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FETAL PROGRAMMING AND GESTATIONAL DIABETES MELLITUS

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23 **Abstract**

24 Gestational diabetes mellitus is defined by new-onset glucose intolerance during
25 pregnancy. About 2-5% of all pregnant women develop gestational diabetes during
26 their pregnancies and the prevalence has increased considerably during the last
27 decade. This metabolic condition is manifested when pancreatic β -cells lose their
28 ability to compensate for increased insulin resistance during pregnancy, however,
29 the pathogenesis of the disease remains largely unknown. Gestational diabetes is
30 strongly associated with adverse pregnancy outcome as well as with long-term
31 adverse effects on the offspring which likely occurs due to epigenetic modifications
32 of the fetal genome. In the current review we address gestational diabetes and the
33 short and long term complications for both mothers and offspring focusing on the
34 importance of fetal programming in conferring risk of developing diseases in
35 adulthood.

36

37 **Keywords:** gestational diabetes mellitus, fetal programming, epigenetics

38

39 1. Gestational Diabetes Mellitus- overview

40 Gestational diabetes mellitus (GDM) is defined by glucose intolerance of various
41 degrees with first recognition during pregnancy [1-3]. In the USA, GDM affects up to
42 10% of all pregnancies and immediately after pregnancy, 5 to 10% of women with
43 GDM are found to have type 2 diabetes mellitus (T2DM) [4]. Although GDM usually
44 resolves within 6 weeks of delivery, approximately 50% of women diagnosed with
45 this metabolic condition are expected to develop T2DM over 10-30 years [4,5].
46 Women with GDM experience an increased risk of developing other pregnancy
47 complications, such as preeclampsia, and their offspring are at higher risk of
48 developing short-term adverse outcomes such as macrosomia, neonatal
49 hypoglycemia and neonatal cardiac dysfunction, and long-term complications, such
50 as obesity, impaired glucose tolerance (IGT), and diabetes in adolescence or early
51 adulthood [2,4,6].

52 During pregnancy, glucose metabolism changes to meet the nutritional demands of
53 the mother and fetus [7]. It has been demonstrated that fasting glucose
54 concentrations of women with normal glucose tolerance decreases as gestation
55 progresses [8]. Although the mechanism is complex and still not well understood
56 potential contributing factors have emerged, including: increased plasma volume in
57 early gestation, increased glucose consumption due to increased feto-placental
58 glucose intake in late gestation, and/or inadequate hepatic glucose production
59 comparative to circulating glucose concentrations [3,7,8]. Nonetheless, despite the
60 decrease in fasting glucose, hepatic glucose production is increased in normal
61 pregnancy [7]. Insulin resistance occurs to some degree in all pregnancies [2,9]. In
62 fact, by late pregnancy, women's insulin sensitivity declines to one third in

63 comparison to their non-pregnant state. This increased insulin resistance facilitates
64 continuous glucose transfer to the fetus [10]. In order to maintain proper glucose
65 control, β -cell mass as well as the amount of insulin secreted from β -cells increases
66 during pregnancy [7]. Pregnant women who develop GDM, however, are unable to
67 increase insulin production to compensate for their increased resistance to insulin
68 [3,7,9,11].

69 GDM is considered to result from interaction between genetic and environmental risk
70 factors [12]. Studies have suggested that pregnancy triggers a series of metabolic
71 imbalances that lead to a diabetic state in some women who are already genetically
72 predisposed to develop diabetes [3]. Indeed, a study by Shaat *et al*, has identified a
73 variant in the *transcription factor-7-like 2 (TCF7L2)* gene to be associated with an
74 increased risk of GDM [13]. Furthermore, women with mutations in *maturity onset*
75 *diabetes of the young (MODY)* genes, with common variants in *potassium inwardly-*
76 *rectifying channel subfamily J, member 11 (KCNJ11)*, *glucokinase (GCK)* and
77 *hepatocyte nuclear factor-1alpha (HNF1 α)* have been demonstrated to be at higher
78 risk of developing GDM [12]. More recently, a two-stage genome-wide association
79 analysis in Korean women found genetic variants in the *CDK5 Regulatory Subunit*
80 *Associated Protein 1-Like (1CDKAL1)* gene and near the *Melatonin Receptor 1B*
81 *(MTNR1B)* gene to be strongly associated with GDM. Interestingly, they also provide
82 evidence that GDM and T2DM share a similar genetic background [14].

