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Increased DNA Methylation and Decreased Expression of PDX-1 in Pancreatic Islets from Patients with Type 2 Diabetes

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Mutations in pancreatic duodenal homeobox 1 (PDX-1) can cause a monogenic form of diabetes (maturity onset diabetes of the young 4) in humans, and silencing Pdx-1 in pancreatic β-cells of mice causes diabetes. However, it is not established whether epigenetic alterations of PDX-1 influence type 2 diabetes (T2D) in humans. Here we analyzed mRNA expression and DNA methylation of PDX-1 in human pancreatic islets from 55 nondiabetic donors and nine patients with T2D. We further studied epigenetic regulation of PDX-1 in clonal β-cells. PDX-1 expression was decreased in pancreatic islets from patients with T2D compared with nondiabetic donors (P = 0.0002) and correlated positively with insulin expression (rho = 0.59, P = 0.000001) and glucose-stimulated insulin secretion (rho = 0.41, P = 0.005) in the human islets. Ten CpG sites in the distal PDX-1 promoter and enhancer regions exhibited significantly increased DNA methylation in islets from patients with T2D compared with nondiabetic donors. DNA methylation of PDX-1 correlated negatively with its gene expression in the human islets (rho = -0.64, P = 0.0000029). Moreover, methylation of the human PDX-1 promoter and enhancer regions suppressed reporter gene expression in clonal β-cells (P = 0.04). Our data further indicate that hyperglycemia decreases gene expression and increases DNA methylation of PDX-1 because glycosylated hemoglobin (HbA1c) correlates negatively with mRNA expression (rho = -0.50, P = 0.00004) and positively with DNA methylation (rho = 0.54, P = 0.00024) of PDX-1 in the human islets. Furthermore, while Pdx-1 expression decreased, Pdx-1 methylation and Dnmt1 expression increased in clonal β-cells exposed to high glucose. Overall, epigenetic modifications of PDX-1 may play a role in the development of T2D, given that pancreatic islets from patients with T2D and β-cells exposed to hyperglycemia exhibited increased DNA methylation and decreased expression of PDX-1. The expression levels of PDX-1 were further associated with insulin secretion in the human islets. (Molecular Endocrinology 26: 1203–1212, 2012)}
sion and diabetes in postnatal life (6). These epigenetic changes include both increased DNA methylation and histone modifications. Although this study demonstrates that epigenetic alterations of the Pdx-1 gene are associated with reduced Pdx-1 expression, β-cell dysfunction and diabetes in rodents, it is not established whether epigenetic alterations of the PDX-1 gene participate in the development of type 2 diabetes (T2D) in humans. The aim of the present study was therefore to analyze DNA methylation of the PDX-1 gene in islets from 55 non-diabetic donors and nine patients with T2D. DNA methylation of the PDX-1 gene was further related to PDX-1 gene expression and glycosylated hemoglobin (HbA1c) levels. Luciferase assays were used to examine whether DNA methylation of the human PDX-1 promoter and enhancer regions influences its transcriptional activity. Finally, we tested whether high levels of glucose affect the degree of Pdx-1 expression and DNA methylation as well as the expression of three DNA methyltransferases in clonal rat β-cells.

Materials and Methods

Pancreatic islets

Pancreatic islets from 55 non-diabetic and nine T2D deceased donors were obtained from the Human Tissue Laboratory at Lund University Diabetes Centre and the Nordic Network for Clinical Islet Transplantation. Islets were prepared by collagen digestion and density gradient purification. After isolation, islets were cultured floating in CMRL 1066 culture medium (ICN Biomedicals, Costa Mesa, CA) supplemented with 10 mmol/liter HEPES, 2 mmol/liter l-glutamine, 50 µg/ml gentamicin, 0.25 µg/ml Fungizone (GIBCO BRL, Gaithersburg, MD), 20 µg/ml ciprofloxacin (Bayer Healthcare, Leverkusen, Germany), and 10 mmol/liter nicotinamide at 37°C (5% CO2) before RNA and DNA preparation. Gene expression of endocrine (somatostatin and glucagon) and exocrine (pancreatic lipase, amylase α2A, and chymotrypsin 2) markers and dithi- zone staining were used to determine islet purity (7). Islet purity was similar for non-diabetic and T2D donors (72% vs 68%, P = 0.29). Glucose-stimulated insulin secretion from the human islets was measured in vitro in static incubations as previously described. The population ancestry of the human donors is not available. The donor before death or her/his relatives upon admission to the intensive care unit had given their consent to donate organs and the local ethics committees approved the protocols.

