Destruction of Pancreatic \( \beta \)-Cells by Transgenic Induction of Prostaglandin E\(_2\) in the Islets*

Type 2 diabetes mellitus is characterized by insulin resistance of peripheral tissues and dysfunction of pancreatic \( \beta \)-cells. Furthermore, the number of pancreatic \( \beta \)-cells decreases as a secondary effect of advanced type 2 diabetes, although the molecular mechanism has not been elucidated. Recently, it has been shown that hyperglycemic conditions induce the expression of cyclooxygenase-2 in pancreatic islets and increase the downstream product prostaglandin E\(_2\) (PGE\(_2\)). To investigate whether high glucose-induced PGE\(_2\) has an adverse effect on pancreatic \( \beta \)-cells, we generated transgenic mice (RIP-C2mE) that express cyclooxygenase-2 and microsomal prostaglandin E synthase-1 in their \( \beta \)-cells using the rat insulin-2 gene promoter (RIP). 

The homozygous RIP-C2mE (Tg/Tg) mice showed severe hyperglycemia from six weeks of age. Although the heterozygous RIP-C2mE (Tg/−) mice showed normal blood glucose levels throughout their lifetime, this level increased significantly compared with that of wild-type mice when glucose was loaded. The relative number of \( \beta \)-cells to the total islet cell number was reduced to 54 and 14% in the RIP-C2mE (Tg/−) and (Tg/Tg) mice, respectively, whereas that in the wild-type mice was 84%. Importantly, the proliferation rate in the islets of the RIP-C2mE (Tg/Tg) mice at four weeks of age decreased significantly in comparison to that in the wild-type mice. Because \( \beta \)-cells replicate not only during the postnatal period but also in the adult pancreas at a basal level, it is possible that increased PGE\(_2\) signaling thus contributes to the reduction of the pancreatic \( \beta \)-cell mass through inhibition of proliferation, thereby aggravating diabetes further.

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EXPERIMENTAL PROCEDURES

Transgenic Mice—The RIP fragment (704 bp; nucleotide position -695 to +8 of the rat insulin-2 gene) was amplified by PCR using rat genomic DNA and the primers 5'-GGGATC-CCCAACCACT-3' and 5'-TTAGGGCTGCGGGTGTTAC-3'. After confirming the nucleotide sequences, the RIP fragment was subcloned into both expression vectors of COX-2 and mPGES-1 at the 5' position in the same orientation as that of cDNAs. Both expression vectors contained RIP, a synthetic chimeric intron excised from pCI (Promega, La Jolla, CA), cDNA for mouse COX-2 or mPGES-1, and a SV40 poly(A) cassette (see Fig. 1A). Mouse COX-2 and mPGES-1 cDNAs were cloned by reverse transcription (RT)-PCR as previously described (16). The transcription unit was excised from each expression vector, purified, and co-microinjected into fertilized eggs from a cross between F1 (C3H and C57BL/6) hybrid females and C57BL/6 males. We obtained 14 founder mice that carried both the COX-2 and mPGES-1 transgenes. Among the F1 progeny of these 14 lines, two lines (RIP-C2mE mouse line 8 and RIP-C2mE mouse line 9) showed high amounts of both COX-2 and mPGES-1 mRNAs in their pancreatic tissues. These two transgenic lines showed essentially the same phenotypes. N2-backcrossed transgenic mice with C57BL/6 were intercrossed to generate homozygous RIP-C2mE (Tg/Tg) and heterozygous RIP-C2mE (Tg/−) mice. Backcrossing was performed using wild-type C57BL/6 mice. Mice of the N2F1 generation were used for the experiments. Littermate wild-type mice were used as controls for the experiments. Genotyping was performed by genomic PCR using tail DNA and the following primer sets: COX-2, 5'-CAGGCCGGCTAG-3' and 5'-ATCACT-3'; mPGES-1, 5'-CAGGAATGCATCAGTCAG-3' and 5'-GTCAGCAGTAGCCTCATC-3'. Homozygotes were identified by increased band intensities of the genomic PCR products in comparison to those of heterozygotes.

Pancreatic Islet Isolation—Pancreata injected with 0.2% collagenase Type I (InVitrogen) in Hanks' buffered saline solution via the bile duct were collected and incubated for 20 min at 37 °C. After digestion, islets were then hand-picked using a dissecting microscope.

