

Toxicology Research

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16 **Abstract**

17 Developmental exposure to bisphenol A (BPA) has been linked to impaired glucose
18 homeostasis and pancreatic function in adulthood, which has been hypothesized to result from
19 the disruption of pancreatic β -cell development at early life. Here we evaluated whether
20 maternal BPA exposure disrupts β -cell development and glucose tolerance and the role of
21 epigenetic modifications of key regulator in this process. We found that maternal exposure to
22 BPA (10 $\mu\text{g}/\text{kg}/\text{d}$) reduced the pancreatic β -cell mass and the expression of pancreatic and
23 duodenal homeobox 1 (*Pdx1*) at birth, as well as the expression of *Pdx1* at gestational day
24 (GD) 15.5. In parallel with the decreased expression of *Pdx1*, histones H3 and H4
25 deacetylation, along with demethylation of histone 3 lysine 4 (H3K4) and methylation of
26 histone 3 lysine 9 (H3K9), were found at the promoter of *Pdx1*, while no significant changes
27 in DNA methylation status were detected at this region. Moreover, these alterations were
28 observed in adult life along with impaired glucose tolerance. We conclude that maternal
29 exposure to BPA reduces pancreatic β -cell mass at birth by reducing PDX1^+ progenitors
30 during fetal development through altering the histone modifications of *Pdx1*, which can be
31 propagated to later life and increase the susceptibility to glucose intolerance.

32

33 **Keywords:** Bisphenol A; pancreatic β -cell; pancreatic and duodenal homeobox 1; histone
34 modification; DNA methylation; glucose homeostasis

35 Introduction

36 The rapidly increasing prevalence of obesity and type 2 diabetes (T2D) has posed huge health
37 and economic burden globally in recent years. Data from the World Health Organization
38 revealed that diabetes was responsible for 1.5 million deaths and 89 million
39 disability-adjusted life years (DALYs) in 2012.¹ Although genetic predisposition, lifestyles
40 and socioeconomic are the generally accepted risk factors for developing T2D, it is now
41 recognized that early-life chemical exposure also play a significant role in the growing
42 epidemic of diabetes and obesity in later life.² For example, prenatal exposure to nicotine has
43 been proved to be a risk factor for obesity and metabolic disorders.³ Endocrine disrupting
44 chemicals (EDCs), to which people are widely exposed, have recently drawn much attention
45 because of their associations with energy imbalance, obesity and T2D.⁴

46 Bisphenol A (BPA) is one of the highest production-volume EDCs used in manufacturing
47 polycarbonate plastics and epoxy resins. Data from more than 80 biomonitoring studies all
48 over the world indicates that human are widespread exposed to BPA.⁵ Animal studies have
49 raised the concern that perinatal exposure to BPA may induce obesity and/or metabolic
50 syndrome.^{6,7} However, the underlying mechanisms are still not clarified.⁸ Previous studies
51 have suggested that pancreatic β -cell may serve as the target of BPA. Prenatal exposure to
52 BPA has been shown to lead to alterations in Ca^{2+} signaling and insulin secretion in islets of
53 Langerhans in adult male offspring, and reduction in proliferating insulin-secreting β -cells.⁹
54 Exposure to di-2-ethylhexyl phthalate (DEHP), another kind of EDCs, through gestation and
55 lactation reduced pancreatic β -cell mass, pancreatic insulin content and the expression of
56 pancreatic and duodenal homeobox 1 (*Pdx1*) in weaning Wistar rats.¹⁰

57 Previous studies have also linked the development of T2D with impaired pancreatic β -cell
58 development in early-life.³ The development of pancreatic β -cells represents a concert of a
59 hierarchy of transcription factors,¹¹ which is initiated by the expression of *Pdx1* in
60 endodermal cells.¹² *Pdx1* is a critical regulator of pancreatic development and β -cell ontogeny
61 during fetal development. Both genetic and acquired reduction in expression of *Pdx1* have
62 verified the role of *Pdx1* in pancreatic development in both humans and animal models,^{13, 14}
63 while overexpression of *Pdx1* in pancreatic β -cells has been shown to restore cell mass and
64 prevent the development of diabetes.^{15, 16}

65 The fact that maternal exposure to environmental chemicals lead to metabolic disorders even
66 long after the exposure was removed indicates that epigenetic mechanisms may be involved
67 in this process. A number of studies have linked EDCs with the potential role of epigenetics in
68 the development of T2D.¹⁷ Interestingly, it is reported that point mutations of the proximal
69 promoter drastically impaired the *Pdx1* promoter activity, indicating that epigenetic
70 modifications in this region may have huge influences on the *Pdx1* expression.¹⁸ Indeed,
71 altered epigenetic modifications of *Pdx1* has been implicated as the reason of β -cell anomaly
72 and occurrence of T2D in intrauterine growth retarded (IUGR) rats.¹⁹ However, to our
73 knowledge, no evidence has ever linked maternal exposure to BPA with the pancreatic β -cell
74 development and the role of epigenetic modifications of *Pdx1* in this process.

75 In the present study, we aim to verify the hypothesis that maternal BPA exposure disturbs
76 epigenetic modifications of key regulators in the development of pancreatic β -cell, which may
77 contribute to the development of the T2D in adulthood.

78

79 Materials and methods**80 Animals and treatment**

81 Wistar rats were purchased from Hubei Research Center of Experimental Animals (Wuhan,
82 China) and were housed on a 12:12-h light-dark cycle. Rats were given ad libitum access to
83 water and a standard rat chow. The water bottles and cages were made of BPA-free
84 polypropylene. Two female rats were mated with 1 male rat after acclimatization for one
85 week. The day on which a vaginal plug or a sperm positive vaginal smear was found was
86 defined as gestational day (GD) 0.5. Pregnant rats were randomly assigned to two
87 weight-matched treatment groups: BPA (10 µg/kg/d) or the vehicle corn oil (both were from
88 Sigma-Aldrich, Saint louis, MO). This exposure dose was proved to make the internal
89 exposure level similar to that detected in human.²⁰ BPA was first dissolved in corn oil to make
90 a 10 µg/mL solution and both reagents were given at a volume of 1mL/kg body weight via
91 gavage throughout gestation and lactation. Neonates were weighed and distributed within
92 each group to balance the litter size (4 males and 4 females per dam), and caged with dams
93 until weaning. For all experiments, both male and female animals were used due to the
94 technical challenge of simultaneously identifying fetal sexes when isolating pancreatic buds.
95 All the procedures were reviewed and approved by the Ethics Committee of Tongji Medical
96 College (Huazhong University of Science and Technology, Wuhan, China).