Gene expression analysis

Total RNA was extracted from human islets and rat clonal β-cells using the All Prep DNA/RNA kit and cDNA was synthesized using QuantiTect reverse transcription kit (Qiagen, Hilden, Germany). PDX-1 mRNA levels were analyzed using TaqMan real-time PCR with an ABI Prism 7900 HT system and gene-specific probes and primer pairs (Assays-on-Demand, Hs00426216_A1, Applied Biosystems Inc., Foster City, CA). The PDX-1 transcript level was normalized to the mRNA level of cyclophilin A (4326316E; Applied Biosystems) and quantified using the ΔΔCt method. Insulin mRNA levels were analyzed in the human islets as previously described (9). The mRNA expression of Pdx-1, Dnmt1, Dnmt3a, and Dnmt3b was analyzed in rat clonal β-cells using the following Assays-on-Demand from Applied Biosystems: Pdx-1, Rn00755591_m1; Dnmt1, Rn00709664_m1; Dnmt3a, Rn01469994_g1; and Dnmt3b, Rn01536414_g1. We further used Normfinder (10) to test whether the expression of two housekeeping genes, cyclophilin A and HPRT (Assay-on-Demand; Applied Biosystems), is stable in human islets and clonal rat β-cells exposed to hyperglycemia.

DNA methylation analysis

Sequenom’s MassARRAY EpiTYPER protocol was applied to measure DNA methylation (Sequenom, San Diego, CA). Two EpiTYPER assays were designed (EpiDesigner; Sequenom), of which one assay covered 15 CpG sites of the human distal PDX-1 promoter and the other assay covered 14 CpG sites of the human PDX-1 enhancer region, respectively. These assays generated successful data for 11 and 12 CpG sites, respectively. A number of CpG sites did not generate any methylation data using the EpiTYPER, due to either low or high mass of the cleavage product. Also, one assay covering 10 CpG sites of the rat Pdx-1 promoter was designed, and it generated successful data for six CpG sites. The primer sequence and the location of the human and the rat EpiTYPER assays are given in Supplemental Table 1, published on The Endocrine Society’s Journals Online web site at http://mend.endojournals.org. Genomic DNA was extracted using the All Prep DNA/RNA kit (Qiagen). Five hundred nanograms of genomic DNA were bisulfite converted. Methylation analysis was performed on human and rat clonal β-cells using All Prep DNA/RNA kit and cDNA was synthesized using QuantiTect reverse transcription kit (Qiagen, Hilden, Germany) and quantified using the ΔΔCt method.

Table 1. Characteristics of the human pancreatic donors

<table>
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<th>Nondiabetic donors</th>
<th>T2D donors</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>n (male/female)</td>
<td>55 (29/26)</td>
<td>9 (5/4)</td>
<td></td>
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<tr>
<td>Age (yr)</td>
<td>56.7 ± 9.8</td>
<td>57.0 ± 13.1</td>
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<tr>
<td>BMI (kg/m²)</td>
<td>25.9 ± 3.6</td>
<td>28.5 ± 4.7</td>
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<tr>
<td>HbA1c</td>
<td>5.7 ± 0.8</td>
<td>7.3 ± 1.2</td>
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</tr>
<tr>
<td>Basal insulin secretion (ng/islet-h)</td>
<td>0.37 ± 0.27</td>
<td>0.22 ± 0.17</td>
<td>0.22</td>
</tr>
<tr>
<td>Glucose-stimulated insulin secretion (ng/islet-h)</td>
<td>1.42 ± 0.95</td>
<td>1.05 ± 1.56</td>
<td>0.045</td>
</tr>
</tbody>
</table>

Data are expressed as mean ± SD.
and ribonuclease (RNase) cleavage reaction were conducted using
the MassCleave kit according to the manufacturer’s recommendations. The cleavage reaction was dispensed onto a 384-
element SpectroCHIP bioarray, and mass spectra were acquired
using a MassARRAY mass spectrometer (Sequenom, San Di-
ego, CA). The spectra were analyzed and the methylation ratios
were obtained by the EpiTYPER software version 1.0.1 (Seque-
nom). Due to the cleavage pattern, the following 10 Cpg sites
were analyzed in five Cpg units: −857, −852, −746, −741,
−3504, −3502, −3420, −3416, −3408, and −3404.