RT-PCR—Total RNA was extracted from the isolated islets using ISOGEN (Nippon Gene, Tokyo, Japan). The extracted RNA was reverse-transcribed and PCR-amplified. The primer sets used for genotyping were also used for RT-PCR analyses of COX-2 and mPGES-1. Glyceraldehyde-3-phosphate dehydrogenase was used as an internal control.

Measurement of Pancreatic PGE$_2$ Level—The PGE$_2$ levels were measured at SRL (SRL Inc, Tokyo, Japan) using six RIP-C2mE (Tg/−) and six wild-type mice at 20 weeks of age, and four RIP-C2mE (Tg/−) and four RIP-C2mE (Tg/Tg) mice at three weeks of age. Briefly, the pancreata were homogenized in a lysis buffer, and PGE$_2$ was extracted with ethanol. The PGE$_2$ levels were measured using the prostaglandin E$_2$ [125I]RIA kit (PerkinElmer Life Sciences). According to the manufacturer's instruction manual, the cross-reactivity of this kit is as follows: PGE$_2$ (100%), PGF$_2\alpha$ (0.9%), PGD$_2$ (0.3%), 6-keto-PGF$_1\alpha$ (1%), and thromboxane B$_2$ (0.01%). The islet PGE$_2$ levels of the RIP-C2mE (Tg/Tg) mice relative to (Tg/−) mice at three weeks of age was calculated using the ratio of the islet area in the pancreas. To determine the ratio of the islet area in the RIP-C2mE (Tg/−) and (Tg/Tg) mice, five sections/pancreas of each genotype were scanned using an ImageJ program (NIH), and then the islet area was quantified versus the total pancreas area.

Measurement of Blood Glucose, Plasma Insulin, and Plasma Glucagon Levels—The blood glucose levels were measured using Glutest AceR (Sanwa Chemical, Nagoya, Japan). For chronologic observation, the blood glucose level was examined when the mice were 3, 6, 9, and 12 weeks of age. In this experiment, six wild-type, 12 RIP-C2mE (Tg/−), and 11 RIP-C2mE (Tg/Tg) mice were used. The plasma insulin levels were examined through use of the High-Sensitive insulin measurement Kit that is based on an enzyme-linked immunosorbent assay test (Morinaga, Yokohama, Japan) at 0 and 20 min of the glucose tolerance test. The plasma glucagon levels were measured by a radioimmunoassay that uses the glucagon kit Daiichi II at SRL (Tokyo, Japan), with 10 wild-type and 4 RIP-C2mE (Tg/Tg) mice.

Glucose Tolerance Test—The mice were fasted for 14 h following an intraperitoneal injection of glucose (1 g/kg body weight). Blood samples were obtained from a tail vein at 10, 20, 30, 60, and 120 min after the glucose injection. The blood glucose and plasma insulin levels were measured as described above. In the glucose tolerance test, seven wild-type and eight RIP-C2mE (Tg/−) mice at 50 weeks of age were used.

Histopathology and Immunohistochemistry—Pancreatic tissues of the mice were fixed in 4% paraformaldehyde,
embedded, and sectioned at a thickness of 4 μm. These sections were stained with H & E and were processed further for immunostaining. Rabbit polyclonal antibody for insulin (Progen Biotechnik, Heidelberg, Germany) and sheep polyclonal antibody for glucagon (Biogenesis, England, UK) were used as the primary antibody for an immunohistochemistry to detect β- and α-cells, respectively. Rat monoclonal antibodies for CD3ε (BD Biosciences), F4/80 (Serotec, Oxford, UK), and Gr-1/Ly-6G (BD Biosciences) were used as the primary antibodies to detect T-cells, macrophages, and neutrophils, respectively. Staining signals were visualized using the Vectorstain Elite kit (Vector Laboratories, Burlingame, CA). Alexa Fluor 594 donkey anti-sheep IgG or Alexa Fluor 488 donkey anti-rabbit IgG (Molecular Probes, Eugene, OR) was used as the secondary antibody.

Apoptosis Analysis—The pancreatic tissues of the mice at four weeks of age were fixed in 4% paraformaldehyde, embedded, and sectioned at a thickness of 4 μm. Apoptosis was determined based upon the terminal deoxynucleotidyltransferase-mediated dUTP nick-end labeling (TUNEL) method, which uses the ApopTag Peroxidase in situ apoptosis detection kit (Chemicon, Temecula, CA) according to the manufacturer’s protocol.