97 Isolation of the pancreatic islets

98 Pancreatic islets of Langerhans from adult rats were isolated as previously described.²¹ Briefly,
99 rats were first anesthetized. Then the peritoneal cavity was opened and the hepatopancreatic
100 ampulla of the duodenal was located following the common bile duct and the pancreatic duct.

101 After the duodenum was clamped off with hemostats at both up and downstream of the
102 ampulla, the common bile duct was injected with collagenase V (1 mg/ml, Sigma-Aldrich,
103 Saint Louis, MO) dissolved in Hank's balanced sodium solution (HBSS) plus 1% w/v BSA
104 until the pancreas was fully distended. The pancreas was removed to a 15 ml conical tube and
105 put in 37 °C water bath for 18 min. Following washing for twice, the resulting tissue debris
106 was re-suspended in a discontinuous Ficoll 400 gradient (25%, 23%, 20.5% and 11% w/v;
107 Amresco, Solon, OH, USA) and centrifuged at 800 g for 20 min. The tissue debris at 23/20.5
108 and 20.5/11 interface was collected and washed twice with cold HBSS.

109 **Immunostaining**

110 For immunofluorescence, fetuses from 6 dams were delivered by caesarean at GD 15.5 and
111 fixed in 4% w/v paraformaldehyde overnight, followed by being embedded in paraffin.
112 Four-micrometer sagittal sections were cut, of which contained the pancreas were stained
113 with rabbit antiserum (Millipore, Temecula, CA), and visualized with goat anti-rabbit
114 secondary antibody conjugated to Alexa Fluor 555 (CST, CA). PDX1⁺ cell fraction was
115 calculated by dividing PDX1⁺ cell number with the whole cell number in the pancreas area of
116 the section. Given the regional variation in islet distribution and cell composition, every 30th
117 section was analyzed, which yielded 5 to 7 sections from each pancreas. For
118 immunohistochemistry, pancreas was excised from neonates from six randomly chosen dams.
119 Pancreas were sectioned and immunostained with a mouse anti-insulin + proinsulin
120 monoclonal antibody (Abcam, Cambridge, MA) at a dilution of 1:1250. Sections were
121 detected by a secondary anti-mouse macromolecule ligated to horse radish peroxidase (Vector
122 Laboratories, Burlingame, CA) and visualized in brown with 3,3'-Diaminobenzidine. As

123 described above, every 30th section was analyzed and 5 to 7 sections were yielded from each
124 pancreas. All images were taken by Olympus IX71 (Olympus, Tokyo, Japan) equipped with
125 Image-Pro Plus software (version 5.0; Media Cybernetics, Inc., Rockville, MD USA).
126 Pancreatic β -cell mass was calculated by multiplying the total weight of the unfixed pancreas
127 by the β -cell fraction, which was calculated as the ratio of insulin-positive area to the total
128 tissue area of the section.

129 **Real-time PCR**

130 At GD 15.5 and birth, total RNA and DNA were extracted from pancreas using an AllPrep
131 DNA/RNA Micro Kit (QIAGEN, Hilden, Germany). The mRNA was first reversely
132 transcribed to cDNA using a RevertAid First Strand cDNA Synthesis Kit (Carlsbad, CA,
133 USA). The resulting cDNA was subjected to real-time PCR using FastStart Universal SYBR
134 Green Master (Rox) (Roche, Germany) on a 7900HT Fast Real-Time PCR system. The
135 primers for *Pdx1* amplification were as follows: forward, 5'-CGGACATCTCCCCATACG-3';
136 reverse, 5'-AAAGGGAGATGAACGCGG-3'. Primers for insulin amplification were: forward,
137 5'-TCTTCTACACCCCATGTCCC-3'; reverse, 5'-GGTGCAGCACTGATCCAC-3'. The
138 PCR conditions were as follows: initial denaturing at 95 °C for 10 min; followed by 40 cycles
139 of denaturing at 95 °C for 15 s, annealing and extension at 60 °C for 1 min. Data was
140 analyzed using the $2^{-\Delta\Delta Ct}$ method,²² with cyclophilin used as the internal control.

141 **DNA methylation analysis of the proximal promoter of *Pdx1***

142 DNA extracted from fetal and neonatal pancreas, as well as from islets isolated from 8
143 week-old offspring were treated with bisulphite and subjected to methyl-specific PCR
144 amplification. Pancreas from three fetuses at GD 15.5 and pancreas from two neonates were

145 pooled together to get 1 tube of DNA. The primer pair used in this amplification was as
146 follows: forward, 5'-GGGGGATTAGTATTGAATTTTGGTA-3'; reverse,
147 5'-AAACCTCCTTCTTAAAACAAAACCA-3'. The resulting PCR products were transcribed
148 to RNA using the T7 RNA polymerase in vitro, followed by RNase A cleavage into
149 fragments containing the CpG sites. These RNA fragments were finally analyzed by the
150 Matrix-Assisted Laser Desorption/Ionization Time of Flight (MALDI-TOF) Mass
151 Spectrometry.

152 **Chromatin immunoprecipitation assay**

153 Pancreas from fetuses and neonates, and islets from 8 week-old offspring were cut into pieces
154 and cross-linked in PBS containing 1% w/v formaldehyde (Sigma-Aldrich, Saint louis, MO)
155 and protease inhibitor cocktail for 10 min on a rocking platform. Cells were lysed using SDS
156 lysis buffer and the resulting chromatin was sheared into fragments ranging from 200 to 1000
157 bp. DNA shearing was conducted using a VCX 750 ultrasonic processor with a time-course of
158 six 15 s pulses at 50% output with 60 s ice-rest between pulses. Supernatants were precleared
159 with protein A-sepharose (Millipore, Temecula, CA). An aliquot of supernatant was 1:100
160 diluted and used as the input control. The precleared supernatants were incubated with rabbit
161 anti-acetyl-histone H3/H4, rabbit anti-dimethyl-histone H3 (Lys 4) or mouse
162 anti-trimethyl-histone H3 (Lys 9) (all were purchased from Millipore, Temecula, CA)
163 overnight at 4 °C on a rocking platform. DNA-protein-antibody complexes were precipitated
164 by protein A-sepharose and washed serially with low-salt buffer, high-salt buffer, IP wash
165 buffer and TE buffer. Precipitated complexes were eluted from protein A with an elution
166 buffer (1% w/v NaHCO₃, 1% w/v SDS), followed by reverse cross-linking using 5M NaOH

167 and thoroughly digestion by proteinase K. The resulting DNA was purified with QIAquick
168 PCR Purification Kit (QIAGEN, Hilden, Germany) and subjected to PCR amplification. The
169 primer set used in this study was learned from previous research (15), which was as follows:
170 forward, 5'-GCAGGACAGGAGAGATCAGC-3'; reverse,
171 5'-CCCAGATCGCTTTGACAGTT-3'.