Pyrosequencing (QIAGEN) was used to analyze DNA meth-
ylation of the human proximal PDX-1 promoter because it was
not possible to design an assay for this region using EpiTYPER
(Sequenom). PCR and sequencing primers were designed using
the PyroMark assay design software version 2.0 (QIAGEN)
(Supplemental Table 1). This assay covered 12 Cpg sites and
successful runs were generated for all Cpg sites. The reverse
primer was biotinylated at its 5’ end. Bisulfite-converted DNA
was amplified by PCR using the PyroMark PCR kit (QIAGEN).
Biotinylated PCR products were immobilized onto streptavidin
coated beads (GE Healthcare, Uppsala, Sweden). DNA strands
were separated using denaturation buffer (QIAGEN). After
washing and neutralizing using the vacuum prep station
(Biotage, Uppsala, Sweden), the sequencing primer was an-
nealed to the immobilized strand. Pyrosequencing was per-
duced with the SQ HS96A (Biotage) and PyroMark Gold
CDT kit (QIAGEN) according to the manufacturer’s instruc-
tions. Data were analyzed using the Pyro Q-CpG software pro-
gram (Biotage).

The DNA methylation assays were selected and designed to
cover gene regions of PDX-1 that previously have been shown
to regulate gene expression due to the binding of transcription
factors (11).

**Luciferase assay**

Three different DNA fragments containing 908 bp of the human
PDX-1 promoter, 606 bp of the human PDX-1 en-
hancer region, or 3800 bp of a sequence containing both the
PDX-1 promoter and the enhancer regions (sequences are given
in Supplemental Fig. 1) were inserted into a CpG-free firefly
luciferase reporter vector (pCpGL-basic) kindly provided by Dr.
Maja Klug and Dr. Michael Rehli (Department of Hematology
and Oncology, University Hospital Regensburg, Regensburg,
Germany) (12). Amplification of the three human PDX-1 se-
quencies and insertion into the pCpGL-basic vector was done by
GeneScript (Piscataway, NJ). The constructs were either mock
methylated or methylated using two different DNA methyl-
transferases: SssI and HhaI (2.5 U/μg DNA) (New England Bio-
labs, Frankfurt am Main, Germany). While SssI methylates all
cytosine residues within the double-stranded dinucleotide rec-
ognition sequence CG, HhaI methylates only the internal cyto-
sine residue in CGCG sequence.

Clonal rat insulinaoma-derived INS 832/13 β-cells (kindly
provided by Professor C. Newgard, Duke University Medical
Center, Durham, NC) were cultured in RPMI 1640 medium
with 11.1 mM glucose, which is the standard glucose concentra-
tion for culture of these cells, supplemented with 10% fetal calf
serum, 1 mM sodium pyruvate, 10 mM HEPES, 50 μM β-mer-
captoethanol, 100 U/ml penicillin, and 100 μg/ml streptomycin
at 37 C in a humidified atmosphere containing 95% air and 5% 
CO₂. INS-1 832/13 β-cells were seeded onto a 96 well plate in
100 μl medium (25 × 10³ cells/well) and incubated overnight.
Cells were then cotransfected with 100 ng pCpGL-vector either
without (control) or with respective PDX-1 insert (see above)
together with 2 ng of pRL renilla luciferase control reporter
vector (pRL-CMV vector; Promega) as a control for transfec-
tion efficiency using 0.3 μl FuGENE HD transfection reagent
(Promega) in 50 μl serum-free medium, and the mixture was
incubated for 15 min at room temperature. Each construct was
transfected in five replicate wells. Then 50 μl of medium was
added to the transfection complex and cells were incubated for
48 h before performing the dual-luciferase assay (Promega).
One hundred microliters of 1× Passive Lysis Buffer was first
used to lyse the cells and then the cell lysate was diluted 1:10
with 1× PLB. One hundred microliters Luciferase Assay Re-
agent II reagent were added to 10 μl of diluted cell lysate to
detect the luciferase signal, and 100 μl Stop and Glo reagent was
used to detect the Renilla signal using the TD-20/20 luminom-
eter (Turner Designs, Sunnyvale, CA). Firefly luciferase activity
of each construct was normalized against renilla luciferase ac-
tivity, and it is shown relative to the activity of the mock-meth-
ylated construct including both the enhancer and promoter
regions. The results represent the mean of four independent
experiments and the values in each experiment are the mean of
five replicates. Furthermore, in each experiment, cells were
transfected with an empty pCpGL-vector as a background
control.