83 In addition, obesity or overweight, advanced maternal age, glycosuria, personal
84 history of GDM or a strong first-degree family history of T2DM and gestational
85 diabetes are important factors and warning signs which increase the risk of GDM
86 [3,15-17].

87 Numerous reports demonstrate the prevalence of GDM is increasing globally. Over
88 the past 20 years, GDM has increased by approximately 10-100% [17-23],
89 particularly in populations immigrating from less- to more-developed areas [24].
90 Population ageing, urbanization, obesity, sedentary lifestyles and stressful modern
91 life are thought to be contributing factors in this emerging public health problem. In
92 addition to adverse consequences for infants in the newborn period, GDM also
93 contributes to the increasing incidence of diabetes and obesity in women with GDM
94 and their offspring later in life [17,25]. Indeed, the Exploring Perinatal Outcomes
95 among Children (EPOCH) study found that youth exposed to maternal GDM *in utero*
96 had significantly higher average BMI over this range ($p=0.01$) and an accelerated
97 BMI growth trajectory ($p=0.008$) compared with unexposed youth (Figure1) [26].
98 While all these factors are attributed to the epidemic of GDM, intrauterine exposures
99 and gestational programming also play a role [25]. Coordinated efforts are required
100 to provide better perinatal management and postpartum diabetes prevention
101 strategies in order to alter these trends and to evade the 'vicious cycle' in which
102 diabetes begets more diabetes.

103 **2. GDM and perinatal programming**

104 Fetuses exposure to maternal diabetes have a higher risk of abnormal glucose
105 homeostasis in later life beyond that attributable to genetic factors [25,27,28].
106 Indeed, it is currently widely accepted that an abnormal *in utero* stimulus or 'insult'
107 has the ability to disrupt the normal pattern of fetal development, permanently
108 changing its body's structure, physiology and metabolism, thereby, predisposing to
109 chronic diseases in later life. This phenomenon is referred to as fetal or gestational

110 programming [28-32]. This hypothesis was first introduced by David J. Barker [29]
111 who proposed “...that poor fetal and early post-natal nutrition imposes mechanisms
112 of nutritional thrift upon the growing individual” leading to increased rates of future
113 cardiovascular disease [33-35], hypertension [36-38], and T2DM [33,39]. Since the
114 discovery that low birth weight is associated with increased risk of developing T2DM
115 and the metabolic syndrome [33,39], numerous epidemiologic and experimental
116 studies have confirmed these associations. In the current review, we will revise
117 epidemiological studies that support the fetal programming theory and analyze the
118 link between maternal diabetes and altered glucose homeostasis in the offspring. We
119 will also discuss the possible cellular and molecular mechanisms behind this
120 association.

121 *2.1 Epidemiology and clinical observations of fetal programming*

122 Dörner was among the first to provide epidemiological evidence that gestational
123 diabetes or even slightly impaired glucose tolerance during pregnancy increases the
124 risk of obesity and diabetes in offspring [40,41]. More direct evidence that adverse
125 intrauterine environment might predispose to long-term T2DM came from a follow-up
126 study of men and women from Hertfordshire, UK, in middle and later life whose body
127 measures at birth had been recorded, showing, for the first time, that those who had
128 had low birthweights presented increased risk of developing T2DM and impaired
129 glucose tolerance in adult life [39]. When this theory was first proposed, it was
130 regarded with much skepticism. The main criticism was that the sample selection
131 was biased due to losses to follow-up owing to missing data on birth or incomplete
132 identification. Other issues regarding the associations observed are potential
133 confounding socioeconomic and environmental factors which could attribute to the

