de 2003 a 2013, e estima-se que atualmente ultrapasse os 827 bilhões de dólares (WHO, 2016), correspondendo a 12% das despesas globais em saúde (IDF, 2015).

Do ponto de vista social, o diabético pode apresentar redução da capacidade funcional e consequente desempenho prejudicado no trabalho. Aliás, em situações mais graves, como no caso de amputações, o indivíduo pode se tornar dependente de outras pessoas (ADA, 2017). Frente às mudanças que o DM pode significar na vida de quem convive com o problema, é importante levar em consideração o aspecto psicológico e constatar precocemente situações como baixa adesão ao tratamento, desinteresse pelo autocuidado e isolamento social, fatores que aumentam o risco de complicações e pioram o prognóstico da comorbidade (SBD, 2018).

Para evitar o estabelecimento de complicações e amenizar os impactos econômicos, sociais e psicológicos, podem ser adotados tratamentos que abrangem a reeducação alimentar, a prática de atividade física e o uso de medicamentos (IDF, 2015). O transplante de ilhotas pancreáticas também é uma opção para a melhora da qualidade de vida dos pacientes com DM1 que não apresentam controle glicêmico, mesmo fazendo uso de combinações dos métodos supracitados, tanto por proporcionar dieta mais flexível, quanto pela interrupção do incômodo das injeções de múltiplas doses de insulina e das medições diárias de glicemia capilar (FROUD et al., 2005; RYAN et al., 2002; SBD, 2018).

3.2.1 Fisiopatologia do DM1 e DM2

A gênese do DM1 se dá quando infecções virais ou processos inflamatórios promovem a apoptose das células beta e consequente liberação de antígenos. A partir disso, as células apresentadoras de antígeno são ativadas e podem recrutar linfócitos T naive, causadores de infiltração no pâncreas. A infiltração mediada pelas células T leva à geração de EROs e de citocinas pró-inflamatórias como TNFα, IL-1β e IFN-γ. Esses agentes ativam os fatores de transcrição fator nuclear kappa B (NF-Kb) e transdutor de sinal e ativador de transcrição 1 (STAT-1), que diminuem a expressão do fator promotor de insulina 1 (PDX1) e de GLUT2, reduzindo a produção e secreção de insulina. A ativação de NF-Kb e STAT-1 também desencadeia estresse de retículo endoplasmático, processos apoptóticos e liberação de mais citocinas pelas células beta, levando a um ciclo vicioso de inflamação e de destruição dessas células que mantém e amplifica o ataque autoimune (HASKINS et al., 2003; VEGA-MONROY; FERNANDEZ-MEJIA, 2012).

A falha na secreção de insulina observada no DM2 pode ser ocasionada pela diminuição da massa e/ou da disfunção das células beta, induzidas pela (CANTLEY; ASHCROFT. 2015; hiperglicemia prolongada POITOUT: ROBERTSON, 2008). Essa condição aumenta a produção de EROs pela cadeia transportadora de elétrons da mitocôndria, os quais ativam vias de morte celular (HUNT; DEAN; WOLFF, 1988; TANAKA et al., 1996). Além disso, a hiperglicemia promove mudanças na expressão dos fatores de transcrição característicos das células beta e diminuição do mRNA, conteúdo e secreção de insulina, o que é denominado desdiferenciação (WEIR; AGUAYO-MAZZUCATO; BONNER-WEIR, 2013). Inclusive, em animais diabéticos já foram observadas células beta que passam a expressar glucagon. Ainda não está claro se essas células são convertidas para alfa ou se há um tipo celular intermediário que expressa tanto glucagon quanto proteínas de células beta (BRERETON et al., 2014).

Outra característica preponderante do DM2, a resistência à insulina, é decorrente da fosforilação de resíduos serina dos IRS, ao invés da fosforilação em tirosina, o que diminui a transdução de sinal a partir desses substratos e consequentemente a ativação das vias PI3K e MAPK (HOTAMISLIGIL et al., 1996; MARTYN; KANEKI; YASUHARA, 2008). Em outras palavras, a insulina não ativa adequadamente suas vias de transdução de sinal, resultando em falha na captação de glicose, na síntese de glicogênio e na inibição da gliconeogênese e lipólise. Em última análise, todos esses eventos culminarão em hiperglicemia (LUCA; OLEFSKY, 2008), e estão relacionados à fosforilação em serina proteínas como a c-jun-N-terminal quinase (JNK), p38 e I-kappa-B-quinase beta (IKKβ). O EO está entre os fatores que levam à ativação dessas quinases (EVANS; MADDUX; GOLDFINE, 2005).

3.3 Estresse oxidativo (EO) e as espécies reativas de oxigênio (EROs)

O estresse oxidativo (EO) é um desequilíbrio entre a produção de espécies moleculares altamente reativas (oxidantes) e as defesas antioxidantes, levando a prejuízos na sinalização redox e/ou a danos moleculares (SIES, 2015). Entre os

agentes oxidantes, merecem destaque as EROs, classificadas em "radicais livres" e "não radicais". Os radicais livres são átomos, íons ou moléculas que têm oxigênio com um ou mais elétrons não pareados em sua órbita externa, ou seja, o elétron está sozinho no orbital. Exemplos desse grupo são a hidroxila (OH⁻), o superóxido (O₂⁻) e o hidroperóxido (HO₂⁻). No caso dos não radicais, não há elétron não pareado e o principal exemplo é o H₂O₂ (HALLIWELL et al., 1995).

Diferentes compartimentos celulares são responsáveis pela produção das EROs, principalmente a membrana plasmática e a mitocôndria, essa responsável por produzir 90% dessas moléculas (BALABAN; NEMOTO; FINKEL, 2005). O complexo enzimático da NADPH-oxidase presente na membrana plasmática é utilizado pelas células fagocíticas para a eliminação de microrganismos patógenos (BROWNLEE, 2005; NEWSHOLME et al., 2007). Em células como fibroblastos, musculares lisas, endoteliais, mesangiais renais e tubulares renais, esse complexo é a maior fonte de produção de EROs (LI, 2003). Várias subunidades constituem a NADPH-oxidase e em estado inativo algumas ficam localizados no citosol, enquanto outras se situam na membrana plasmática. No citosol são encontradas as subunidades p40fox, p47fox, p67fox e rac, e na membrana plasmática as subunidades p22fox e gp91fox. A fosforilação da subunidade p47fox, PKC. promove principalmente pela а translocação das subunidades citoplasmáticas à membrana e ativa o complexo. A NADPH-oxidase catalisa a doação de um elétron do NADPH para o O_2 , formando o O_2^- (Figura 1) (BABIOR, 2004).



Figura 1. Complexo NADPH-oxidase ativado. Fonte: RABELO L. A. et al. Arquivo Brasileiro de Cardiologia. 2010.

A cadeia transportadora de elétrons está localizada nas cristas da membrana mitocondrial interna, e a formação de EROs a partir dela envolve a atividade dos complexos I, II, III e IV da cadeia respiratória, durante a fosforilação oxidativa. Os elétrons provenientes de vias catabólicas, como do metabolismo de glicose e ácidos graxos pelo ciclo do ácido tricarboxílico, são transferidos para aceptores universais de elétrons: Nicotinamida Adenina Dinucleotídeo (NAD) e a Flavina Adenina Dinucleotídeo (FAD) que são convertidos em NADH e FADH₂ quando reduzidos (BROWNLEE, 2005; NEWSHOLME et al., 2007).

O complexo NADH desidrogenase (I) catalisa a transferência dos elétrons do NADH para a coenzima Q. O mesmo processo é realizado pelo complexo succinato desidrogenase (II); porém, nesse caso, quem fornece elétrons é o succinato. O complexo citocromo c-oxidorredutase (III), por sua vez, transporta elétrons da coenzima Q até o citocromo c. Por fim, o complexo citocromo oxidase (IV) conduz elétrons do citocromo c para o oxigênio molecular (O₂), reduzindo-o à água. O fluxo de elétrons é acompanhado pelo bombeamento de prótons através da membrana, produzindo um gradiente eletroquímico ou de voltagem. Esse gradiente impulsiona a síntese de ATP pela ATP sintase. Alternativamente, as proteínas de desacoplamento (UCPs) podem diminuir o gradiente de voltagem para gerar calor, como forma de manter constante a geração de ATP (KORSHUNOV; SKULACHEV; STARKOV, 1997). Uma pequena proporção de elétrons, escapa pelos complexos l e II, reage com o oxigênio e forma o O_2^- (Figura 2).



Figura 2. Produção de superóxido pela cadeia transportadora de elétrons mitocondrial. CI: complexo I; CII: complexo II; CIII: complexo III; CIV: complexo IV; CoQ: coenzima Q; CytC: citocromo C; UCPs: proteínas de desacoplamento; SOD: superóxido dismutase; CAT: catalase; GPx: glutationa peroxidase; NADH: Nicotinamida Adenina Dinucleotídeo; O₂⁻: superóxido; H₂O₂: peróxido de hidrogênio. Adaptado de MC MURRAY F., PATTEN D. A., HARPER, M. E. Obesity. 2016.

A produção de EROs em concentrações fisiológicas, até 100 nM (SIES, 2017), é necessária para a expressão gênica, para a supressão de células tumorais e para a ativação de fatores de transcrição nuclear e de crescimento celular (LEE; KOO; MIN, 2004). As EROs também atuam no mecanismo inflamatório de defesa desempenhado pelas células do sistema imunológico, como os macrófagos e os neutrófilos, visando à eliminação de microrganismos patogênicos. Para isso, as EROs oxidam proteínas, lipídeos e o material gênico do patógeno, induzindo sua morte celular (NATHAN; BUSSEL, 2011; NEWSHOLME et al., 2007).