**Culturing rat clonal β-cells in normal or high glucose levels for DNA methylation analysis**

Clonal rat insulinaoma-derived INS 832/13 β-cells were cul-
tured in RPMI 1640 medium with 11.1 mM glucose, which is the
standard glucose concentration for culture of these cells, as de-
scribed above. The cells were plated out in six-well plates and
allowed to attach overnight. The medium was then replaced
with fresh medium containing either 11.1 or 16.7 mM glucose.
The cells were further cultured for 72 h, with the medium ex-
changed after 48 h. DNA was isolated with the All Prep kit
(QIAGEN, Hilden, Germany) and kept at −20 C until analysis.
DNA extracted from the cells was then used for analysis of DNA
methylation.

**β-Cell purification**

β-Cells and α-cells were purified from pancreatic islets of
three human donors [54, 55, and 74 yr old, with a body mass
index (BMI) 21.5–23.1 kg/m²], different from the donors de-
scribed in Table 1, using a method previously described (13, 14).
Dissociation of islet cells was achieved by incubation with con-
stant agitation for 3 min at 37 C in 0.05% trypsin-EDTA (In-
vitrogen) supplemented with 3 mg/ml deoxyribonuclease I
(DNase I) (Roche, Basel, Switzerland) followed by vigorous pi-
petting. Labeling and fluorescence-activated cell sorting (FACS)
of the β- and α-cell fractions was performed as previously de-
scribed (13, 14). Sorted β- and α-cells were applied to microscope
slides and coimmunostained for insulin and glucagon to detect the
amount of α-cells in the β-cell fraction, and vice versa. Using this
method, a β-cell purity of 89 ± 9% (mean ± SD) was achieved (14).

**Statistical analysis**

Differences between T2D patients and nondiabetic donors
were analyzed using nonparametric Mann-Whitney U tests. All
Values analyzed for the human islets were two tailed. The false discovery rate (FDR) was used to correct for multiple testing for the CpG sites analyzed using EpiTYPER in human islets, and CpG sites with a Q value of 0.05 or less were considered to be significantly changed. Correlations were calculated using Spearman correlation coefficient. Differences in DNA methylation between FACS sorted /H9252/ and /H9251/ cells as well as between clonal rat /H9252/ cells cultured in 11.1 or 16.7 mM glucose were analyzed using paired nonparametric one-tailed tests. Differences in expression of /Dnmt1/, /Dnmt3a/, and /Dnmt3b/ and the luciferase data were analyzed using paired two-tailed tests. P < 0.05 was considered significant. Statistical calculations were performed using NCSS software (NCSS Statistical Software, Kaysville, UT) and PASW Statistics for Windows (SPSS, Chicago, IL).

**Results**

**PDX-1 expression in human pancreatic islets**

The characteristics of the donors included in this study are described in Table 1. PDX-1 mRNA expression was decreased in pancreatic islets from patients with T2D compared with nondiabetic donors (T2D 0.40 ± 0.076 vs. nondiabetic 1.29 ± 0.15, P = 0.0002; Fig. 1). Furthermore, while islet PDX-1 mRNA expression correlated positively with insulin mRNA expression (rho = 0.59, P = 0.000001) and glucose-stimulated insulin secretion (rho = 0.41, P = 0.005), it correlated negatively with HbA1c levels and BMI (rho = -0.50, P = 0.0004 and rho = -0.28, P = 0.04, respectively).