172 **Intraperitoneal glucose or insulin tolerance tests**

173 Rat offspring randomly chosen at 4 weeks, 8 weeks and 20 weeks were subjected to
174 intraperitoneal glucose tolerance test (ipGTT) or intraperitoneal insulin tolerance test (ipITT)
175 to evaluate the glucose homeostasis and insulin sensitivity. For ipGTT, rats were fasted
176 overnight and injected with 2 g/kg glucose dissolved in saline intraperitoneally. Blood
177 glucose was measured at 0, 15, 30, 60, and 120 min later using an Accu-chek glucometer and
178 test strips (Roche, Mannheim, Germany). For ipITT, rats were fasted for 6 h and given an i.p.
179 injection of 0.75 IU/kg human insulin (Novo Nordisk, Bagsvaerd, Denmark) and the time
180 points for blood glucose measurement was 0, 15, 30, 45, and 60 min. Rats were excluded
181 from data analysis if they did not exhibit a rise in blood glucose greater than 20 mmol/L (360
182 mg/dl) in the first 15 min or if they exhibited diarrhea.

183 **Statistics**

184 Statistical analysis was carried out with SPSS 13.0. A repeated measure analysis of variances
185 (ANOVA) was used in the analysis of data from ipGTT and ipITT. Other statistical analyses
186 were performed using two-tailed Student's t-test. Data were presented as mean \pm SEM, $p <$
187 0.05 was considered significant in all the analyses.

188

189

190 **Results**191 **Maternal exposure to BPA reduces pancreatic β -cell mass at birth.**

192 The results of birth weight, pancreas weight, and organ coefficient are shown in Table 1.

193 Birth weight and pancreas weight were significantly reduced ($p < 0.001$) due to maternal

194 exposure to BPA, while no significant variation in the pancreas organ coefficient (organ

195 weight/body weight) was observed. Fig. 1 shows that BPA exposure significantly reduced (p 196 < 0.001) the pancreatic β -cell mass (BCM) at birth (Fig. 1A, B, and C). However, this

197 reduction in cell mass did not alter the content of mRNA for insulin in isolated pancreas (Fig.

198 1D).

199 **Maternal exposure to BPA disrupts the expression and epigenetic modifications of *Pdx1***200 **at birth**

201 We also examined the expression of mRNA for some key regulators which are important for

202 the pancreatic β -cell development. The expression of mRNA for *Pdx1* was decreased in the

203 BPA group, whereas no changes were observed in the expression of pancreas transcription

204 factor 1 subunit alpha (*Ptfla*), glucagon (*Gcg*), and amylase (*Amy*) (Fig. 2A).205 We next investigated whether this change in expression of *Pdx1* was correlated with206 epigenetic modifications of the proximal promoter of *Pdx1*. The acetylation status of core

207 histones H3 and H4, trimethylation of lysine 4 at H3 (H3K4me3) and dimethylation of lysine

208 9 at H3 (H3K9me2) were determined by chromatin immunoprecipitation (ChIP). Maternal

209 exposure to BPA significantly reduced the abundance of histones H3 ($p < 0.001$) and H4 ($p <$ 210 0.05) acetylation and H3K4me3 ($p < 0.01$), whereas increased the abundance of H3K9me2 (p

211 < 0.05), leading to repressed chromatin structure (Fig. 2B). In addition to histone
212 modifications, we also determined the DNA methylation status of the proximal promoter of
213 *Pdx1*. The CpG sites examined in the present study were illustrated in Fig. 2C. However, no
214 substantial changes in the DNA methylation status were observed at birth. Two sites (2 and
215 12) were consistently methylated across the study.

216 **Maternal exposure to BPA disrupts the expression and epigenetic modifications of *Pdx1***
217 **at GD 15.5**

218 Since the development of pancreatic β -cell initiates and develops under the control of *Pdx1* at
219 fetal stages before birth, we also examined the expression and epigenetic modifications of
220 *Pdx1* at gestational day (GD) 15.5. The expression of mRNA for *Pdx1* and *Ptf1a* were
221 reduced by 30.9% and 63.6% respectively, indicating a potential decrease in the abundance of
222 pancreatic progenitor cells, while the expression of mRNA for insulin (*Ins*), *Gcg*, *Amy*, and
223 neurogenin 3 (*Ngn3*) remained unchanged (Fig. 3A). In addition to the reduction in
224 expression of mRNA for *Pdx1*, morphological results also showed that BPA exposure
225 significantly reduced the PDX1⁺ cell fraction ($p < 0.01$) at GD 15.5 compared to the control
226 group (Fig. 3B and C).

227 At this life stage, BPA also significantly reduced the acetylation of histones H3 and H4, as
228 well as the H3K4me3 ($p < 0.05$), while H3K9me2 was not detected in control group. Still,
229 we did not observe any changes in DNA methylation status at the promoter of *Pdx1*.

230 **Altered epigenetic modifications of *Pdx1* propagates to 8 weeks of age**

231 To verify the continuity and progressiveness of the epigenetic modifications, we also
232 investigated the epigenetic modifications of *Pdx1* at 8 weeks of age. The difference in histone

233 code between two groups was strengthened at this life stage. Acetylated histones H3 and H4
234 were barely detected by 8 weeks in BPA exposed group whereas the H3K9me2 was
235 significantly increased compared to the control (Fig. 4A). Surprisingly, DNA methylation
236 status still did not show any changes between two groups (Fig. 4B).

237 **Maternal exposure to BPA induces glucose intolerance and insulin resistance in**
238 **adulthood**

239 We also tried to verify if the disrupted pancreatic β -cell development at birth correlates with
240 the glucose homeostasis at adulthood. There was no significant difference in both ipGTT and
241 ipITT at 4 weeks (Fig. 5A, G). At 8 weeks, the results of ipGTT and ipITT showed slight
242 differences after the injection (Fig. 5B, H), with the area under curve (AUC) of ipGTT
243 showed a marginal difference ($p = 0.088$; Fig. 5E). At 20 weeks, repeated measures ANOVA
244 showed significant differences in interaction between treatment and time ($p = 0.001$ and 0.026
245 for ipGTT and ipITT respectively). The BPA group exhibited higher blood glucose levels at
246 15, 30 and 60 min after glucose injection (Fig. 5C). There were significant differences in
247 blood glucose at 0 and 15 min after the injection during the ipITT (Fig. 5I). The AUC also
248 showed significant differences at this stage (Fig. 5F, L).