Para as células beta, as EROs têm importante papel na secreção de insulina. O H₂O₂ exógeno e maleato de dietilo, que aumenta o H₂O₂ intracelular, estimulam a secreção de insulina em linhagem de células beta e ilhotas isoladas de ratos (PI et al., 2007). Acredita-se que esse efeito ocorra pelo aumento do Ca²⁺ intracelular, que estimula a exocitose das vesículas de insulina (JANJIC et al., 1999; MAECHLER; JORNOT; WOLLHEIM, 1999). Por outro lado, a inibição da cadeia transportadora de elétrons por vários agentes, como rotenona, antimicina A, oligomicina, que aumentam as EROs derivadas de mitocôndrias, mas inibem a geração de ATP, levou à diminuição da secreção de insulina estimulada pela glicose. Ou seja, as EROs participam do mecanismo de secreção de insulina; contudo, por si mesmas não promovem esse efeito. É necessário, principalmente, o aumento da concentração do ATP intracelular pelo metabolismo da glicose (HENQUIN, 2000; WOLLHEIM; MAECHLER, 2002).

Entretanto, quando a concentração de EROs ultrapassa o limite fisiológico em qualquer tipo celular, são observados efeitos deletérios sobre proteínas, lipídeos e DNA. A oxidação de proteínas pode gerar carbonilas, metionina sulfóxido e 2-oxohistidina, compostos que alteram mecanismos de transdução de sinal, sistemas de transporte e atividades enzimáticas (STADTMAN, 2001). Além disso, as proteínas oxidadas são mais suscetíveis à desnaturação e à hidrólise (CECARINI et al., 2007). A bicamada fosfolipídica das membranas celulares é alvo direto da oxidação lipídica, que tem como consequência o aumento da polaridade da fase lipídica e da diminuição da fluidez das membranas e da resistência à desnaturação pela temperatura (LEE; KOO; MIN, 2004; ORRENIUS; GOGVADZE; ZHIVOTOVSKY, 2007). Ademais, a oxidação do DNA pode provocar alterações em suas bases nitrogenadas, como a formação do 8-hidroxiguanosina, utilizado como marcador de dano genético. E a modificação permanente do DNA pode desencadear a mutagênese, carcinogênese e envelhecimento (VALKO et al., 2007).

Algumas condições, como a hiperglicemia, são capazes de acrescer a produção de EROs pelas células beta, principalmente pelo complexo enzimático da NADPH-oxidase e pela mitocôndria (EL-BENNA et al., 2005). O aumento das concentrações intra e extracelulares de glicose induz a formação de EROs pela NADPH-oxidase, pois essa condição aumenta a produção do diacilglicerol (DAG), que estimula a atividade da PKC, e essa é responsável pela ativação do complexo (BROWNLEE, 2001; MORGAN et al., 2007). Com relação à produção de EROs pela mitocôndria, na presença do DM, há mais glicose e lipídeos sendo oxidados no ciclo do ácido tricarboxílico, o que leva mais NADH e succinato para a cadeia respiratória dessa organela. Como resultado, o gradiente de voltagem da membrana mitocondrial aumenta até atingir um limiar crítico. A partir daí a transferência de elétrons no interior do complexo III é bloqueada, fazendo com que eles retornem à coenzima Q, a qual doa os elétrons para o O₂, aumentando a

produção de O2⁻.

3.3.1. Modelos de indução de estresse oxidativo

Para melhor compreensão da gênese do EO e como ele se relaciona com as mais diversas doenças, podem ser utilizados compostos, tanto *in vivo* quanto *in vitro*, que induzem a formação das EROs e/ou mimetizam sua ação, como: dieta *high-fat* (60% lipídeos, 20% proteínas e 20% carboidratos) (TACHIBANA et al., 2015); elevada concentração de carboidratos como ribose (BENSELLAM et al., 2015) e glicose (LIU et al., 2014); ácido palmítico (SHEN et al., 2014), terc-butil hidroperóxido (t-BHT) (FERNÁNDEZ-MILLÁN et al., 2014) e peróxido de hidrogênio (H₂O₂) (FIORY et al., 2014; LEE et al., 2009), sendo que esse último foi utilizado neste trabalho.

O H₂O₂ é uma ERO não radical extremamente abundante em organismos aeróbicos e relativamente estável in vivo, se comparado a outras EROs. Sua meia vida em linfócitos, por exemplo, é 1 ms, enquanto do O_2^- é 1 µs (RETH, 2002). O H₂O₂ entra nas células por meio das aquaporinas e é capaz de se difundir pelas membranas celulares (BIENERT; SCHJOERRING; JAHN. 2006). Sua concentração fisiológica é entorno de 10 nM (SIES, 2014) e o acréscimo da sua produção faz com que oxide proteínas, principalmente nos resíduos cisteína (BIENERT; SCHJOERRING; JAHN, 2006; RETH, 2002). O H₂O₂ induz danos no DNA via formação de OH⁻, radical altamente reativo, pela sua reação com metais de transição (SLAMENOVA et al., 2013).

3.3.2 Defesas antioxidantes

Para que possa ocorrer equilíbrio entre a produção e a eliminação das EROs, é necessário que as células tenham sistemas de defesa antioxidante que abrangem enzimas como a CAT, a glutationa peroxidase (GPx) e o superóxido dismutase (SOD) (VALKO et al., 2007). Existem oito isoformas conhecidas de GPx, sendo a GPx1 (citosólica) a mais abundante (MEHMETI et al., 2017; PAPP et al., 2007) e três isoformas de SOD, a SOD1 (citosólica, CuZn SOD), a SOD2 (mitocondrial, Mn SOD) e a EC-SOD (extracelular) (MARITIM; SANDERS; WATKINS, 2003; MARKLUND, 1982). O O₂⁻ proveniente, principalmente, de organelas como a membrana plasmática e a mitocôndria é dismutado pela SOD, formando o H₂O₂. O H₂O₂ pode ser metabolizado pela CAT ou pela GPx. No primeiro caso, ocorrerá a produção de uma molécula de H₂O e O₂ e no segundo, duas moléculas de H₂O (LEE; KOO; MIN, 2004). O H₂O₂ pode ainda reagir com metais de transição como Fe²⁺ ou Cu²⁺ (reação de Fenton) e com o superóxido (Reação de Haber-Weiss), formando a mais deletéria das EROs, a OH⁻ (HALLIWELL; GUTTERIDGET, 1984). Para esse radical livre; entretanto, não há enzimas que promovem a sua metabolização, por isso, provoca-se extensa destruição tecidual (LEE; KOO; MIN, 2004).

Em comparação com outros tecidos, as células beta pancreáticas apresentam menor expressão da CAT, GPx e SOD. Por exemplo, a expressão de SOD nas células beta e da CAT e GPx nas ilhotas corresponde a 50% e 1%, respectivamente, da observada no tecido hepático (LENZEN; DRINKGERN; TIEDGE, 1996; TIEDGE et al., 1997). Isso poderia contribuir para a suscetibilidade das células secretoras de insulina à danos mediados pelo EO (LENZEN; DRINKGERN; TIEDGE, 1996).

Normalmente, as enzimas antioxidantes não estão expressas na sua capacidade máxima, mas são altamente induzíveis pelos fatores de transcrição. Fatores de transcrição são proteínas que podem ativar ou reprimir a transcrição de um gene por meio de sua interação com sequências específicas do DNA (VILLARD, 2004). A ativação clássica da transcrição das enzimas antioxidantes envolve a via de sinalização Keap1-Nrf2-ARE. Keap1 (*Kelch-like ECH-associated protein 1*) é uma proteína repressora que retém o Nrf2 (fator nuclear eritroide 2 relacionado ao fator 2) no citoplasma e estimula a sua degradação proteassomal. Substâncias oxidantes e eletrófilos, por exemplo, podem reagir com resíduos de cisteína da Keap1, provocando a sua alteração conformacional e a liberação do Nrf2. O Nrf2 migra para o núcleo onde forma um heterodímero com proteínas da família *small* Maf, o qual se liga ao ARE (elementos de resposta antioxidante). A transativação de ARE permite recrutar elementos transcricionais para a expressão dos genes regulados (ITOH et al., 1999; KENSLER; WAKABAYASHI; BISWAL, 2007; SYKIOTIS; BOHMANN, 2010).

Apesar de esse mecanismo ser amplamente estabelecido, outras vias de

sinalização parecem ter influência sobre a transcrição das enzimas antioxidantes, como a via dos receptores ativados por proliferadores de peroxissoma (PPARs). Os PPARs são fatores de transcrição da família dos receptores nucleares que regulam diversos eventos biológicos com destaque para diferenciação e desenvolvimento celular, homeostase da glicose, metabolismo de lipídeos e inflamação. Estão presentes em três subtipos: α , β/δ e γ (BERGER; MOLLER, 2002). O PPAR α é expresso predominantemente no fígado, e em menor abundância no coração e no rim; o PPAR β/δ é ubíquo, embora a sua expressão seja maior no tecido adiposo, na pele e no músculo esquelético (SEMPLE; CHATTERJEE; RAHILLY, 2006); o PPAR γ tem três isoformas. O PPAR γ 1 é expresso em ampla variedade de tecidos incluindo coração, músculo, rim, baço e pâncreas; o PPAR γ 2 está presente no tecido adiposo; e o PPAR γ 3, em macrófagos e no intestino grosso (TYAGI et al., 2011).

Os PPARs ativam a transcrição de genes a partir da formação de um heterodímero com o receptor x retinoide (RXR), que se liga a sequências específicas do DNA, chamadas de elementos responsivos aos proliferadores de peroxissoma (PPRE), na região promotora dos genes alvo. Na ausência de um ligante, o complexo PPAR/RXR se mantém ligado a co-repressores transcricionais que impedem sua interação com o PPRE. Na presença de um ligante agonista, uma alteração conformacional leva à liberação do correpressor, recrutamento de coativadores, transativação de promotores relacionados ao PPRE e indução da transcrição (DEBRIL et al., 2001). Os coativadores e os correpressores transcricionais existem em complexos multiproteicos contendo enzimas modificadoras de histonas, tais como histonas acetiltransferases e histonas deacetilases. A atividade dessas enzimas modificadoras de histonas afeta a transcrição gênica por alterar a estrutura da cromatina (MCKENNA; MALLEY, 2002).