**DNA methylation of PDX-1 in human pancreatic islets**

We next analyzed DNA methylation of PDX-1 in pancreatic islets from patients with T2D and nondiabetic donors using three assays that cover the PDX-1 proximal and distal promoter regions as well as the PDX-1 enhancer region, respectively (11) (Fig. 2A). These regions of PDX-1 were selected based on previous studies that identified regions that regulate the expression of PDX-1 (11). All analyzed CpG sites located in the proximal promoter region close to the PDX-1 transcription start site (Fig. 2A) showed very low levels of DNA methylation in islets from both nondiabetic and T2D donors, and there was no difference in methylation between the two groups (1.9 vs. 2.0%; P = 0.57) (Fig. 2B). On the other hand, 10 of the analyzed CpG sites located further upstream (5') in the distal promoter region and the enhancer region of PDX-1 showed increased DNA methylation in pancreatic islets from patients with T2D compared with nondiabetic donors (Fig. 2, C and D and Supplemental Table 2). Also, the average degree of PDX-1 methylation of the distal promoter and enhancer regions but not the proximal pro-

![FIG. 1. PDX-1 mRNA expression levels in human pancreatic islets from nondiabetic donors and patients with T2D. Expression was analyzed using quantitative RT-PCR. Results are expressed as mean ± SEM. *, P < 0.05, nondiabetic vs. T2D islets.](image1)

![FIG. 2. Impact of T2D on DNA methylation of PDX-1 in human pancreatic islets. A, A schematic representation of 3500 bp of the human PDX-1 promoter and enhancer region. The three regions analyzed for DNA methylation, representing 93 bp of the proximal promoter, 436 bp of the distal promoter, and 475 bp of the enhancer region, are visualized. DNA methylation of the proximal PDX-1 promoter (B), distal PDX-1 promoter (C), and enhancer region (D) in human pancreatic islets of nondiabetic donors (white bars) and patients with T2D (black bars). Results are expressed as mean ± SEM. FDR was used to correct for multiple testing with *, Q < 0.05 nondiabetic vs. T2D islets.](image2)
moter region was increased in T2D compared with non-diabetic islets (Fig. 2, B–D). The absolute increase in degree of DNA methylation in T2D islets ranged between 6.2 and 18.0% for the analyzed regions, representing fold changes between 1.15 and 1.47 (Supplemental Table 2).

Impact of DNA methylation on gene expression of PDX-1

Because increased DNA methylation has been associated with transcriptional silencing, we further tested whether the degree of PDX-1 DNA methylation correlated negatively with PDX-1 mRNA expression in islets of all studied subjects. Indeed, for a number of analyzed CpG sites, PDX-1 DNA methylation correlated negatively with its gene expression (Table 2). The strongest correlations were found for CpG sites located in the enhancer region, proposing a key role for this region in the regulation of PDX-1 expression. An example of the negative correlation between PDX-1 expression and DNA methylation of one of the CpG sites is illustrated in Fig. 3A. These data suggest that increased DNA methylation may suppress PDX-1 gene expression.

To further examine if DNA methylation of the PDX-1 promoter is associated with reduced expression, three reporter gene constructs were made by inserting the human PDX-1 promoter and/or enhancer sequences into a luciferase expression plasmid pCpGL that completely lacks CpG dinucleotides (12) and that hence could be used to study the effect of promoter DNA methylation in transfection assays (Fig. 3B and Supplemental Fig. 1). Each construct was then mock methylated or methylated with the methyltransferases HhaI and SssI. While SssI methylates all CpG sites, HhaI methylates only the internal cytosine residue in a CGCG sequence. Hence, SssI results in totally methylated constructs and HhaI gives point meth-

<table>
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<tr>
<th>CpG site</th>
<th>PDX-1 gene expression</th>
<th></th>
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<th>HbA1c levels</th>
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FDR was used to correct for multiple testing and to generate Q values. **Bold** values represent significant P and Q values after the FDR analysis.
On the other hand, for the promoter region alone, reporter gene expression was reduced (from 4.6 ± 0.8 to 0.24 ± 0.21%; P = 0.023) only when the construct was totally methylated by Sss1, and there was no effect on gene expression by point methylation by Hha1 (P = 0.26).