249 Separated analyses of data for males and females revealed no differences for both sexes at 4
250 weeks of age (supplementary Fig. S1A-H). At 8 weeks, BPA exposed males first exhibited
251 insulin resistance (supplementary Fig. S2C), which was confirmed by the increased AUC in
252 BPA rats (supplementary Fig. S2D), whereas females showed no difference between control
253 and BPA group (supplementary Fig. S2E-H). At 20 weeks, BPA exposed males showed both
254 glucose intolerance and insulin resistance compared to control males (supplementary Fig.

255 S3A-D). Glucose intolerance was also detected in BPA exposed females at this age
256 (supplementary Fig. S3E, F).

257 **Discussion**

258 Previous studies have demonstrated that in utero exposure to low-dose BPA disrupts glucose
259 homeostasis and induces diabetes^{6, 9, 17}. However, the underlying molecular mechanisms
260 remain unclear. In this study, we found that perinatal exposure to BPA impaired the fetal
261 development of pancreatic β -cell, characterized by decreased PDX1⁺ cell fraction at GD 15.5,
262 and reduced pancreatic β -cell mass at birth. Furthermore, alterations in histone modification
263 of *Pdx1* promoter towards an inactivated chromatin were observed in parallel with reduction
264 in PDX1⁺ cell fraction at GD 15.5. These alterations propagated to 8 weeks of age, when
265 glucose intolerance and insulin resistance were observed. To our knowledge, this is the first
266 study to report the correlation between pancreatic β -cell development and the histone
267 modification of *Pdx1* gene in a BPA exposure model. We believe this will help understand the
268 underlying mechanisms by which early life exposure to BPA may impact on the development
269 of diabetes in adulthood.

270 This research further verifies that perinatal period is the critical time window for BPA
271 exposure. Rodent models and human studies have shown that BPA can be transferred across
272 the placenta,^{23, 24} and through the milk,²⁵ which makes the developing organ systems
273 particularly susceptible to the potential adverse effects of BPA, including brain and
274 behavior,^{26, 27} reproductive system,²⁸ and metabolism.²⁹ The perinatal period being one of the
275 most crucial time windows is due to not only directly exposure but also the effects of BPA on
276 maternal behaviors.³⁰

277 Both *in vivo* and *in vitro* studies have suggested that pancreatic β -cell as the potential target,
278 by which BPA may exert its effects on blood glucose homeostasis and diabetes.^{31,32} However,
279 to our knowledge, no evidence has ever linked BPA exposure with the development of
280 endocrine pancreas *in vivo*, of which impairment has been proposed to greatly increase the
281 susceptibility to the development of T2D.³³ In our present study, we found that perinatal
282 exposure to BPA significantly reduced the pancreatic β -cell mass at birth, which, at least in
283 part, account for the association between prenatal exposure to BPA and the onset of T2D. The
284 involvement of endocrine pancreas in the development of T2D has been verified by various
285 previous studies involving developmental malnutrition and/or developmental exposure to
286 environmental chemicals. Both maternal low-protein and low-energy diet during pregnancy
287 significantly decreased the rat fetal β -cell mass.³⁴ Similar results have been demonstrated in
288 vitamin A deficiency and exposure to DEHP, nicotine, and dexamethasone models during
289 development.^{10, 35-37} Furthermore, studies indicate that even a 37% increase in pancreatic
290 β -cell proliferation in IUGR animals at 3 months of age, the pancreatic β -cell mass remained
291 less than that of the normally nourished ones, indicating a persistent reduction in β -cell mass
292 in adulthood.³⁸ This may in turn strengthen the reduction in β -cell mass, because adult
293 pancreatic β -cells are maintained by self-duplication of existing cells rather than stem-cell
294 differentiation.³⁹ When this persistent reduction in pancreatic β -cell mass encounters aging,
295 glucose intolerance was triggered.⁴⁰ Intriguingly, the reduced beta cell mass by BPA was not
296 mirrored by a reduction of insulin mRNA, suggesting a higher insulin content per beta cell.³⁴
297 *Pdx1* is a key regulator in determining cell lineage in pancreatic development and maintaining
298 β -cell function in adulthood. Increasing evidence suggests that decreased expression level of

299 *Pdx1* in development may be responsible for the reduction in pancreatic β -cell mass induced
300 by developmental deficiency in nutrition.^{19,34} Restoration of expression of *Pdx1* by neonatal
301 administration of exendin-4 counteracted the progressive reduction in pancreatic β -cell mass
302 after intrauterine growth retardation.¹⁶ In consistent with the reduction in pancreatic β -cell
303 mass, our data suggest that the expression of *Pdx1* was significantly reduced by BPA
304 exposure at birth. We also found that the expression level of *Pdx1* and *Ptf1a* were
305 significantly reduced compared to that of the control group at GD 15.5. Genetic tracing
306 experiments have demonstrated that both endocrine and exocrine cells of the pancreas derive
307 from a pool of progenitor cells that express the transcription factors *Pdx1*⁴¹ and *Ptf1a*.⁴²
308 These results indicate that reduction in the PDX1⁺ progenitor cells at an early developmental
309 stage may be responsible for the impairment of pancreatic β -cell development in our
310 experiment. Conditional progenitor cell ablation revealed that pancreas size was limited by
311 the size of the progenitor cell pool that was set aside in early development and was not subject
312 to growth compensation.⁴³ The same study also suggested that early ablation of the PDX1⁺
313 progenitor cells decreased insulin⁺ cell area at E18.5 while amylase⁺ (exocrine) and DBA⁺
314 (duct) cell area showed small non-significant changes, and adult mice derived from early
315 ablation of pancreatic progenitor cells exhibited glucose intolerance at 11 weeks.⁴³ These
316 results indicate that BPA induced reduction in PDX1⁺ progenitor cells may have profound and
317 permanent effects on pancreatic β -cell development and glucose homeostasis in adulthood.
318 Indeed, in addition to the reduced pancreatic β -cell mass at birth, we also observed slight
319 changes in glucose metabolism and insulin response in BPA exposed offspring at as early as 8
320 weeks, and this propagated to insulin resistance at 20 weeks of age. Although we believe that

321 perinatal exposure to BPA may possibly decrease the pancreatic β -cell mass by reducing the
322 PDX1⁺ progenitor cell pool at early stage, studies are still needed to elucidate the exact events
323 mediating the effects. It is worth noting that previous studies indicate that females are more
324 resistant to the toxicity of BPA on glucose homeostasis.⁹ However, identifying the fetal sexes
325 when isolating the pancreatic buds at GD 15.5 turned out to be technically challenging for us.
326 In this case, following experiments were conducted on rats irrespective of the sexes. However,
327 we still tried to analyze the GTT and ITT data separately by sex (see supplementary
328 materials), and found that the emerging time of glucose intolerance for females was later than
329 that for males, which is in consistent with previous studies.⁶