Cell Proliferation Analysis—Mice were injected intraperitoneally with 1 ml of a BrdUrd solution (1 mg/ml). At 3 h post-injection, pancreatic tissues were fixed in 4% paraformaldehyde, embedded, and sectioned at a thickness of 4 μm. The sections were immunostained with an anti-BrdUrd antibody using the BrdUrd In-Situ detection kit (BD Biosciences). The number of BrdUrd-labeled cells and the total number of islet cells were scored from 10 islets, and a mean BrdUrd labeling index was calculated.

Scoring the Ratio of α- and β-Cells in the Pancreatic Islets—At least six non-overlapping fields of the fluorescence-immunostained sections were photographed (total number of islets >12), and the number of glucagon-positive α-cells and insulin-positive β-cells were scored. The ratio of α-cells and β-cells in the islet was calculated by dividing each number with the total number of islet cells. The total cell number in each islet was scored using the same sections under a differential interference microscope (DM5000B, Leica Microsystems, Wetzler, Germany).

Statistical Analysis—Statistical analyses were carried out using the unpaired Student’s t test, and a p value of <0.05 was considered to be significant.
Pancreatic β-Cell Destruction by PGE₂ Signaling

To investigate the effects of PGE₂ on the pancreatic β-cells in mice, we generated transgenic (RIP-C2mE) mice expressing both COX-2 and mPGES-1 by co-microinjection of the two expression vectors (Fig. 1A). We used RIP to target the β-cells in the pancreatic islets. To increase the expression level of the transgenes, we introduced a synthetic intron between the RIP and cDNAs for COX-2 and mPGES-1 (16). Two transgenic lines (RIP-C2mE mouse line 8 and RIP-C2mE mouse line 9) essentially exhibited the same phenotype (data not shown). Accordingly, we present the results with RIP-C2mE mouse line 8 (hereafter referred to as RIP-C2mE). We detected high amounts of mRNA of COX-2 and mPGES-1 by RT-PCR in the isolated islets from the RIP-C2mE (Tg/–) mice, whereas the expression of both genes was found in the wild-type islets at a basal level (Fig. 1B). We consistently found strong immunostaining signals for COX-2 and mPGES-1 in the pancreatic islets of the RIP-C2mE (Tg/–) mice compared with those of the wild-type mice (Fig. 1C). As shown in Fig. 1D, pancreatic PGE₂ levels at 20 weeks of age increased significantly in the RIP-C2mE (Tg/–) mice (10.9 ± 2.2 pg/mg) in comparison to that in the wild-type mice (4.2 ± 0.5 pg/mg), indicating that the simultaneous transgenic expression of COX-2 and mPGES-1 produced PGE₂ in vivo.

The blood glucose level in the RIP-C2mE (Tg/–) mice did not differ from that in the wild-type mice at four months of age (data not shown). To examine whether increased PGE₂ affects β-cell function under hyperglycemic conditions, we carried out the glucose tolerance test using fasted RIP-C2mE (Tg/–) mice. As shown in Fig. 2A, the RIP-C2mE (Tg/–) mice showed a significant increase in the blood glucose level in comparison to that in the wild-type mice from 10 to 60 min after the glucose injection. In the wild-type mice, the plasma insulin level at 20 min post-glucose injection increased significantly in comparison to that at 0 min (Fig. 2B). However, the plasma insulin level in the RIP-C2mE (Tg/–) mice at 20 min was significantly lower than that in the wild-type mice, although it had increased 1.3-fold of the basal level at 0 min. These results indicate that increased PGE₂ in the pancreatic β-cells causes impaired insulin secretion under hyperglycemic conditions.

To further investigate the role of PGE₂ signaling in pancreatic β-cells, we intercrossed heterozygous RIP-C2mE (Tg/–) mice to generate homozygous RIP-C2mE (Tg/Tg) mice that carried double the copy number of each transgene. The mean PGE₂ level in the pancreas of the RIP-C2mE (Tg/Tg) mouse at three weeks of age was higher than that in the pancreas of the RIP-C2mE (Tg/–) mice, although it was not significant (Fig. 3A). However, the ratio of the islet area in the pancreas of the RIP-C2mE (Tg/Tg) mice was lower than that in the RIP-C2mE (Tg/–) mice (0.39 and 0.59% of the total pancreas in the Tg/Tg and Tg/– mice, respectively). Consequently, the relative islet PGE₂ level in the RIP-C2mE (Tg/Tg) mice was 1.9-fold higher than that in the RIP-C2mE (Tg/–) mice (Fig. 3B).