Atuam como ligantes do complexo PPAR/RXR tanto substâncias endógenas como esteroides, ácidos graxos, vitaminas e hormônios (REPA; EVANS; MANGELSDORFZI, 2001), quanto sintéticas, como os fibratos e as tiazolidinedionas (TZDs) (BERGER; AKIYAMA; MEINKE, 2005).

Os fibratos, ligantes do PPARα como o fenofibrato, são prescritos principalmente para o tratamento da hipertrigliceridemia (SAHEBKAR et al., 2017) e na prevenção da aterosclerose (SAHEBKAR et al., 2016). Esse fármaco também

atua sobre as células beta pancreáticas, restabelecendo a secreção de insulina prejudicada pelas EROs (SUN et al., 2008) e diminuindo a hiperglicemia de animais com diabetes induzido pelo estresse oxidativo, por aumentar a atividade da CAT e SOD (YARIBEYGI et al., 2018).

As TZDs, ligantes de PPARγ, como a pioglitazona, são indicadas para o tratamento do DM2 em humanos por aumentarem a captação de glicose estimulada pela insulina no músculo esquelético e tecido adiposo, por inibirem a produção hepática de glicose e por reduzirem a hipertrigliceridemia e a concentração de ácidos graxos livres no plasma (DEBRIL et al., 2001; SEMPLE; CHATTERJEE; RAHILLY, 2006). Em modelos animais diabéticos db / db e obesos pré-diabéticos, as TZDs aumentam a proliferação e reduzem a apoptose de células beta (KANDA et al., 2010; ZENDER et al., 2004) e estimulam a secreção de insulina (HIGA et al., 1999), respectivamente. Diante do estresse oxidativo, a pioglitazona previne a formação de EROs, protegendo as ilhotas pancreáticas e as células beta da apoptose (SAITOH et al., 2008; VANDEWALLE et al., 2008). Nesse sentido, os promotores dos genes das enzimas antioxidantes têm PPRE (CHUNG et al., 2011; GIRNUN et al., 2002; YOO; CHANG; RHO, 1999) e estudos mostram que as TZDs aumentam a expressão de CAT, GPx e SOD2, tanto em ilhotas quanto em células beta (KANDA et al., 2010; CHUNG et al., 2011).

3.4 Prolactina

Descoberta em 1960, a Prolactina (PRL) é um hormônio constituído por 199 aminoácidos e tem aproximadamente 23 kDa. É secretada, predominantemente, pela hipófise anterior (FRIESEN; GUYDA; HARDY, 1970; GUELHO et al., 2016), apesar de também ser verificada a sua produção em linfócitos, glândula mamária, glândula prostática, fibroblastos cutâneos e tecido adiposo (GOUVEIA et al., 2014).

Normalmente, a liberação da PRL é controlada pelo hipotálamo, que exerce sobre ela uma inibição por meio da secreção de dopamina na eminência média. Por esse motivo, as drogas que interferem na síntese ou na ação da dopamina aumentam a secreção de PRL (LYONS; BROBERGER, 2014).

A secreção da PRL pode ser estimulada por situações de estresse, como cirurgia, medo, exercício físico e sono, embora elevada concentração desse

hormônio seja encontrada principalmente durante o período gestacional. Homens e mulheres apresentam concentrações séricas basais normais semelhantes (FREEMAN et al., 2000).

Uma vez na corrente sanguínea, a PRL não se liga a proteínas séricas e, por essa razão, tem uma meia-vida relativamente curta de cerca de 20 minutos. A transdução de sinal a partir da PRL ocorre após a ligação do hormônio ao seu receptor (PrIr), causando a sua dimerização e consequente ativação da janus quinase 2 (JAK2). A JAK2, por sua vez, fosforila os resíduos de tirosina do domínio intracelular do receptor, proporcionando locais de ligação para diversas proteínas sinalizadoras, destacando-se as transdutoras de sinal e ativadoras de transcrição (STAT), particularmente as STAT5. As STATs, como fatores de transcrição citoplasmática latentes, se separam do complexo e migram até o núcleo, onde ativam a transcrição gênica de proteínas (IGNACAK et al., 2012).

Apesar de a PRL ter sido associada inicialmente à estimulação da produção de leite, atualmente apresenta dezenas de ações reconhecidas, entre elas: diminuição da excreção renal de sódio e potássio (IBARRA et al., 2005); aumento da absorção intestinal de água e sais; influência na resposta ao estresse e à ansiedade; regeneração do sistema nervoso central (MÖDERSCHEIM et al., 2007); lipogênese (STEWART et al., 2004); proteção contra o desenvolvimento de cardiomiopatia pós-parto (HILFIKER-KLEINER et al., 2007); estimulação ou inibição da resposta imune de acordo com sua concentração (TOMIO et al., 2008), além de diversos efeitos sobre o pâncreas.

Durante o período de gestação, ocorrem alterações morfofisiológicas nas células beta de humanas e ratas, dentre elas o aumento da massa celular e da secreção de insulina (BRELJE et al., 1993; SORENSON; BRELJE, 1997) como mecanismo adaptativo para compensar a resistência à insulina que é verificada nessa fase. O aumento da massa da ilhota pancreática pode alcançar 50% e se deve pela hipertrofia e hiperplasia de células e redução da morte celular (AMARAL et al., 2004).

O Prlr está presente nas ilhotas pancreáticas e a sua expressão aumenta durante a prenhez/gravidez. Em estudo realizado com camundongos que não apresentavam o Prlr, verificou-se hipoplasia das ilhotas e das células beta e o surgimento de intolerância discreta à glicose (FREEMARK et al., 2002). Amaral e colaboradores (2004) demonstraram que proteínas das vias PI3K e MAPK têm

expressão aumentada em ilhotas de ratas prenhas e grande parte desse efeito é dependente do PrIr. Esses achados confirmam que os ligantes desse receptor, dentre eles a PRL, estão associados ao aumento da massa e da sensibilidade à glicose das ilhotas de ratas, observados durante a prenhez.

Um efeito muito semelhante é observado em ilhotas de ratos neonatais tratadas com PRL, em que ocorre aumento da secreção de insulina estimulada pela glicose (BOSCHERO et al., 1992), da fosforilação dos IRS 1 e 2 (AMARAL et al., 2003), da expressão proteica do GLUT2 (DE MAZANCOURT et al., 1994) e de proteínas das vias PI3K e MAPK (AMARAL et al., 2003).

Diante desses resultados, somados ao fato de a PRL melhorar a viabilidade de células beta pancreáticas humanas em cultura (YAMAMOTO et al., 2009), passou-se a investigar se a PRL poderia ser uma alternativa para aumentar a eficácia do transplante de ilhotas. Apesar de o transplante de ilhotas ter emergido como um tratamento alternativo para o DM1 (RYAN et al., 2002), a perda de células saudáveis durante o processo de isolamento das ilhotas é um fator que limita o sucesso da técnica. Como elas são avasculares e, portanto, isquêmicas desde o isolamento até ao período necessário para a revascularização, algumas substâncias nocivas podem ser produzidas, como as EROs e citocinas pró-inflamatórias, causando prejuízos no funcionamento das células e/ou induzindo a apoptose (MONFARED; LARIJANI; ABDOLLAHI, 2009).

O tratamento de ilhotas de camundongos com PRL, precedendo o transplante, fez com que animais diabéticos se tornassem normoglicêmicos mais rapidamente, bem como tivessem aumento da vascularização pela redução da expressão do inibidor da angiogênese, TSP-1 (JOHANSSON et al., 2009). Além disso, a pré-incubação de ilhotas de humanos com PRL aumentou a proliferação e diminuiu a apoptose de células beta induzida por citocinas pró-inflamatórias e H₂O₂, após o transplante (YAMAMOTO et al., 2010). A PRL protege as células beta contra a apoptose induzida por citocinas por aumentar a expressão de proteínas anti-apoptóticas da família BCL2 (TERRA et al., 2011) e prevenir a ativação da via JNK e da NF-Kb (NARDELLI et al., 2018). Entretanto, ainda é desconhecido o mecanismo pelo qual esse hormônio protege as células beta do estresse oxidativo.

Nesse sentido, é possível que a PRL possa modular a expressão de enzimas antioxidantes, visto que o aumento da expressão gênica da SOD1 e da EC-SOD foi verificado em ilhotas de ratas e em linhagem celular de fibroblastos, respectivamente, tratados com esse hormônio (ADACHI et al., 2004; BORDIN et al., 2004). Além do mais, a PRL exerce efeito protetor sobre células da retina submetidas a estresse oxidativo, embora não esteja completamente esclarecido de que maneira isso ocorre. Em camundongos sem a atividade do Prlr ocorreu a diminuição do mRNA da CAT nas células da retina. E quando realizado tratamento com PRL em camundongos com receptor ativo, o hormônio aumentou a atividade da GPx (THÉBAULT, 2017). Ademais, em linhagem celular de pré-adipócitos e em tecido adiposo de ratos, a PRL aumentou a expressão gênica do PPARγ (NANBU-WAKAO et al., 2000), que tem influência sobre a expressão de enzimas antioxidantes.