330 Epigenetic modifications provide a mechanism, by which the activity of gene expression can
331 be reprogrammed and propagated to later life stage. The dynamic epigenome is sensitive to
332 environmental signals, which makes it an interface between the dynamic environment and the
333 static genome.⁴⁴ Moreover, pancreas development and T2D have both been implicated to be
334 associated with epigenetic modifications.^{45, 46} In mammals, epigenetic modifications are
335 mainly mediated by DNA methylation and chromatin modifications. In vitro studies suggest
336 that the proximal promotor region of *Pdx1* contains a highly conserved CpG island and is
337 heavily acetylated at histone H3 and H4.^{18, 47} We first observed a decrease in the acetylated
338 H3 and H4, and H3K4me3 at GD 15.5 in BPA exposed fetuses, followed by an increase in
339 H3K9me2 at birth. These results indicate that BPA significantly altered the chromatin
340 modifications of *Pdx1* promotor towards an inactive direction, through which the expression
341 level of *Pdx1* was significantly decreased. Moreover, these epigenetic modifications were
342 progressively propagated to 8 weeks of age, indicating permanent impairments of expression

343 level of *Pdx1*.

344 We also detected the DNA methylation status of the proximal promotor region in parallel with
345 histone modifications in the same region. Surprisingly, we did not detect any significant
346 changes at all the 19 CpG sites at different time points. Emerging evidence supports the view
347 that DNA methylation and histone modifications may be mutually reinforcing and
348 interdependent, and histone modifications are readily reversible whereas DNA methylation is
349 stable.⁴⁸ Given that methylation of H3K9 precedes DNA methylation,⁴⁹ it is possible that the
350 histone modifications of the *Pdx1* promoter in BPA exposed group may represent an early
351 stage of DNA methylation in this study. However, to our knowledge, no previous studies have
352 ever identified the DNA methylation status of the promoter of *Pdx1* in primary islet tissue
353 when exposed to BPA during fetal development. Future studies are required to fully verify the
354 long-term effects of BPA on DNA methylation of the *Pdx1* promoter and the molecular
355 interactions in this process.

356 **Conclusions**

357 In conclusion, our study demonstrates that perinatal exposure to BPA induces altered histone
358 modifications towards an inactive status in the proximal promotor of *Pdx1*. This leads to the
359 reduction in PDX1⁺ progenitor cells during development, which in turn impairs the
360 development of the pancreatic β -cell. And these finally disrupt glucose homeostasis at
361 adulthood. We believe that our research provides new insights of the mechanisms by which
362 perinatal exposure to BPA may impair pancreatic β -cell development and induce T2D.

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371 **Conflicts of interest**

372 There are no conflicts of interest to declare.

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507

508 **Table 1. General parameters of neonatal rats.**

	Body weight (g)	Pancreas weight (g)	Organ coefficient
Control (n = 61)	4.638 ± 0.011	0.027 ± 6.557E-5	0.006 ± 5.882E-6
BPA (n = 73)	3.954 ± 0.010*	0.022 ± 6.849E-5*	0.006 ± 1.127E-5

509 Data are represented as mean ± SEM; * $p < 0.001$ by two-tailed Student's t-test.

510 **Figure captions**

511 **Fig. 1 Pancreatic β -cell mass and insulin expression at birth.** (A, B) Representative images
512 of pancreatic β -cells (brown) in pancreas isolated from the control (A) and BPA (B) group at
513 birth ($n = 6$). Bars = 50 μm . (C) The pancreatic β -cell mass at birth. Mean pancreatic β -cell
514 fraction was used to calculate the absolute pancreatic β -cell mass as described in the Materials
515 and Methods section ($n = 6$). (D) The relative mRNA expression level of insulin at birth ($n =$
516 6). Data are represented as mean \pm SEM, *** $p < 0.001$ by two-tailed Student's t-test.

517 **Fig. 2 The expression and epigenetic profiling of *Pdx1* at birth.** (A) The expression level
518 of mRNA for *Pdx1* was determined at birth ($n = 6$). (B) The abundance of acetylated H3
519 (AceH3), acetylated H4 (AceH4), H3K4me3, and H3K9me2 at the *Pdx1* promoter ($n = 3$).
520 Data are represented as percent of input control, which went through the analyses exactly as
521 the test samples except for the IP step. (C) A schematic illustration of the analyzed CpG sites
522 at *Pdx1* proximal promoter. CpG sites are marked with open circles relative to translational
523 start site (+1 bp). (D) DNA methylation status of the *Pdx1* promoter ($n = 3$). Data are
524 represented as mean \pm SEM. * $p < 0.05$, ** $p < 0.01$; *** $p < 0.001$ by two-tailed Student's t-test.

525 **Fig. 3 The expression and epigenetic profiling of *Pdx1* at GD 15.5.** (A) The expression
526 level of mRNA for *Pdx1* was determined at GD 15.5 ($n = 6$). (B) PDX1⁺ cell was stained red
527 with anti-PDX1 antibody and the pancreas at GD 15.5 was outlined ($n = 6$). Bars = 50 μm . (C)
528 PDX1⁺ cell fraction at GD 15.5 ($n = 6$). (D) The abundance of AceH3, AceH4, H3K4me3,
529 and H3K9me2 at the *Pdx1* promoter ($n = 3$). Data are represented as percent of input control,
530 which went through the analyses exactly as the test samples except for the IP step. (E) DNA
531 methylation status at the *Pdx1* promoter ($n = 3$). Data are represented as mean \pm SEM. * $p <$

532 0.05, ** $p < 0.01$ by two-tailed Student's t-test.

533 **Fig. 4 Epigenetic profiling of *Pdx1* at 8 weeks of age.** (A) The abundance of AceH3, AceH4,
534 H3K4me3, and H3K9me2 at the *Pdx1* promoter. Data are represented as percent of input
535 control, which went through the analyses exactly as the test samples except for the IP step (n
536 = 3). (B) DNA methylation status at the *Pdx1* promoter ($n = 3$). Data are represented as mean
537 \pm SEM. * $p < 0.05$, *** $p < 0.001$ by two-tailed Student's t-test.