134 chronic diseases, *per se*, such that low birthweight alone might not be dictated as an
135 independent risk factor. Notwithstanding, several other studies have confirmed this
136 association [33,42-48], further suggesting that maternal undernutrition is able to
137 permanently change insulin-glucose metabolism in the fetus, thus programming
138 insulin resistance and T2DM in the offspring. These observations indicate that there
139 is a linear inverse correlation between birthweight and T2DM. Nevertheless, *in utero*
140 exposure to high glucose concentrations and to maternal diabetes, forces the fetus
141 to increase its own insulin production, generally leading to excessively growth, a
142 condition known as large for gestation age or macrosomic fetus [3,49]. Among Pima
143 Indian Americans, a population with a particularly high prevalence of diabetes and
144 obesity, it was reported, for the first time, that the prevalence of T2DM was greatest
145 in those with the lowest and highest birthweights and the risk for subsequent
146 diabetes among higher birthweight infants (over 4.5 kg) was entirely associated with
147 maternal diabetes during pregnancy [45]. This demonstrates the importance of
148 intrauterine exposure to impaired maternal glucose metabolism, even within a
149 population that may have increased genetic susceptibility to T2DM. Further
150 epidemiologic [50-52] and experimental [53,54] studies have demonstrated that high
151 birthweight is associated with increased risk of T2DM in later life to the same extent
152 as low birthweight. Taken together, these data indicate that, in fact, not a linear-
153 inverse but a U-shaped relationship exists between weight at birth and future risk of
154 developing T2DM and obesity (“diabesity”), with increased risk at both ends of the
155 birthweight curve [31,32,45,51,52].

156 Given the increasing prevalence of “diabesity” among women of reproductive age in
157 developed and Westernized developing countries, this may decisively contribute to
158 the increasing frequency of high birth weight and therefore to greater diabetes

159 susceptibility in the offspring. Indeed, various studies have provided further evidence
160 that offspring of mothers with uncontrolled diabetes, either pre-existing or originating
161 during pregnancy, are 4-8 times more likely to develop diabetes in later life
162 compared to those born from non-diabetic mothers. And a female born from a GDM
163 pregnancy has a higher chance of developing GDM during her pregnancy, thus,
164 creating a recurring disease cycle [55-57]. A way to counteract this tendency would
165 be to avoid and/or adequately correct maternal overweight and/or maternal diabetes
166 during pregnancy [17,25]. In line with this, a recent follow-up study of children of
167 women un-treated versus treated for mild GDM demonstrated that treatment during
168 pregnancy is associated with lower fasting glucose in female offspring at ages 5-10
169 years but not in male offspring. However, none of the children of treated or untreated
170 mothers had diabetes at 5-10 years, suggesting that treatment of mild maternal
171 diabetes may not affect childhood obesity or metabolic health [58]. Therefore, the
172 possibility that fetal programming in the setting of maternal diabetes can have a
173 beneficial offspring effect that can be modified by treatment remains unknown.
174 Larger follow-up studies in pregnancy randomized trials are needed to provide
175 evidence that the diabetes cycle can be interrupted.

176 *2.2 Mechanisms*

177 *2.2.1 Pancreatic Development*

178 Accumulated evidence points for a fetal developmental programming of later glucose
179 metabolism dysfunction, however, the molecular mechanisms by which intrauterine
180 exposure to hyperglycemia contributes to the development of obesity and diabetes
181 are still not well understood. It is generally accepted that fetal programming results
182 from a combination of mechanisms acting at organ, tissue, cellular and molecular

183 levels [32]. For example, current knowledge on the development of the pancreas in
184 humans suggests that it may be particularly sensitive to an altered glucose and
185 amino acid environment as it achieves complete development during late gestation
186 and the perinatal period [29,32]. In fact, reduced β -cell mass was demonstrated in rat
187 fetuses of hyperglycemic dams, with reduced expression of insulin-like growth factor
188 2 [59]. Moreover, as recently reviewed by Portha *et al.*, the offspring of mild diabetic
189 mothers, induced experimentally by streptozotocin (STZ) that selectively destroys β -
190 cells, presented normal weight and enhanced percentage of pancreatic endocrine
191 tissue, leading to higher β -cell mass. On the other hand, fetuses from severe diabetic
192 dams were small at birth and had decreased pancreatic weight and degranulated β -
193 cells, leading to low pancreatic insulin content and low plasma insulin. The long-term
194 consequences evaluated in the progeny of these models revealed impaired glucose
195 tolerance in the offspring of mild STZ diabetic rats due to lower insulin secretion in
196 response to glucose, while insulin resistance was reported in the offspring of the
197 severe STZ diabetic mothers [60]. Additionally, Hales *et al.* suggest that poor early
198 development of islets of Langerhans and β -cells is a major factor in the etiology of
199 T2DM [29]. Such alteration in the pancreas development, though, only compromise
200 function later in life, when increasing physiologic requirements and over-solicitation
201 of insufficient organ mass start to induce organ damage [32].