4. METODOLOGIA

4.1 Cultivo celular e tratamento

Células beta pancreáticas da linhagem INS-1E, gentilmente cedidas pelo Prof. C. Wolheim (Centro Médico Universitário, Genebra, Suíça), foram cultivadas em meio RPMI 1640 (Vitrocell®, SP, Brasil) e suplementadas com 5% v/v de soro fetal bovino (FBS), HEPES 10 mmol/L, piruvato de sódio 1 mmol/L e 2mercaptoetanol 50 µmol/L com 11 mmol/L de glicose. As células foram semeadas em placas de 96 poços (15.000 ou 50.000 células por poço), em triplicata, para avaliação da viabilidade celular, mitoSOX e mito-roGFP2-Orp1 e em placas de 24 poços (100.000 células por poço) para os demais experimentos. Para o tratamento com PRL e H₂O₂, as células foram mantidas em meio sem FBS, com 1% p/v de BSA e 5,6 mmol/L de glicose. Os experimentos foram realizados 24h após o prétratamento com PRL (0,5 µg/mL; Programa Nacional de Hormônio e Peptídeos, #AFP7547B) ou veículo (NaHCO₃ 0,01 mmol/L + BSA 0,3% p/v) e subsequente exposição a H₂O₂ (Sigma, H1009). A PRL e o veículo foram mantidos no meio de tratamento durante a exposição ao H₂O₂. Células INS-1E expostas apenas à PRL foram usadas no experimento de time-course.

4.2 Avaliação da viabilidade celular

A viabilidade celular foi avaliada a partir de: a) células coradas com intercalantes de DNA Hoechst 33342 (ThermoFisher, H3570; 10 µg/mL) e iodeto de propídio (ThermoFisher, P1304MP; 5 µg/mL). Foram removidos 100 µL do meio de tratamento de cada poço e adicionados 100 µL de meio de cultura contendo os corantes Hoechst 33342 (ThermoFisher, H3570; 10 µg/mL) e iodeto de propídio (ThermoFisher, P1304MP; 5 µg/mL). Após 15 min de incubação, a 37 °C, foram removidos 100 µL do meio de cada poço e adicionados 100 µL de meio RPMI-1640. A porcentagem de células necróticas/apoptóticas foi determinada em High Content Imaging System (ImageXpress; Molecular Devices) por meio do módulo *Live and Dead* do software MetaXpress (Molecular Devices). Para identificar as populações de células viáveis e mortas, foram aplicadas máscaras para os comprimentos de onda DAPI (excitação em 350 nm e emissão em 470 nm; Hoescht) e Texas *red* (excitação em 596 nm e emissão em 615 nm; iodeto de propídio); b) Western blot da caspase 3 clivada (ver detalhes abaixo).

4.3 Western Blot

As células foram lavadas com PBS 1x e coletadas com 60 μ L de tampão de extração de proteínas Laemmli. As amostras foram aquecidas a 100 °C, por 5 min, para posterior aplicação de 20 μ L de seu conteúdo em SDS-PAGE com 12% de acrilamida. Após separação eletroforética em aparatos, as proteínas foram transferidas por transferência líquida, com 20% de metanol, para membrana de nitrocelulose (com poro de 0,22 μ m), e o bloqueio de ligações inespecíficas foi realizado com tampão TBS-T (50 mM Tris pH 7,5, NaCl 150 mM, 0,1% Tween 20) contendo 10% de leite desnatado, durante 60 min. As membranas foram incubadas durante 16h, a 4 °C, com anticorpos primários para a α -tubulina (Santa Cruz, 8095), β -actina (Santa Cruz, 81178), caspase 3 clivada (Abcam, 4051), catalase (Abcam, 16731), glutationa peroxidase 1 (abcam, 22604), superóxido dismutase 1 (abcam, 16831) e superóxido dismutase 2 (Santa Cruz, 30080). Em seguida, as membranas foram incubadas por 60 min com anticorpos secundários conjugados com peroxidase, em temperatura ambiente. O conteúdo proteico foi detectado pelo
ImageQuant LAS 4000 (Healthcare Bio-Sciences) após a reação de quimiluminescência com o Substrato Quimioluminescente SuperSignal West Femto (Thermo Scientific). Finalmente, a densitometria das bandas de proteínas foi determinada com o software ImageQuantTL (Healthcare Bio-Sciences). Os valores obtidos foram normalizados pelos controles internos, α -tubulina ou β -actina.

4.4 PCR quantitativa em tempo real (qRT-PCR)

A extração do RNA total foi realizada com o reagente TRIzol (Invitrogen, 15596026), de acordo com as instruções do fabricante. Em seguida, o RNA das amostras foi guantificado no leitor multimodal Spectramax i3 (Molecular Devices). A síntese de cDNA foi feita por meio do kit High Capacity cDNA Reverse Transcription (Applied Biosystems, 4668814) e a amplificação de cDNA foi realizada com o reagente Power SYBR Green Master Mix (Applied Biosystems, 5´-4367659), juntamente os primers (Senso, com para pparg CCTTGCTGTGGGGGATGTCTC-3'; anti-senso, 3'-CGCCAACAGCTTCTCCTTCT-5') e para o gene controle, rps 26 (Senso, 5'-TTTTTCCTCCTTGGGCGTCTG-3'; anti-senso, 3'-GGTAGACAGTCGAATCATCCATTCA-5'). O qRT-PCR foi realizado com o Applied Biosystems StepOne real-time PCR system (Applied Biosystems) e a expressão do mRNA foi determinada após a normalização pelo método 2-ΔΔCT (LIVAK; SCHMITTEGEN, 2001).

4.5 MitoSOX

As células foram incubadas durante 20 min com a sonda mitoSOX (Invitrogen, M36008; 5 µg/mL) e o corante intercalante de DNA Hoechst 33342 (ThermoFisher, H3570; 5 µg/mL). O mitoSOX é um indicador de O₂⁻ mitocondrial, uma vez que sofre oxidação por essa espécie reativa e é convertido em um produto fluorescente. A aquisição da fluorescência foi realizada de acordo com as instruções do fabricante, em um leitor de microplacas, utilizando o *High Content Imaging System* (ImageXpress; Molecular Devices), com o módulo de análise *Cell Scoring of MetaXpress* (Molecular Devices). Apenas a fluorescência do mitoSOX

no citoplasma foi considerada, uma vez que essa sonda migra para o núcleo das células em processo de apoptose (LIVAK; SCHMITTEGEN, 2001). Os valores obtidos foram normalizados pelo número de células, determinado pela fluorescência do corante Hoechst.

4.6 Mito-roGFP2-Orp1

Células INS-1E expressando estavelmente a sonda mito-roGFP2-Orp1 foram obtidas por transdução retroviral. Resumidamente, células Phoenix-AMPHO foram transfectadas com pLPCX/mito-roGFP2-Orp1 (codificando a sonda roGFP2-Orp1 com uma sequência de direcionamento mitocondrial N-terminal) pelo método do fosfato de cálcio. Após 6h de transfecção, as células foram lavadas duas vezes com PBS e transferidas para meio fresco. Após 24 e 48h de transfecção, o sobrenadante foi recolhido e passado através de um filtro de 0,22 mm. As células INS-1E (semeadas a 2,7 x 10⁵ células por poco em uma placa de seis pocos, durante 24h antes de cada experimento) foram incubadas com o sobrenadante contendo o vírus, suplementado com Polybrene, (4 mg/mL) a 37°C por 24h, em uma atmosfera de 5% de CO₂. As células foram então cultivadas por vários dias em meio contendo puromicina (0,5 mg/mL). Uma população celular altamente fluorescente (~ 6% da população total) foi selecionada por citometria de fluxo (FACSAria). As células coletadas foram expandidas no meio contendo puromicina (0,5 mg/mL) e gentamicina (50 mg/mL). Imagens com um microscópio de fluorescência foram capturadas para confirmar a localização mitocondrial da sonda. A mito-roGFP2-Orp1 é uma sonda sensível ao H₂O₂ com dois picos de excitação diferentes e redox dependes, em 405 nm e 488 nm, e um único pico de emissão, em 510 nm. Enquanto a oxidação da sonda por H₂O₂ resulta em um aumento do pico de excitação de 405 nm, a redução da sonda aumenta a excitação em 488 nm. Consequentemente, a razão entre 405/488 nm pode ser usada como um indicador da quantidade relativa de mito-roGFP2-Orp1 oxidada/reduzida e da concentração mitocondrial de H₂O₂ (MORGAN, SOBOTTA, DICK, 2011). Após o pré-tratamento, as células foram expostas ao H2O2 e imediatamente submetidas à leitura de fluorescência em 405 e 480 nm, por cerca de 1h, pelo CLARIOstar (BMG LABTECH). Foram analisadas fluorescências obtidas 10 min após a adição de

H₂O₂, em um intervalo de 10 min. A razão entre as fluorescências (400/480) foi normalizada pela razão entre fluorescências da sonda maximamente reduzida e maximamente oxidada, mensurada após a adição de diidrotreitol (10 mM) e diamida (2 mM).

4.7 Ensaio in silico

Foram obtidos dados de transcriptoma a partir do macroarray de 1176 genes, previamente realizado por nosso grupo de pesquisa, utilizando ilhotas de ratas Wistar (90 a 120 dias de vida; controle) e ilhotas de ratas Wistar prenhes (15º dia de gestação). As análises subsequentes foram realizadas com os genes que apresentaram diferenças relativas acima de 2 *fold change* em relação ao grupo controle e com p <0,05. Esses dados foram importados para o software DAVID (*Database for Annotation, Visualisation and Integrated Discovery v6.8*), no qual foi avaliado o enriquecimento das vias KEGG (*Kyoto Encyclopedia of Genes e Genomes*). Também analisou-se o enriquecimento de ontologia de genes por "componentes celulares" através do GOterms-CC (<u>http://www.geneontology.org</u>).