Impact of hyperglycemia on DNA methylation of PDX-1

We next examined whether HbA1c levels, which are used as long-term measurements of blood glucose levels, correlate with the degree of PDX-1 DNA methylation in the human islets. HbA1c levels correlated positively with the degree of DNA methylation for a number of analyzed CpG sites, indeed suggesting that hyperglycemia may increase DNA methylation of PDX-1 (Table 2). A correlation between HbA1C and PDX-1 DNA methylation is shown in Fig. 4A. To examine whether hyperglycemia has a direct impact on gene expression and DNA methylation of Pdx-1, we cultured clonal rat β-cells in normal and high levels of glucose for 72 h. While mRNA expression of Pdx-1 decreased (P = 0.016, Fig. 4B), DNA methylation of Pdx-1 increased nominally (P = 0.045, Fig. 4C) in β-cells exposed to high glucose. We next examined whether high levels of glucose could affect the expression of three key DNA methyltransferases compared with cells cultured in low levels of glucose. While mRNA expression of Dnmt1 increased (P = 0.015), mRNA expression of Dnmt3a and Dnmt3b did not change (P = 0.52 and P = 0.27, respectively) in the clonal β-cells exposed to high compared with low levels of glucose (Fig. 4D).

DNA methylation of PDX-1 in α- and β-cells

Finally, because epigenetic factors are known to regulate cell specific gene expression and because it is established that the mature pancreas mainly expresses PDX-1 in pancreatic β-cells, we examined whether the degree of DNA methylation of PDX-1 differed in FACS-sorted α- and β-cell fractions from islets of three human donors. Although all three donors showed increased PDX-1 DNA methylation in α- compared with β-cells, the increase was only nominally significant (Fig. 5).
To our knowledge, this study presents the first analysis of DNA methylation of PDX-1 in pancreatic islets from human donors with or without T2D. We found that CpG sites of the distal PDX-1 promoter and its enhancer exhibited increased DNA methylation with a concomitant decrease in PDX-1 mRNA expression in islets from patients with T2D. It is well established that a decrease in PDX-1 expression results in impaired insulin secretion (4, 5, 15, 16). It has also been previously shown that PDX-1 regulates insulin gene transcription through binding to the insulin promoter in β-cells (17–19). In agreement with these previous studies, we found that both glucose-stimulated insulin secretion and insulin mRNA expression correlated positively with PDX-1 expression in the human islets. It is hence possible that the low levels of PDX-1 expression found in islets from donors with T2D contribute to the impaired insulin expression and secretion seen in these patients (9).

Park et al. (6) have previously shown that an adverse intrauterine environment leads to reduced pancreatic Pdx-1 expression and hence impaired insulin secretion and diabetes in adult rats. An explanation for this phenotype is that epigenetic modifications of Pdx-1, including both increased DNA methylation and histone modifications, are associated with reduced gene transcription in rat islets (6). Our study proposes that epigenetic modifications, i.e., increased DNA methylation, of PDX-1 may also be associated with reduced gene expression and consequently impaired insulin secretion and diabetes in humans. In contrast to the rodent studies, in which epigenetic modifications of the proximal promoter close to the transcription start site seem critical for reducing islet Pdx-1 expression, our data propose that increased DNA methylation of the enhancer region and a more distal part of the promoter may be critical in reducing PDX-1 expression in human islets, i.e., the strongest inverse correlations between DNA methylation and gene expression, were found for CpG sites located in the enhancer region. Moreover, the CpG sites located in the PDX-1 enhancer region showed the largest increase in DNA methylation in islets from patients with T2D compared with nondiabetic donors. In support for this theory, when we tested whether DNA methylation affects expression of the human PDX-1 promoter using several reporter gene constructs, we found that methylation of the construct including both the enhancer and promoter regions indeed reduced the transcriptional activity of the human PDX-1 gene the most. It is previously known that the enhancer region plays a key role for transcriptional activity of the human PDX-1 gene (11, 20). Ma et al. (21) have recently shown that the reduced expression of PDX-1 seen in gastric cancer may be due to increased DNA methylation and reduced histone acetylation of the PDX-1 gene, further supporting the importance of epigenetic regulation of PDX-1 in human diseases.
Hyperglycemia has previously been associated with decreased expression of PDX-1 in β-cells (22). Here we identified an inverse correlation between HbA1c levels, representing the time-averaged mean levels of glycemia in vivo, and PDX-1 mRNA expression, proposing a negative effect of hyperglycemia on PDX-1 expression in human islets. We further demonstrate that high levels of glucose decrease Pdx-1 expression in clonal rat β-cells. Previous studies have shown that hyperglycemia can have direct effects on the epigenetic pattern, which may result in transcriptional changes (9, 23). The positive correlations we identified between HbA1c levels and DNA methylation of PDX-1 in the human islets indicate that this may also be the case for the PDX-1 gene. In support of this, we found nominally increased DNA methylation of the Pdx-1 gene in clonal rat β-cells exposed to high levels of glucose. Furthermore, glucose increased mRNA expression of one DNA methyltransferase, Dnmt1, but not Dnmt3a and Dnmt3b in the clonal β-cells. Using chromatin immunoprecipitation, Park et al. (6) have previously shown that Dnmt1 is the primary DNA methyltransferase associated with the Pdx-1 gene in islets from rats exposed to an adverse intrauterine environment, proposing that Dnmt1 may affect the level of DNA methylation of Pdx-1. The binding of Dnmt1 to Pdx-1 was prevented by treatment with exendin-4, a glucagon-like peptide-1 analog used in diabetes treatment (24). This resulted in decreased DNA methylation and increased expression of Pdx-1 (24). However, pancreatic islets from patients with T2D exhibit only a small but not significant increase in DNM1T1 expression (data not shown), and future studies are needed to test whether DNA methylation changes of PDX-1 precede the manifestation of T2D.