538 **Fig. 5 Glucose homeostasis and insulin sensitivity in adult rats.** ipGTT was performed at 4
539 weeks (A), 8 weeks (B), and 20 weeks (C), $n = 10-19$ and $8-17$ for control and BPA
540 respectively. Panels D-F show the ipGTT AUC. The ipITT was performed in the same groups
541 at 4 weeks (G), 8 weeks (H) and 20 weeks (I), $n = 11-16$ and $12-17$ for control and BPA
542 respectively. Panels J-L show the ipITT AUC. Data are represented as mean \pm SEM. * $p < 0.05$,
543 ** $p < 0.01$, *** $p < 0.001$ by two-tailed Student's t-test.

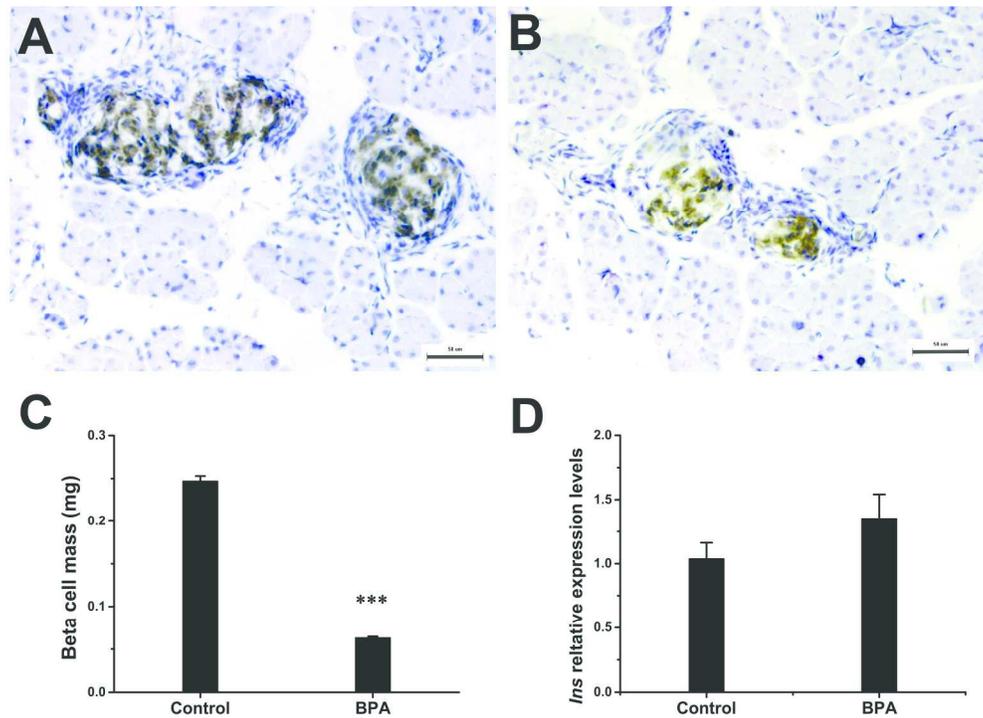


Fig. 1 Pancreatic β -cell mass and insulin expression at birth. (A, B) Representative images of pancreatic β -cells (brown) in pancreas isolated from the control (A) and BPA (B) group at birth ($n = 6$). Bars = 50 μm . (C) The pancreatic β -cell mass at birth. Mean pancreatic β -cell fraction was used to calculate the absolute pancreatic β -cell mass as described in the Materials and Methods section ($n = 6$). (D) The relative mRNA expression level of insulin at birth ($n = 6$). Data are represented as mean \pm SEM, *** $p < 0.001$ by two-tailed Student's t -test.

212x153mm (300 x 300 DPI)

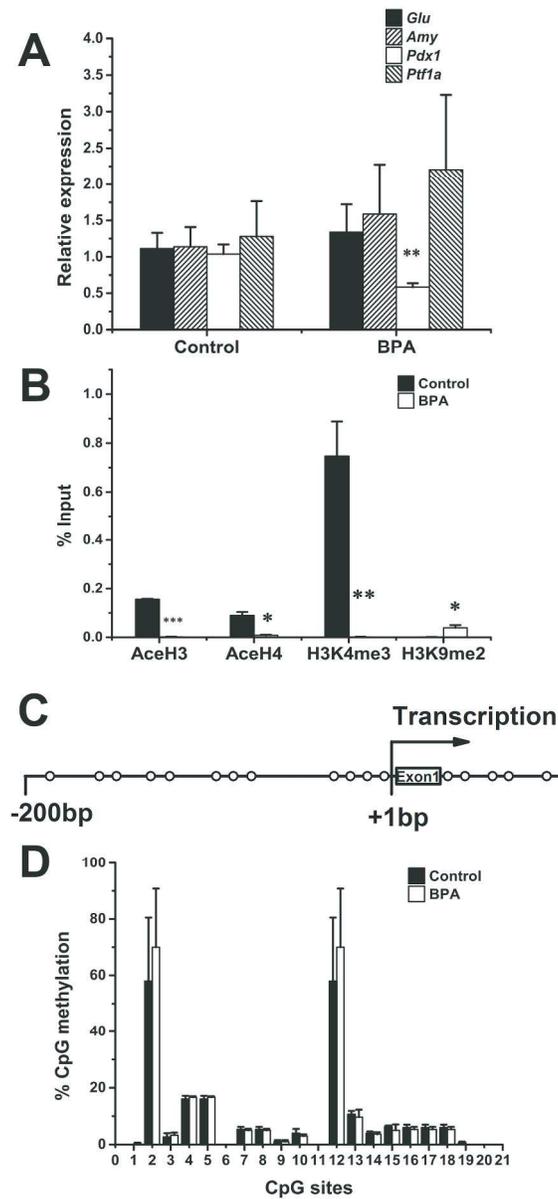


Fig. 2 The expression and epigenetic profiling of Pdx1 at birth. (A) The expression level of mRNA for Pdx1 was determined at birth ($n = 6$). (B) The abundance of acetylated H3 (AceH3), acetylated H4 (AceH4), H3K4me3, and H3K9me2 at the Pdx1 promoter ($n = 3$). Data are represented as percent of input control, which went through the analyses exactly as the test samples except for the IP step. (C) A schematic illustration of the analyzed CpG sites at Pdx1 proximal promoter. CpG sites are marked with open circles relative to translational start site (+1 bp). (D) DNA methylation status of the Pdx1 promoter ($n = 3$). Data are represented as mean \pm SEM. * $p < 0.05$, ** $p < 0.01$; *** $p < 0.001$ by two-tailed Student's t-test. 131x279mm (300 x 300 DPI)