4.8 Ensaio de promotor repórter

As células foram transfectadas por 16h utilizando meio RPMI 1640, meio Opti-MEM (Gibco, 31985070) e Lipofectamina 3000 (Invitrogen, L3000015) com 0,5 mg de pRL-SV40 (luciferase renilla; Promega, E2231) e 30 ng de pPPRE X3- TK-luciferase (elemento responsivo ao PPAR - PPRE; Dr. Bruce Spiegelman, Addgene, 1015) por poço. Em seguida, o meio de transfecção foi substituído pelo meio RPMI 1640 e após 24h as células foram tratadas com veículo ou PRL (0,2 µg/mL, 0,5 µg/mL ou 1,0 µg/mL) durante esse mesmo período. As amostras foram coletadas com 100 µL de tampão de lise (Promega, E1500) e a atividade da luciferase foi mensurada em 20 µL do lisado em placa branca de 96 poços (costar), utilizando o sistema Dual luciferase assay (Promega) de acordo com as instruções do fabricante. Por fim, os valores obtidos da atividade de pPPRE X3-TK-luciferase foram normalizados pela atividade da renilla luciferase.

4.9 RNA de interferência (siRNA)

Dois siRNAs diferentes para o PPARγ (siPPARγ-1 e siPPARγ-2; Sigma-Aldrich) foram usados para reduzir a expressão desse gene nas células INS-1E. *AllStars Negative Control* siRNA (Qiagen) foi utilizado como controle negativo. As células foram incubadas por 16h com meio RPMI 1640, meio Opti-MEM e lipofectamina RNAiMAX (Invitrogen, 13778075) com 40 nM de siPPARγ e 40 nM do siRNA *AllStars Negative Control* (Qiagen, 1027281). Em seguida, o meio de transfecção foi substituído pelo meio RPMI 1640 e após 24h foi realizado o tratamento.

4.10 Análise estatística

Os resultados foram expressos como a média \pm erro padrão da média (EPM). Para a avaliação estatística, utilizou-se o teste t de Student e ANOVA (*one or two way*), seguido de pós-teste de Bonferroni. O nível de significância adotado foi de p <0,05 e as análises foram feitas por meio do software GraphPad Prism 6.00. O número de amostras utilizadas foi descrito na legenda dos gráficos. No método *in silico*, os valores de corte usados para a análise de enriquecimento de vias KEGG foi de p <0,1 e *Fold enrichment* p≥1,5 (HUANG; SHERMAN; LEMPICKI, 2009). Os resultados dessa análise foram apresentados em *-log Fold Change*.

5. RESULTADOS E DISCUSSÃO

ARTIGO: Prolactina aumenta a expressão de enzimas antioxidantes e ativa o receptor ativado por proliferador de peroxissoma (PPAR) em células INS-1E

Prolactin increases the expression of antioxidant enzymes and activates peroxisome proliferator-activated receptor (PPAR) in INS-1E cells

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Abstract

Oxidative stress causes functional damage to pancreatic beta cells and contribute to the development of diabetes mellitus. Prolactin, a hormone highly secreted in the gestational and lactation period, has known beneficial effects on insulin-secreting cells, including the protection of beta cells against H₂O₂-induced cell death, although the mechanism is still unknown. In this sense, prolactin modulates the expression of antioxidant enzymes in pancreatic islets, retinal cells and fibroblasts. Thus, we investigated whether the protection of prolactin in pancreatic beta cells against oxidative stress occurs by an increase of antioxidant enzymes and which pathway would be involved in this effect. We found that prolactin increases the protein content of antioxidant enzymes and decreases mitochondrial concentration of H₂O₂ in INS-1E cells. Bioinformatics analyzes of genes upregulated in islets of pregnant rats revealed enrichment of the peroxisome proliferator-activated receptor (PPAR) pathway, which is involved in the expression of antioxidant enzymes in different cell types. Performing a promoter reporter assay we found that PRL activates PPAR. Next, we evaluated whether PRL would be dependent on PPAR γ to avoid cell death caused by H₂O₂, once PPAR_γ expression is increased by PRL in pre-adipocyte cell line and rat adipose tissue. However, the knockdown of this transcription factor did not alter the efficiency of PRL in protecting beta cells from oxidative stress. For the first time we demonstrated that PRL increases the production of antioxidant enzymes in INS-1E cells and activates a transcription factor important for the functioning of pancreatic beta cells.

Keywords

Pancreatic beta cell; Oxidative stress; Cell death; Prolactin; PPAR; Diabetes

Highlights

PRL exerts a protective effect against H₂O₂-induced beta cell death Antioxidants enzymes protein content are increased by PRL PRL decreases mitochondrial concentration of H₂O₂ PRL actives PPAR

1. Introduction

Diabetes mellitus (DM) is a chronic disease characterized by permanent hyperglycemia [1] caused by defects in insulin secretion [2], insulin action, or both [3]. Oxidative stress, an increase in the ratio between highly reactive molecular species and antioxidant defenses [4], is among the factors that cause functional damage to pancreatic beta cells and contribute to the development of the disease [5-8].

Among the reactive molecular species, the oxygen species (ROS) are the most abundant in the cells and have as representatives the hydroxyl (OH⁻), superoxide (O_2^{-}), hydroperoxide (HO_2^{-}) and hydrogen peroxide (H_2O_2) [4]. To maintain the physiological concentration of ROS and avoid oxidative stress, the cells have antioxidant defense systems that include enzymes such as catalase (CAT), glutathione peroxidase (GPx) and superoxide dismutase (SOD) [9].

Prolactin (PRL), is a protein hormone secreted predominantly by adenohypophysis. High concentration of this hormone is observed during the gestational period [10-12]. In this phase, morphophysiological alterations in the pancreatic beta cells of human and rats are verified, among them the increase of the cellular mass and the insulin secretion [13,14] as an adaptive mechanism to compensate the insulin resistance that occurs in pregnancy and the PRL receptor is related to these alterations [15]. In cell culture, in addition to the previously mentioned effects [16,17], PRL has also been shown to protect against cell death induced by proinflammatory cytokines and H₂O₂ [18]. Recently, pathways involved in the protection of beta cells by PRL against insult caused by pro-inflammatory cytokines have been described [19]. However, the mechanism by which this hormone protects beta cells from oxidative stress remains unknown. In this sense, studies have already shown that PRL increases the gene expression of SOD in pancreatic islets [20] and in fibroblast cell line [21]. In retinal cells of mice subjected to oxidative stress, the absence of the PRL receptor decreased the mRNA of CAT [22].

In this way, we investigate whether the protection exerted by prolactin against oxidative stress is due to the increased production of the antioxidant enzymes and whhicht pathway would be involved in this effect. Our results demonstrated for the first time that PRL increases the protein content of antioxidant enzymes, prevents the mitochondrial concentration of H_2O_2 and activates the transcriptional factor peroxisome proliferator-activated receptor (PPAR) in INS-1E beta cell line.

2. Material and Methods

2.1 Cell culture and treatment. Insulin-producing INS-1E cells, kindly given by the Prof. C. Wolheim (Centre Médical Universitaire, Geneva, Switzerland), were cultured in RPMI 1640 medium (Vitrocell®, SP, Brazil) and supplemented with 5% v/v of fetal bovine serum (FBS), HEPES 10 mmol/L, sodium pyruvate 1 mmol/L and 2-mercaptoethanol 50 μ mol/L with 11 mmol/L glucose. The cells were seeded in 96-well plates (15,000 cells by well or 50,000 cells), in triplicate, to the assessment of cell viability, mitoSOX and mito-roGFP2-Orp1 and in 24-well plates (100,000 cells by well) to the others experiments. For the PRL and H₂O₂ treatment, the cells were maintained in a medium with 1% w/v of BSA and 5.6 mmol/L glucose without FBS. The experiments were performed 24h after pretreatment with PRL (0.5 μ g/mL; National Hormone and Peptide Program, #AFP7547B) or vehicle (0.01 mmol/L NaHCO3 + 0.3% w/v BSA) and subsequent exposure to H₂O₂ (Sigma, H1009). PRL or vehicle were also kept in the medium during H₂O₂ exposure. INS-1E cells exposed only to PRL were also used in the time course studies.

2.2 Assessment of cell viability. The cell viability was measure by: a) staining cells with DNA-binding dyes Hoechst 33342 (ThermoFisher, H3570; 10 μ g/mL) and propidium iodide (ThermoFisher, P1304MP; 5 μ g/mL). 100 uL of culture medium was removed from each well and added 100 uL of culture medium containing the DNA-binding dyes hoechst 33342 (ThermoFisher, H3570; 10 μ g/mL) and propidium iodide (ThermoFisher, P1304MP; 5 μ g/mL). After 15 min incubation, at 37 °C, 100 uL of culture medium was removed from each well and added 100 uL of RPMI-1640 medium. The percentage of necrotic/apoptotic cells was determined on High Content Imaging System (ImageXpress; Molecular Devices) through the Live and Dead module of MetaXpress (Molecular Devices) software. In order to identify the viable and dead cell populations, masks were applied for the DAPI (350 nm excitation and 470 nm emission; Hoescht) and Texas Red (596 nm excitation and 615 nm emission; propidium iodide) wavelengths; b) western blot for cleaved caspase 3 (see details below).

2.3 Western blot assay. The cells were washed with PBS 1x and collected with 60 μ L of protein extraction buffer Laemmli. The samples were heated at 100 ° C, for 5 min, for further application of 20 μ L of their content on 12% acrylamide SDS-PAGE. After electrophoretic separation in apparatus, the proteins were transferred by liquid transfer with 20% methanol to nitrocellulose membrane (with a pore of 0.22 μ m) and non-specific binding blockade was

performed with TBS-T buffer (50 mM Tris pH 7,5, 150 mM NaCl, 0,1% Tween®20) containing 10% skim milk, for 60 min. The membranes were incubated for 16 h, at 4 ° C, with primary antibodies to α -tubulin (Santa Cruz, 8095), β -actin (Santa Cruz, 81178), cleaved caspase 3 (abcam, 4051), CAT (abcam, 16731), GPx1 (abcam, 22604), SOD1 (abcam, 16831) and SOD2 (Santa Cruz, 30080). Next, the membranes were incubated for 60 min with appropriate horseradish peroxidase-conjugated secondary antibodies, at room temperature. Protein content was detected by ImageQuant LAS 4000 (Healthcare Bio-Sciences) after the chemiluminescence reaction with SuperSignal West Femto Chemiluminescent Substrate (Thermo Scientific). Finally, the densitometry of the protein bands was determined with ImageQuantTL (Healthcare Bio-Sciences) software. The values obtained were normalized by internal controls, α -tubulin or β -actin.