202 *2.2.2 Placental role in GDM*

203 The placenta fulfills several critical roles during pregnancy: not only is the regulator
204 of materno-fetal transport of nutrients and gases but also a source of hormonal
205 signals that influence maternal and fetal metabolism [30]. The placenta is in a
206 continuous state of development throughout pregnancy with regulated periods of

207 branching angiogenesis, non-branching angiogenesis, trophoblast differentiation and
208 syncytium formation [30]. Thus, when exposed to intrauterine adverse conditions, the
209 placenta either changes the pattern of developmental (hormonal) signals to the fetus
210 or the amount of nutrients/oxygen transported to the fetus [30,61] to such an extent
211 that fetal development is altered, leading to long-term consequences throughout life
212 [30,61,62]. The timing of the disruption of this development pattern is critical to
213 determine the consequence on placental function and hence programming of the
214 fetus [30,32].

215 Placentas from GDM pregnancies present characteristic histological features such
216 as villous immaturity, villous fibrinoid necrosis, chorangiosis, and increased
217 angiogenesis [63]. Generally, if impaired glucose metabolism is diagnosed in the
218 early pregnancy, mainly structural dysfunctions are observed, whereas if detected in
219 late gestation, GDM will affect placental function to a greater extent inflammation and
220 oxidative stress that can lead to the chronic fetal hypoxia Diabetic insults at the
221 beginning of gestation instigates placenta adaptive responses to the diabetic
222 environment, such as buffering excess maternal glucose or increased vascular
223 resistance, which may lead to limited fetal growth. If the duration or extent of the
224 diabetic insult, including maternal hyperglycemia, hyperinsulinemia, or dyslipidemia,
225 exceeds the placental capacity to mount adequate responses, then excessive fetal
226 growth may ensue [64]. Furthermore gene expression studies suggest that GDM is
227 characterized by changes in trophoblast cells that include up-regulation of genes
228 involved in a multitude of cellular functions including, immune response, organ
229 development, regulation of cell death and also genes regulating inflammatory
230 responses and endothelial reorganization reflecting a state of chronic systemic

231 inflammation of placentas of women with GDM that could ultimately lead to the
232 chronic fetal hypoxia [65,66].

233 Fetal glucose production is minimal, therefore, the fetus depends almost completely
234 on the maternal glucose supply. Since glucose is able to cross the placenta, fetuses
235 from hyperglycemic mothers are inevitably predestined to grow in an environment of
236 greater than normal glucose concentration [32]. The transplacental glucose flux
237 follows as maternal-to-fetal concentration gradient and is handled by the transporter
238 isoforms of the glucose transporters (GLUTs) family of proteins. It has been shown,
239 however, that materno-fetal glucose transport is flow-limited and not regulated by
240 transporter availability [61,62]. Indeed, recent observations in placenta perfusion
241 studies found no difference in transplacental glucose transport between placentas
242 from GDM and normal pregnancies at a fixed maternal-to-fetal glucose gradient
243 [67,68]. Hence, these data indicate that the placenta is not involved in enhanced
244 maternal-to-fetal glucose transfer in GDM and that the increased glucose flux across
245 the placenta observed in GDM depends entirely on maternal-to-fetal concentration
246 gradient [61,62]. Regarding the long-term effects of *in utero* exposure to a
247 continuous range of high glucose concentrations throughout pregnancy, the
248 Pedersen hypothesis is generally accepted. According to this proposition, maternal
249 hyperglycemia increases glucose transfer to the fetus, thereby leading to fetal
250 hyperglycemia, which in turn stimulates islet cell proliferation and insulin production
251 [69]. This phenomenon generally leads to macrosomia, which has been associated
252 with increased risk of later obesity and diabetes [70,71]. Moreover the
253 overstimulation of fetal β -cells usually leads to hypertrophy of the tissue. This event,
254 coupled to a higher fetal utilization of glucose could explain several abnormal
255 structure and changes found in the newborn [69]. Indeed, the hyperglycemia and