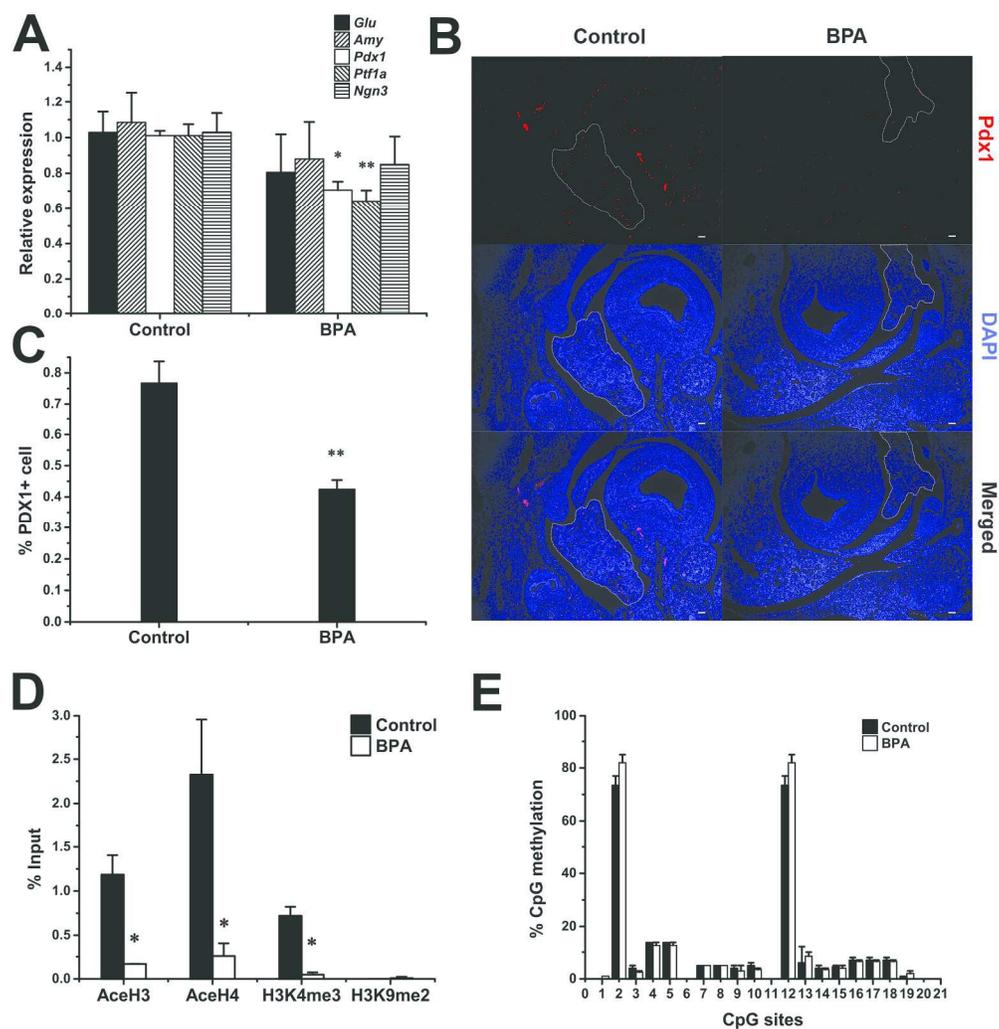


Fig. 3 The expression and epigenetic profiling of Pdx1 at GD 15.5. (A) The expression level of mRNA for Pdx1 was determined at GD 15.5 ($n = 6$). (B) PDX1+ cell was stained red with anti-PDX1 antibody and the pancreas at GD 15.5 was outlined ($n = 6$). Bars = 50 μ m. (C) PDX1+ cell fraction at GD 15.5 ($n = 6$). (D) The abundance of acetylated H3 (AceH3), acetylated H4 (AceH4), H3K4me3, and H3K9me2 at the Pdx1 promoter ($n = 3$). Data are represented as percent of input control, which went through the analyses exactly as the test samples except for the IP step. (E) DNA methylation status at the Pdx1 promoter ($n = 3$). Data are represented as percent of. Data are represented as mean \pm SEM. * $p < 0.05$, ** $p < 0.01$ by two-tailed Student's t-test.

206x218mm (300 x 300 DPI)

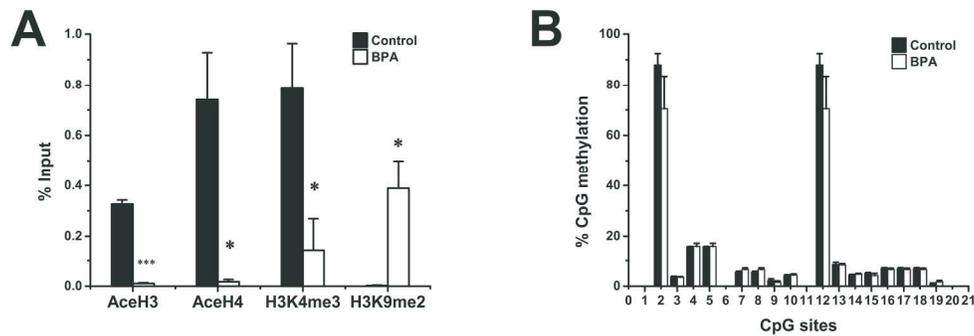


Fig. 4 Epigenetic profiling of Pdx1 at 8 weeks of age. (A) The abundance of acetylated H3 (AceH3), acetylated H4 (AceH4), H3K4me3, and H3K9me2 at the Pdx1 promoter. Data are represented as percent of input control, which went through the analyses exactly as the test samples except for the IP step (n = 3). (B) DNA methylation status at the Pdx1 promoter (n = 3). Data are represented as mean \pm SEM. *p < 0.05, ***p < 0.001 by two-tailed Student's t-test.

215x75mm (300 x 300 DPI)