2.4 Real time quantitative PCR (qRT-PCR). Total RNA extraction was performed using TRIzol reagent (Invitrogen, 15596026), according to the manufacturer's instructions. Then, the RNA of the samples was quantified in a multimodal reader Spectramax i3 (Molecular Devices). The cDNA synthesis was done by means of the High Capacity cDNA Reverse Transcription kit (Applied Biosystems, 4668814) and cDNA amplification was performed with the Power SYBR Green Master Mix reagent (Applied Biosystems, 4367659), along with the primers for *pparg* (Forward, 5'-CCTTGCTGTGGGGGATGTCTC-3'; reverse, 3' - CGCCAACAGCTTCTCCTTCT-5') and to the housekeeping gene, *rps 26* (Forward, 5'-TTTTTCCTCCTTGGGCGTCTG-3'; reverse, 3'-GGTAGACAGTCGAATCATCCATTCA-5'). The qRT-PCR was done with the Applied Biosystems StepOne real-time PCR system (Applied Biosystems) and the mRNA expression was determined after normalization using the 2- $\Delta\Delta$ CT method [23].

2.5 MitoSOX. The cells were incubated for 20 min with mitoSOX probe (Invitrogen, M36008; 5 μ M) and DNA-binding dye Hoechst 33342 (ThermoFisher, H3570; 5 μ g/ml). MitoSOX is a mitochondrial O₂⁻ indicator, once undergoes oxidation by this ROS and is converted in a fluorescent product. The fluorescence acquisition was performed according to the manufacturer's instructions on a microplate reader using a High Content Imaging System (ImageXpress; Molecular Devices) and the module of analysis used was the Cell Scoring of MetaXpress software (Molecular Devices). Only the fluorescence of the mitoSOX in the cytoplasm was considered, since this probe migrates to the nucleus in cells in the process of apoptosis [24]. The values obtained were normalized by the number of

cells, determined by fluorescence of the Hoechst dye.

2.6 Mito-roGFP2-Orp1. INS-1E cells stably expressing mito-roGFP2-Orp1 were established by retroviral transduction. Briefly, Phoenix-AMPHO cells were transfected with pLPCX/mito-roGFP2-Orp1 (encoding the roGFP2-Orp1 probe with an N-terminal mitochondrial targeting sequence) by the calcium phosphate method. After 6 hours of transfection, cells were washed twice with PBS and transferred to fresh medium. After 24 and 48 hours of transfection, supernatant was collected and passed through a 0.22-mm filter. INS-1E cells (seeded at 2.7×105 cells per well in a six-well plate for 24 hours before each experiment) were incubated with the virus-containing supernatant supplemented with Polybrene (4 mg/mL) for 24 hours at 37°C in a 5% CO₂ atmosphere. Cells were then grown in medium containing puromycin (0.5 mg/mL) for several days. A highly fluorescent cell population (~6% of overall population) was selected by flow cytometry (FACSAria). Collected cells were expanded in the medium containing puromycin (0.5 mg/mL) and gentamycin (50 mg/mL). Pictures with a fluorescence microscope were taken to confirm the mitochondrial location of the probe. Mito-roGFP2-Orp1 is a H₂O₂-sensitive probe with two different and redox-dependent excitation peaks at 405 nm and 488 nm, and one single emission peak at 510 nm. While probe oxidation by H₂O₂ results in an increase of the 405 nm excitation peak, probe reduction by H_2O_2 increases excitation at 488 nm. Consequently, the ratio between 405/488 nm can be used as an indicator of the relative amount of oxidized/reduced mito-roGFP2-Orp1 and the H₂O₂ mitochondrial concentration [25]. After the pretreatment, the cells were exposed to H_2O_2 and immediately subjected to fluorescence reading in 405 and 480 nm during about 1h, by the CLARIOstar (BMG LABTECH). Fluorescences obtained 10 min after the addiction of H₂O₂, in a 10 min interval, were analyzed. The ratio of fluorescences (400/480) was normalized by the fluorescence ratio of the maximally-reduced and maximally-oxidized probe measured after addition of dithiothreitol (10 mM) and diamide (2 mM).

2.7 In silico assay. Transcriptome data were obtained from the macroarray of 1176 genes previously performed by our research group, using islets of Wistar rats (90 to 120 days of life; control) and islets of pregnant Wistar rats (15th day of pregnancy). Subsequent analyzes were performed with genes that presented relative differences above 2 fold change in relation to the control group and p value <0.05. These data were imported into the DAVID (Database for Annotation, Visualization and Integrated Discovery v6.8) software, in which evaluated

the enrichment of the KEGG (Kyoto Encyclopedia of Genes and Genomes) pathways. It was also analyzed the enrichment of gene ontology by "cellular components" through GOterms-CC (<u>http://www.geneontology.org</u>).

2.8 Promoter reporter assay. The cells were transfected for 16h using RPMI 1640 medium, Opti-MEM medium (Gibco, 31985070) and Lipofectamine 3000 (Invitrogen, L3000015) with 0.5 μ g of pRL-SV40 (luciferase renilla; Promega, E2231) and 30 ng of pPPRE X3-TK-luciferase (PPAR responsive element - PPRE; Dr. Bruce Spiegelman, Addgene, 1015) per well. After that, the transfection medium was replaced by the RPMI 1640 medium and after 24 h the cells were treated with vehicle or PRL (0.2 μ g/mL, 0.5 μ g/mL or 1.0 μ g/mL) for that same period. The samples were collected with 100 μ L of passive lysis buffer (Promega, E1500) and luciferase activity was measured in 20 μ L of the lysate in a 96-well white plate (costar), using the Dual luciferase assay system (Promega) according to the manufacturer's instructions. Finally, the values obtained from the pPPRE X3-TK-luciferase activity were normalized by the renilla luciferase activity.

2.9 Small Interfering RNA (siRNA). Two different siRNAs against PPAR γ (siPPAR γ -1 and siPPAR γ -2; Sigma-Aldrich) were used to knock down the expression of the target gene. Allstars Negative Control siRNA (Qiagen) was used as a negative control. The cells were incubated for 16h with RPMI 1640 medium, Opti-MEM medium and lipofectamine RNAiMAX (Invitrogen, 13778075) with 40 nM siPPAR γ and 40 nM Allstars negative control siRNA (Negative control; Qiagen, 1027281). Next, the transfection medium was replaced by the RPMI 1640 medium and after 24 hours of recovery the treatment was performed.

2.10 Statistical Analysis. Results are presented as mean \pm standard error of the mean (SEM). For the statistical evaluation was used t test and ANOVA (one or two way), followed by Bonferroni posttest. The level of significance was set at p <0.05 and the analyzes were done through the GraphPad Prism 6.00 software. The number of samples used is described in the graphics legend. In the in silico method the cut-off values used for KEGG pathway enrichment analysis were p <0.1 and Fold enrichment p \geq 1.5 [26]. The results of this analysis are presented in -log Fold Change.

3. Results

3.1 PRL prevents the cell death induced by H₂O₂. Firstly, we tested if PRL could increase the survival of INS-1E cells against oxidative stress. The treatment with PRL reduced the protein content of cleaved caspase 3 by 42% in the presence of 100 μ M and 200 μ M of H₂O₂ (Fig. 1A) and in 82% and 42% the percentage of dead cells compared to 100 μ M and 150 μ M H₂O₂, respectively (Fig. 1B).



Figure 1. Viability of cells treated with vehicle or PRL and oxidative stress inducer. INS-1E cells were pretreated for 24h with vehicle or PRL. After this period, the oxidative stress induction was done adding different concentrations of H_2O_2 for another 24 hours. (A-B) Protein content of the cleaved caspase 3 determined by western blotting. The representative image is in Fig 2I; (C) Percentage of dead cells using the dyes Hoescht 33342 and propidium iodide. The results represent the means \pm SEM. Comparisons were performed by two-way ANOVA followed by the Bonferroni posttest. *p<0.05, **p<0.01, ***p<0.001 and ****p<0.0001 versus vehicle; $\dagger p<0.05$, $\dagger \dagger \dagger p<0.001$ between the bars (n = 4).

3.2 PRL increases the protein content of antioxidant enzymes. We investigated if PRL could modulate the protein content of antioxidant enzymes for the prevention of cell death caused by H_2O_2 . In the time course of PRL, we observed an increase in the protein content of SOD2 with 48h, but not of CAT, GPx1, SOD1 (Fig. 2A, 2C, 2E and 2G). Interestingly, when the cells were pretreated with PRL and treated with H_2O_2 (50 µM and 100 µM), we observed an increase in CAT expression, but not in the other antioxidant enzymes (Fig. 2B, 2D e 2F).

















Figure 2. Protein content of CAT, GPx1, SOD2 and SOD1 in cells treated with vehicle or PRL and oxidative stress inducer. (A, C, E, G and H) INS-1E cells were treated with PRL (0.5 μ g/mL) for 0h, 0.25h, 0.5h, 2h, 8h, 16h, 24h, and 48h. For the statistical evaluation, one-way ANOVA was used, followed by the Bonferroni posttest. (B, D, F and I) INS-1E cells were pretreated for 24h with vehicle or PRL. After this period, the oxidative stress induction was done adding different concentrations of H₂O₂ for another 24 hours. Comparisons were performed by two-way ANOVA followed by the Bonferroni posttest. Protein content of antioxidant enzymes was determined by western blotting and the results represent the means \pm SEM. **p<0.01 versus vehicle, ****p < 0.0001 versus t=0h (n = 4-5).