FIGURE 4. Fluorescence immunostaining of the islets for insulin (β-cell; green) and glucagon (α-cell; red) at 16 weeks of age. Shown are representative results of two islets each for the wild-type mice (A), RIP-C2mE (Tg/–) mice (B), and RIP-C2mE (Tg/Tg) mice (C). Scale bars, 100 μm. Shown is the ratio of β-cells (D) and α-cells (E) to the total islet cells (mean ± S.E.). *, p < 0.05.

RESULTS

To investigate the effects of PGE₂ on the pancreatic β-cells in mice, we generated transgenic (RIP-C2mE) mice expressing both COX-2 and mPGES-1 by co-microinjection of the two expression vectors (Fig. 1A). We used RIP to target the β-cells in the pancreatic islets. To increase the expression level of the transgenes, we introduced a synthetic intron between the RIP and cDNAs for COX-2 and mPGES-1 (16). Two transgenic lines (RIP-C2mE mouse line 8 and RIP-C2mE mouse line 9) essentially exhibited the same phenotype (data not shown). Accordingly, we present the results with RIP-C2mE mouse line 8 (hereafter referred to as RIP-C2mE). We detected high amounts of mRNA of COX-2 and mPGES-1 by RT-PCR in the isolated islets from the RIP-C2mE (Tg/–) mice, whereas the

expression of both genes was found in the wild-type islets at a basal level (Fig. 1B). We consistently found strong immunostaining signals for COX-2 and mPGES-1 in the pancreatic islets of the RIP-C2mE (Tg/–) mice compared with those of the wild-type mice (Fig. 1C). As shown in Fig. 1D, pancreatic PGE₂ levels at 20 weeks of age increased significantly in the RIP-C2mE (Tg/–) mice (10.9 ± 2.2 pg/mg) in comparison to that in the wild-type mice (4.2 ± 0.5 pg/mg), indicating that the simultaneous transgenic expression of COX-2 and mPGES-1 produced PGE₂ in vivo.

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[Image 50x377 to 407x734]

**FIGURE 5.** Fluorescence immunostaining of the pancreatic islets for insulin (β-cell; green) and glucagon (α-cell; red) at three weeks of age. Shown are representative results for three islets each for the wild-type mice (A) and RIP-C2mE (Tg/Tg) mice (B). Scale bars in A and B, 100 μm. Shown are the ratio of β-cells (C) and α-cells (D) to the total islet cells (mean ± S.E.) and immunostaining for BrdUrd in the islets of the wild-type (E), RIP-C2mE (Tg/-) (F), and (Tg/Tg) (G) mice at four weeks of age. Arrowheads indicate BrdUrd-incorporated cells. Scale bars in E-G, 50 μm. H, BrdUrd labeling index per islet of the respective mouse genotypes (mean ± S.E.). *, p < 0.05.

mained the blood glucose level chronologically when the mice were 3, 6, 9, and 12 weeks of age (Fig. 3C). The blood glucose levels in the RIP-C2mE (Tg/-) mice were normal at all examined ages; this was consistent with the results of the glucose tolerance test. However, the homozygous RIP-C2mE (Tg/Tg) mice showed a significant increase in the blood glucose levels from six weeks of age, thus suggesting that insulin secretion was inhibited by PGE₂ signaling in a dose-dependent manner. Importantly, the blood glucose level of the RIP-C2mE (Tg/Tg) mice at three weeks of age was at the normal level, indicating that the dysfunction of the pancreatic β-cells was not caused by the congenital anomaly of the pancreatic islets.