In mature pancreatic islets, PDX-1 is mainly expressed in β-cells. However, some PDX-1 expression has also been found in islet δ-cells and in some other tissues including the developing brain and in the adult hypothalamus (25–27). Epigenetic mechanisms can be used to control cell and tissue-specific gene expression. In this study we had access to FACS-sorted β- and α-cell fractions from islets of only three human donors; nevertheless, our data suggest that DNA methylation may be involved in controlling cell-specific PDX-1 expression in the human islets. In this context, it was recently reported that Dnmt1-mediated methylation of the α-cell-specific transcription factor Arx in β-cells contributes to their specific phenotype (28). Here β-cells deficient in Dnmt1 converted to α-cells, resulting in reduced expression of β-cell specific genes including Pdx-1 and insulin (28). Likewise, suppression of Pdx-1 function in insulin-secreting cells favors an α-cell-like phenotype (29). In contrast to the study by Dhanw et al. (28), we found increased Dnmt1 expression in parallel with decreased expression and increased DNA methylation of Pdx-1 in clonal β-cells exposed to high levels of glucose. The discrepancy between our studies may be explained by the conversion of β- to α-cells in the study by Dhanw et al. (28).

Even though we cannot fully rule out that the changes we find in PDX-1 expression and DNA methylation are due to altered cell composition in islets from patients with T2D, our data from the clonal rat β-cells demonstrate that hyperglycemia specifically increases Pdx-1 promoter DNA methylation and decreases Pdx-1 expression in β-cells. Moreover, if a reduced β-cell mass would cause increased PDX-1 methylation in diabetic islets due to the higher PDX-1 methylation in α- compared with β-cells, then all analyzed CpG sites of PDX-1 would show increased methylation in islets from diabetic compared with nondiabetic donors. However, this is not the case. While the proximal PDX-1 promoter shows similar very low levels of methylation in islets from both diabetic and nondiabetic donors, the distal promoter and enhancer regions of PDX-1 show differential DNA methylation due to T2D. It is hence unlikely that the differences we see in DNA methylation are due to a reduced β-cell number in diabetic islets. In addition, our luciferase experiments provide functional conformation that increased DNA methylation reduces the transcriptional activity of the PDX-1 gene. Moreover, while some investigators have found reductions in β-cell number in human T2D islets (30), others have not seen any changes (31), and this is still a controversial issue. Another study recently reported differential DNA methylation in islets from patients with T2D, which was not associated with a reduced β-cell content (32).

Recent studies from our group and others demonstrate that epigenetic modifications influence genes with important roles in insulin secretion and action, i.e. we found increased DNA methylation of the insulin promoter in pancreatic islets from patients with T2D (9, 33–43). Epigenetic modifications may be passed on from one cell generation to the next (mitotic inheritance) and/or between generations of a species (meiotic inheritance) (44). In plants, epigenetic modifications are known to be inherited from one generation to the next (45). However, there is still limited information about the inheritance of epigenetic traits between generations in mammals (39, 46, 47).

The data from this study demonstrate that epigenetic modifications of PDX-1 may reduce its expression in human diabetic islets, which may lead to impaired insulin expression and secretion. Our data further suggest that hyperglycemia may be a factor behind increased DNA methylation and decreased expression of PDX-1.
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