3.3 PRL prevents the increase of the mitochondrial concentration of H₂O₂. As PRL seems to influence the expression of antioxidant enzymes, we used the MitoSOX and mito-GFP2-ORP1 probes to investigate whether treatment with the hormone prevent the increase in ROS content induced by 50 μ M of H₂O₂ (Appendix, Fig 1A and B). We did not find effect of PRL on the mitochondrial O₂⁻ concentration both in the basal state (Fig. 3A), and in cells exposed to H₂O₂ (Fig. 3B). However, we observed that PRL prevent the oxidation by H₂O₂ in the mitochondria, that is, reduced the mitochondrial concentration of H₂O₂, in the basal state (Fig. 3C) and after the addition of H₂O₂ (Fig. 3D).









Figure 3. Production of O₂⁻ **and H**₂**O**₂ **mitochondrial.** INS-1E cells were pretreated for 24h with vehicle or PRL. After, the oxidative stress was induced with (B) 50 μ M of H₂O₂ for another 6 hours and (D) 50 μ M of H₂O₂, while reading the plate. (A and B) Mitochondrial O₂⁻ detection was performed with the mitoSOX probe, 5 μ M, with reading done in High-Content Imaging System. The values obtained were normalized by the number of cells, determined by using Hoechst 33342 DNA dye (10 μ g/mL). Comparisons were performed t test (n = 3). (C and D) It was performed the fluorescence reading in 400 and 480 nm during about 1h, by the the CLARIOstar (BMG LABTECH). Fluorescences (400/480) was normalized to the fluorescence ratio of the maximally-reduced and maximally-oxidized probe measured after addition of 10 mmol/L dithiothreitol and 100 mmol/L diamide. Comparisons were performed by t test. The results represent the means ± SEM (n = 5).

p < 0.01, **p < 0.0001 versus vehicle. (E) mito-GFP2-ORP1 fluorescences with red light (405 nm; oxidized state of the probe), green light (488 nm; reduced state of the probe) and merged, confirming the mitochondrial location of probe. Scale bar: 40 μ m. (F and G) merged in details. Scale bar: 60 μ m and 100 μ m, respectively.

3.4 PPAR signaling is enriched in islets of pregnant rats. The genes upregulated in the islets of pregnant rats previously identified from macroarray by our research group, were transferred to DAVID. This software grouped the genes according to the pathway that they are related to and caught our attention the enrichment of the PPAR signaling pathway (Fig. 4; Appendix, table 2), which is involved in the production of antioxidant enzymes in different cell types, including beta cells [27-29].



Figure 4. Enrichment of Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways in islets of pregnant rats. The upregulated genes in islets from pregnant rats were imported into the DAVID software that grouped the genes according to the cell signaling pathways available in KEGG. The results are presented in -log Fold Change.

The ontological analysis of these same genes by "cellular components" revealed great influence of pregnancy on the expression of mitochondrial genes (Appendix, table 3) since 16 genes were upregulated in this organelle (Appendix, table 4). In addition, five of these genes are associated with both the fatty acid degradation pathway and PPAR signaling, they are: acyl-CoA synthetase (Acs), responsible for the mitochondrial transport of fatty acids; acyl-CoA oxidase (Aco), carnitine palmitoyltransferase 1 (Cpt-1), carnitine palmitoyltransferase 2 (Cpt-2) and acyl-CoA dehydrogenase (Lcad), related to the oxidation of fatty acids (Appendix, fig. 3).

3.5 PRL actives PPAR, however PPAR γ knockdown does not decreases the beneficial effect of PRL on cell viability. Based on the results of the analysis in silico, we investigated if PRL modulates the activity of PPARs in beta cells. For this purpose, we performed the promoter reporter assay was performed targeting PPAR response element (PPRE), which are specific sequences in the promoter region of genes were PPARs bind to start its transcription. Interestingly, the PRL (0.5 µg/ml and 1.0 µg/mL) promoted PPRE activation (Fig. 5A), indicating that this hormone activates PPARs.

Among the PPAR isoforms, PPAR γ is the most extensively studied in beta cells. Furthermore, PRL increases the expression of PPAR γ in adipocyte cell line and rat adipose tissue [30]. Therefore, we tested whether PPAR γ is involved in the protective action of PRL against the oxidative stress in INS-1E cells. For this, two specific siRNAs (siPPAR γ -1 and siPPAR γ -2) were used to suppress PPAR γ in INS-1E cells. Both siRNA inhibited by, approximately, 55% the expression of PPAR γ (Fig 5B). However, this inhibition did not abrogate the efficiency of PRL in preventing the cell death induced by H₂O₂ (Fig 5C).



Figure 5. Activation of PPRE by PRL and viability of cells treated or not with PRL and oxidative stress inducer, after PPAR γ knockdown. (A) INS-1E cells were transfected for 16 h with 0.5 μ g renilla luciferase and 30 ng pPPRE X3-TK-luciferase per well. After this time the transfection medium was changed to the RPMI 1640, where the cells remained for 24 hours. Then the cells were treated with 0.2 μ g/mL, 0.5 μ g/mL and 1.0 μ g/mL of PRL for 24 hours. The luciferase activity was measured in 20 μ L of lysate using the Dual luciferase assay system. Finally, the values obtained from the pPPRE X3-TK-luciferase activity were normalized by the renilla luciferase values. The results represent the means \pm SEM. Comparisons were performed by one-way ANOVA followed by the Bonferroni posttest. *p<0.05 versus vehicle (n=4). (B) INS-1E cells were transfected for 16 h with 40 nM of two specifics siRNAs for PPARy (siPPARy1 and siPPARy2) or a control siRNA (siCTL). After, the transfection medium was exchanged for RPMI 1640, where the cells remained for 72 hours before being collected. Gene expression was determined qRT-PCR, normalized by the $2^{-\Delta\Delta Ct}$ method (n = 2). (C) INS-1E cells were transfected for 16 h with 40 nM of two specifics siRNAs to PPARy (siPPARy1 and siPPAR γ 2) or a control siRNA (siCTL). 48h after transfection, the cells were pretreated for 24h with vehicle or PRL and the oxidative stress induction was gone adding 100 µM of H₂O₂ for another 24h. The percentage of dead cells was determined using the dyes Hoescht 33342 and propidium iodide. The results represent the means \pm SEM. Comparisons were performed by two-way ANOVA followed by the Bonferroni posttest. *p < 0.05 and ****p < 0.0001 versus vehicle; $\dagger \dagger \dagger \dagger \dagger p < 0.0001$ between the bars (n = 4).

4. Discussion

DM is related, mainly, with the modern life style, unhealthy diet and sedentary life [31], and has been affecting more and more people over time. The severity of the disease is due to the complications that untreated hyperglycemia can cause as: susceptibility to infections, retinopathy with possible vision loss, nephropathy inducing kidney failure, peripheral neuropathy related with the presence of foot lesions, atherosclerosis and cerebrovascular diseases [32]. Taking into account all these injuries that DM can cause, it becomes imperative to investigate molecules and mechanisms that inhibit or even prevent the development of this disease.

Our study demonstrated for the first time that PRL increases the expression of SOD2 and CAT, decreases the mitochondrial concentration of H₂O₂ and is able to activate PPAR in INS-1E cells. Notably, in oxidative stress condition, PRL increased the protein content of CAT after 24h. This enzyme detoxifies H₂O₂ [33] and has an important relationship with the development of diabetes, because knockout mice for the enzyme and acatalasemic mice present pre-diabetic phenotype [34] and are more susceptible to diabetes caused by alloxan [35], respectively. There are controversies regarding the profile of antioxidant enzymes in different tissues in DM but often they are impaired, certainly because hyperglycemia enhances non-enzymatic binding of glucose to proteins (glycation), causing structural and functional changes [36] and alters the availability of micronutrients that serve as cofactors for antioxidant enzymes [37]. Therefore, approaches that favor the production of antioxidant enzymes are important to beta cell protection and functioning of the beta cell.

Our next step was to evaluate whether PRL could reduce ROS content of the cells. Using a specific mitochondrial O_2^- probe, the mitoSOX, we did not observe changes in the

mitochondrial O_2^- levels in INS-1E cells with PRL-pretreatment. As previously mentioned, the increase in the catalase protein content occurred 24 hours after stress induction by H_2O_2 . It is possible that at 6h the increase in CAT synthesis has not yet occurred and, thus, the O_2^- mitochondrial concentration was not altered. In this sense, the enzymatic activity assay can be used to clarify the behavior of the enzyme, regardless of its protein content. Interestingly, using a specific probe for H_2O_2 , the mito-roGFP2-ORP1, we observed that PRL prevented the probe oxidation, both in the basal state and after the addition of H_2O_2 , at the time of reading. Likewise, the expression of CAT has not yet increased, suggesting the participation of another detoxification pathway of H_2O_2 . Another enzyme that detoxifies H_2O_2 is peroxiredoxin and studies have shown its importance for protection of beta cell against death induced by oxidative stress [38, 39].

An experimental approach that has gained increasing prominence in the scientific field is the in silico analysis. Through this bioinformatics tool it is possible to use information available in databases to list research targets, such as genes. Our bioinformatics analysis made from the genes upregulated during pregnancy, a condition in which there is an increase in the hypothalamic secretion of PRL [12], showed the enrichment of transcription factors involved with the production of antioxidant enzymes, the PPARs. This transcription factors are present in three isoforms: α , β/δ and γ . PPARs form a heterodimer with the retinoid x receptor (RXR) that binds to specific sequences in the promoter region of the target genes, the PPRE, promoting changes on chromatin structure and activation of transcription [40]. The promoters of the genes of antioxidant enzymes have PPRE [27,29,41] and the activation of PPAR increases expression and activity of antioxidant enzymes such as CAT [27-29] and SOD [28, 42].