We then examined the pancreatic β-cells by fluorescence immunohistochemistry using pancreatic tissue of the respective mouse genotypes at 16 weeks of age. In the wild-type mice, the insulin-positive β-cells predominated the pancreatic islets, whereas the glucagon-producing α-cells were found scattered in the marginal regions of the islets (Fig. 4A). In the heterozygous RIP-C2mE (Tg/-) mice, the number of β-cells decreased compared with that in the wild-type mice, whereas the α-cell population increased slightly (Fig. 4B). In sharp contrast to the wild-type mice, α-cells predominated the RIP-C2mE (Tg/Tg) mouse islets, and the β-cells were sparsely distributed in the center of the islets (Fig. 4C). The mean relative ratio of β-cells to the total number of islet cells was 84, 54, and 14% in the wild-type, RIP-C2mE (Tg/-), and (Tg/Tg) mice, respectively (Fig. 4D). In contrast, the mean ratio of α-cells increased inversely with the RIP-C2mE (Tg/-) and (Tg/Tg) mice (Fig. 4E). However, the mean plasma glucagon level in the RIP-C2mE (Tg/Tg) mice stayed at a similar level to that found in the wild-type mice (97.0 ± 4.4 pg/ml and 101.3 ± 9.2 pg/ml in the wild-type and RIP-C2mE (Tg/Tg) mice, respectively). These results collectively indicate that an increase in the PGE₂ level causes a diabetic phenotype through a decrease in the number of pancreatic β-cells.

To rule out the possibility that PGE₂ signaling impairs the development of the pancreatic islets, we carried out fluorescence immunohistochemistry with mice at three weeks of age. The number of pancreatic β-cells in the wild-type mice at three weeks of age was less than that found at 16 weeks of age (Fig. 5, A and C; Fig. 4, A and D). It is possible that the number of β-cells was still increasing at three weeks of age, because β-cells rep-
It has been suggested that the COX-2 pathway is involved in the development of the autoimmune disease type 1 diabetes (12–14). It was thus possible that the increased PGE2 signaling is correlated with the severity of the pancreatic β-cell damage. Thus, increased blood glucose is caused by the reduced number of β-cells and not by the increased number of α-cells. We herein found a significant decrease in the cell proliferation rate in the RIP-C2mE (Tg/Tg) mouse islets at four weeks of age. Because β-cells replicate during the postnatal period (17), it is possible that these proliferating cells are β-cells and that PGE2 signaling inhibits this β-cell proliferation. The number of β-cells in the normal adult islets is regulated by a balance between proliferation and apoptosis (19). It has been estimated that it takes three months for the renewal of 50% of the pancreatic β-cells (20) and nine months for the renewal of
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98% (21). Accordingly, it is conceivable that increased PGE₂ signaling suppresses β-cell proliferation in the adult islets, resulting in gradual reduction of the β-cell mass.

Recently, it has been demonstrated that the expression of p27<sup>Kip1</sup> plays a key role in regulation of the pancreatic β-cell mass and that deletion of the gene encoding p27<sup>Kip1</sup> in the type 2 diabetes model (db/db mice) prevents β-cell destruction (22). Therefore, it is important to investigate the underlying relationship between PGE₂ and p27<sup>Kip1</sup> in β-cell destruction.

Type 1 diabetes mellitus is characterized by β-cell destruction due to autoimmune responses, which are critically dependent upon the interaction between antigen-presenting cells and T-cells. Because we did not observe inflammatory or immune cell infiltration around the pancreatic islets in the RIP-C2mE mice, we concluded that the inhibition of β-cell destruction in our mouse model is not caused by host immune responses. However, IL-1β signaling also plays an important role in the β-cell destruction of type 1 diabetes (23). Furthermore, the IL-1β-induced inhibition of insulin secretion is suppressed by COX-2 inhibitors; this is reconfirmed by exogenous PGE₂ stimulation (13). Therefore, it is possible that PGE₂ plays some role as a downstream mediator of the IL-1β pathway during β-cell destruction in type 1 diabetes as well.

It has been suggested that chronic inflammation plays an etiological role in type 2 diabetes (24) and that chronic activation of the immune system causes a decrease in insulin sensitivity, which may contribute to the pathogenesis of type 2 diabetes (25). The present results suggest that chronic inflammatory responses are involved in the decrease of pancreatic β-cells via the induction of COX-2 and PGE₂, which leads to an increased susceptibility to type 2 diabetes. Moreover, an epidemiological study has indicated the association of the promoter variant of the COX-2 gene with type 2 diabetes in Pima Indians (26). Although COX-2 is an inducible enzyme in most tissues, it has been shown to be expressed constitutively in pancreatic islets (27). Therefore, it is probable that an increase in the basal level of COX-2 expression, caused by a promoter polymorphism, enhances the susceptibility to type 2 diabetes via the suppression of the renewing capabilities of islet β-cells. It is therefore possible that the blockade of PGE₂ receptors or the inhibition of mPGES-1 is an effective therapeutic strategy against β-cell destruction in type 2 as well as type 1 diabetes mellitus.

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