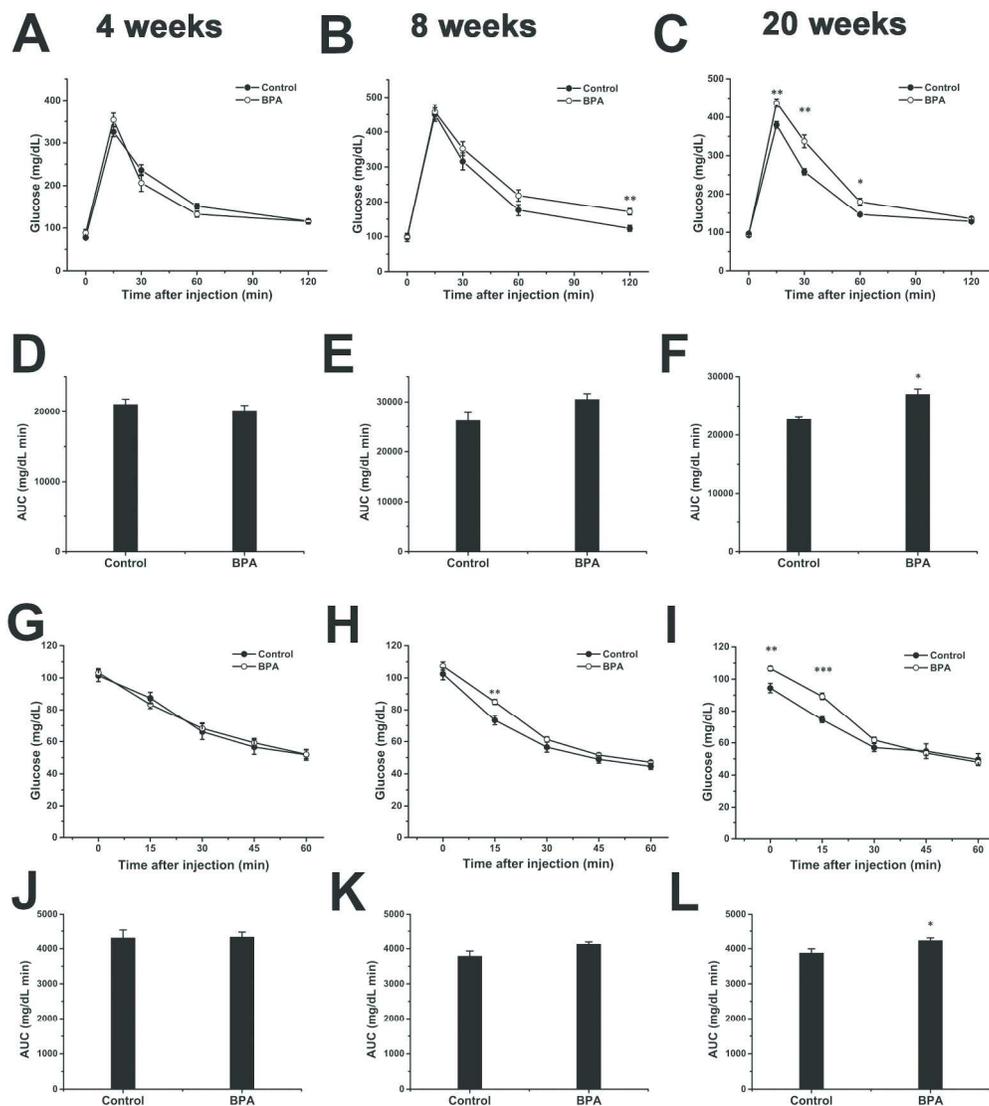
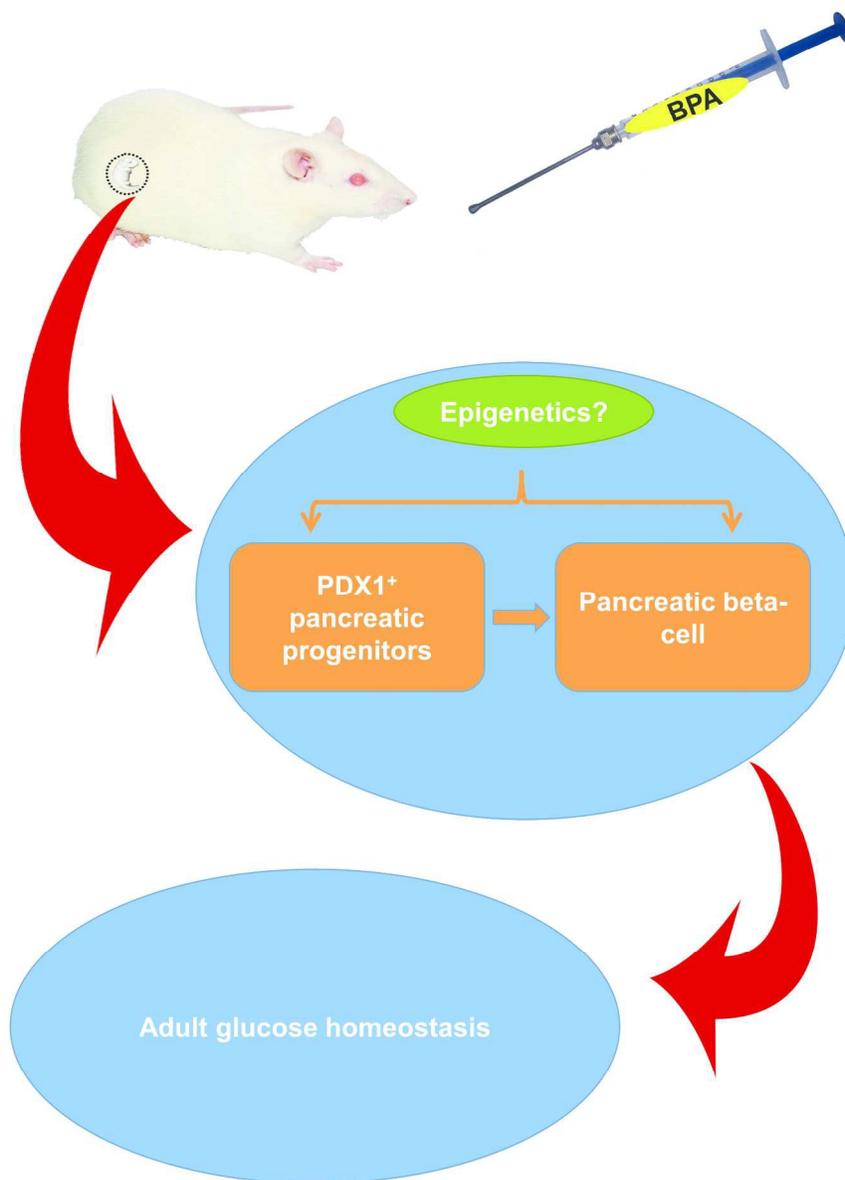


Fig. 5 Glucose homeostasis and insulin sensitivity in adult rats. ipGTT was performed at 4 weeks (A), 8 weeks (B), and 20 weeks (C), $n = 10-19$ and $8-17$ for control and BPA respectively. Panels D-F show the ipGTT AUC. The ipITT was performed in the same groups at 4 weeks (G), 8 weeks (H) and 20 weeks (I), $n = 11-16$ and $12-17$ for control and BPA respectively. Panels J-L show the ipITT AUC. Data are represented as mean \pm SEM. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$ by two-tailed Student's t-test. 200x225mm (300 x 300 DPI)



206x281mm (300 x 300 DPI)