In addition to the enrichment of PPAR pathway, it was remarkable the large number of upregulated genes located in the mitochondria and involved with the metabolism of fatty acids in pancreatic islets during pregnancy. As an important function of PPARs is the control of lipid metabolism [43,44], these results suggest that, in pregnancy, the PPAR pathway is enriched to promote the metabolism of fatty acids [45,46]. In fact, the concentration of circulating lipids increases during this period, as a result, the islets adapt to become more sensitive to fatty acids [47]. Fatty acids metabolism by beta cells, as well as glucose metabolism, increases the ATP/ADP ratio, promoting increased insulin secretion [48,49]. This increase in insulin secretion acts as a compensatory mechanism to resistance to this hormone that is verified during pregnancy [14]. At the same time, the increase in fatty acid metabolism results in more NADH and FADH₂ available to the electron transport chain, adding the production of ATP and also of ROS [50]. It would be possible that, to neutralize the increase of ROS, the PPAR pathway also would act to increase the production of antioxidant enzymes in order to protect beta cells from oxidative stress. That is, alterations in the metabolism and redox state of beta cells could be modulated by a common pathway involving PPARs (Fig 8).



Figure 6. Possible involvement of PPARs pathway in the metabolism and redox state of beta cells.

To test whether PRL has influence on PPARs, as suggested by in silico analyzes, we performed the promoter reporter assay and found that PRL activates these transcription factors. Among PPARs, PPAR γ is the therapeutic target of drugs indicated for the treatment of diabetes, thiazolidinediones (TZDs), such as pioglitazone, for example [51,52]. In diabetic *db/db* and obese pre-diabetic animal models, TZDs increase proliferation and reduce apoptosis of beta cells [53,54] and stimulate insulin secretion [53,55], respectively. Faced with oxidative stress, pioglitazone prevent the formation of ROS protecting pancreatic islets and beta cells from apoptosis [54,56]. In this sense, Kanda et al. 2010 and Chung at al. 2011 demonstrated that TZDs increase expression of CAT, GPx and SOD2, both in islets and beta cells.

Because of the actions that the activation of PPAR γ exerts on the insulin producing cells and knowing that the PRL increases the expression of this isoform of PPAR in adipocyte cell line and rat adipose tissue [30], we evaluated whether PRL is PPAR γ dependent to protect INS-1E cells against oxidative stress. Despite the knockdown of PPAR γ , PRL maintained its beneficial effect on cell viability against H₂O₂-induced death. It is possible that another PPAR isoforms play an important role in the viability, since they are also present in beta cells [57], or that other pathways may be involved, such as the classic pathway of antioxidant enzymes production by the transcription factor nuclear factor erythroid 2–related factor 2 (Nrf-2) which protects beta cells from oxidative damage [58,59]. Another mechanism that deserves to be highlighted is that involves c-Jun N-terminal kinase (JNK) signaling. JNK is activated by ROS to induce cell death by means of phosphorylation of pro-apoptotic proteins [60,61]. In contrast, PRL negatively regulates JNK by preventing the beta cells death by inflammatory cytokines [19] that, like ROS, activate JNK to lead to cell death [62,63].



Figure 7. Mechanism that can be used by PRL to protect beta cells against oxidative stress.

In conclusion, we demonstrate for the first time that PRL is capable of activating PPAR. However, PRL is not dependent on PPAR γ to protect INS-1E cells from H₂O₂-induced death, therefore future researches are needed to reveal the exacts mechanisms of beta cell protection by PRL against oxidative stress. In addition, we also revealed that PRL increases the expression of antioxidant enzymes and decreases the mitochondrial concentration of H₂O₂, important effects in favor of pancreatic beta cell survival (Fig 9).

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6. Appendix



Supplementary figure 1. Production of O₂⁻ and H₂O₂ mitochondrial. INS-1E cells were pretreated for 24h with vehicle. After, the oxidative stress was induced with (A) 50 μ M of H₂O₂ for another 6 hours and (B) 50 μ M of H₂O₂, while reading the plate. (A) Mitochondrial O₂⁻ detection was performed with the mitoSOX probe, 5 μ M, with reading done in High-Content Imaging System. The values obtained were normalized by the number of cells, determined by using hoechst 33342 DNA dye (10 μ g/mL). Comparisons were performed t test (n = 3). (B) It was performed the fluorescence reading in 400 and 480 nm during about 1h, by the the CLARIOstar (BMG LABTECH). Fluorescences (400/480) was normalized to the fluorescence ratio of the maximally-reduced and maximally-oxidized probe measured after addition of 10 mmol/L dithiothreitol and 100 mmol/L diamide. Comparisons were performed by t test. The results represent the means ± SEM (n = 5). *p < 0.05, ****p < 0.0001 versus vehicle.

Term	Count	%	PValue
Fatty acid degradation	7	8.75	5.77E-07
PPAR signaling pathway	7	8.75	1.09E-05
Retinol metabolism	6	7.5	2.15E-04
Fatty acid metabolism	5	6.25	4.38E-04
Adipocytokine signaling pathway	5	6.25	1.52E-03
Arachidonic acid metabolism	5	6.25	2.02E-03
Steroid hormone biosynthesis	5	6.25	2.02E-03
Bladder cancer	3	3.75	2.91E-02
Linoleic acid metabolism	3	3.75	3.04E-02
HIF-1 signaling pathway	4	5	3.20E-02
Calcium signaling pathway	5	6.25	3.46E-02
Proteasome	3	3.75	3.91E-02
Inflammatory mediator regulation	of 4	5	4.12E-02
TRP channels			
Pathways in cancer	7	8.75	4.82E-02
Hepatitis C	4	5	5.47E-02
Glutathione metabolism	3	3.75	5.71E-02
Measles	4	5	6.10E-02
Pancreatic cancer	3	3.75	6.79E-02
Amphetamine addiction	3	3.75	6.79E-02
MicroRNAs in cancer	4	5	7.00E-02

Supplementary table 1. Enrichment of KEGG pathway in islets of pregnant rats.

Term	Count	%	PValue
Organelle membrane	7	8.75	8.75E-07
Endoplasmic reticulum membrane	11	13.75	2.92E-05
Secretory granule	6	7.5	4.07E-05
Membrane	21	26.25	6.54E-05
Intracellular membrane-bounded	11	13.75	1.72E-04
organelle			
Proteasome core complex, alpha-	3	3.75	4.57E-04
subunit complex			
Mitochondrion	16	20	4.93E-04
Intracellular organelle	3	3.75	1.14E-03
Presynaptic membrane	4	5	2.44E-03
Proteasome core complex	3	3.75	2.59E-03
Vesicle	5	6.25	2.76E-03
Apical plasma membrane	6	7.5	5.49E-03
Cell surface	8	10	6.51E-03
Extracellular space	12	15	7.23E-03
Synaptic vesicle	4	5	1.14E-02
Neuron projection	6	7.5	1.38E-02
Cell junction	6	7.5	1.63E-02
Synaptic vesicle membrane	3	3.75	1.93E-02
Proteasome complex	3	3.75	1.93E-02
Cytoplasm	28	35	2.20E-02
Extrinsic component of cytoplasmic	3	3.75	2.52E-02
side of plasma membrane			
Mitochondrial inner membrane	5	6.25	2.67E-02
Plasma membrane	22	27.5	3.71E-02
Basolateral plasma membrane	4	5	3.91E-02
Extracellular exosome	16	20	4.84E-02
Dense core granule	2	2.5	4.95E-02
Postsynaptic density	4	5	5.51E-02

Supplementary table 2. Cellular components in descending order of the number of genes upregulated in the islets of pregnant rats.

Focal adhesion	5	6.25	5.52E-02
Z disc	3	3.75	6.71E-02
Protein complex	6	7.5	7.00E-02
Perinuclear region of cytoplasm	6	7.5	8.25E-02
Dendrite	5	6.25	9.64E-02

ID	Gene Name
Lcad	acyl-CoA dehydrogenase, long chain
Acox1	acyl-CoA oxidase 1
Acsl6	acyl-CoA synthetase long-chain family member 6
Ak3	adenylate kinase 3
Cpt1a	carnitine palmitoyltransferase 1A
Cpt2	carnitine palmitoyltransferase 2
Cox1	cytochrome c oxidase subunit 1
Gsr	glutathione-disulfide reductase
Ghr	growth hormone receptor
Hsd3b1	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-
	isomerase 1
Lypla1	lysophospholipase I
Mmp2	matrix metallopeptidase 2
Mmp3	matrix metallopeptidase 3
Nr3c1	nuclear receptor subfamily 3, group C, member 1
Stat3	signal transducer and activator of transcription 3
Slc16a1	solute carrier family 16 member 1

Supplementary table 3. Mitochondrial genes upregulated in the islets of pregnant rats.



Supplementary figure 2. PPAR signaling pathway. The pregnant rats islets present upregulation of five genes (star) regulated by PPAR and related to degradation of fatty acids. Source: DAVID, 2018.

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4. CONSIDERAÇÕES FINAIS

O estresse oxidativo está entre os fatores que causam danos às células beta pancreáticas e que, consequentemente, levam ao desenvolvimento do DM. A PRL melhora a sobrevivência de células beta frente ao estresse oxidativo, entretanto é desconhecido o mecanismo pelo qual isso ocorre. Uma vez que a PRL modula a expressão gênica de enzimas antioxidantes em diferentes tipos celulares, nosso objetivo foi investigar se a PRL protege as células beta pancreáticas do estresse oxidativo por aumentar a produção de enzimas antioxidantes e qual via de sinalização estaria envolvida nesse efeito.

Demonstramos, pela primeira vez, que a PRL aumenta o conteúdo proteico de enzimas antioxidantes e é capaz de ativar o PPAR em células INS-1E. Entretanto, a PRL não é dependente do PPARγ para proteger as células INS-1E da morte induzida pelo H₂O₂. Sendo assim, pesquisas futuras são necessárias para revelar o exato mecanismo de proteção das células beta pela PRL contra o estresse oxidativo.

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