256 adverse pregnancy outcome (HAPO) study suggested a positive linear correlation
257 between maternal glucose and a range of adverse outcomes for the baby, including
258 high birthweight and hypoglycemia [72].

259 *2.2.3 Development plasticity and epigenetics*

260 Many lines of evidence indicate that early life events play a powerful role in
261 influencing later susceptibility to certain chronic diseases, such as T2DM, coronary
262 heart disease, and hypertension. Despite all the explanations mentioned above, the
263 molecular mechanisms through which the intrauterine exposure to hyperglycemia
264 would translate into the development of diabetes are yet to be unraveled. An
265 increased understanding on the developmental plasticity- defined as the ability of an
266 organism to develop in various ways, depending on the particular environment [73],
267 provides a conceptual basis to understand the association between fetal
268 programming and adult disease. Developmental plasticity requires stable modulation
269 of gene expression, and this appears to be mediated, at least in part, by epigenetic
270 processes. In fact, accumulated evidence suggests that both the genome and the
271 epigenome can interactively influence the phenotype determining sensitivity to later
272 environmental factors and the subsequent risk of disease [74]. Recently published
273 studies provide supporting evidence that epigenetic modifications may establish a
274 better understanding on the mechanism whereby hyperglycemia influences T2DM in
275 the offspring [75,76].

276 Although the genetic code of an organism is homogeneous, each individual cell type
277 possesses its own gene-expression pattern that defines each cell's biological fate.
278 Stable alterations of this gene-expression profile are named 'epigenetic'
279 modifications because they are heritable changes in gene expression without

280 alteration of the DNA sequence [77]. Most of these heritable changes are
281 established during differentiation and are stably maintained through cell division,
282 enabling cells to have distinct identities while containing the same genetic
283 information [78]. DNA methylation and histone modifications are the best-known
284 epigenetic mechanisms [79]. DNA methylation is the most extensively studied
285 epigenetic signature [78] and it involves the covalent modification of cytosine
286 residues that precede guanines- CpG dinucleotides, with the “p” referring to the
287 phosphodiester bond between the cytosine and guanine nucleotides [80]. The CpG
288 dinucleotides are not evenly distributed across the human genome but are instead
289 clustered in CpG-rich regions known as CpG islands, spanning the 5’ regulatory end
290 of many genes [78]. On the other hand, histone proteins which comprise the
291 nucleosome core, contain a globular C-terminal domain and an unstructured N-
292 terminal tail. The N-terminal tails of core histones can normally be altered post-
293 translationally by a variety of modifications, including methylation, acetylation,
294 ubiquitylation, SUMOylation and phosphorylation [78]. Histone modifications can
295 function by changing the accessibility of chromatin or by recruiting and obstructing
296 non-histone effector proteins, leading to either activation or repression depending
297 upon which residues are modified and the type of modifications present. For
298 example, lysine acetylation usually correlates with transcriptional activation, whereas
299 lysine methylation leads to transcriptional activation or repression depending upon
300 which residue is modified and the degree of methylation [78]. Epigenetic marks are
301 mitotically stable but can also be subject to reprogramming in response to
302 environmental stimuli such as changes in diet, physical activity, *in utero* environment,
303 and pharmacological treatment [80]. Therefore, epigenetic signatures serve as a
304 connection between life environment and phenotypes.

305 Although data in humans are still limited, accumulating evidence has provided
306 insights into the involvement of epigenetic mechanisms in the developmental
307 programming of obesity and T2DM later in life. A study of individuals who were
308 prenatally exposed to famine during the Dutch Hunger Winter in 1944-1945
309 revealed, six decades later, lower DNA methylation of the imprinted *insulin-like*
310 *growth factor-2 (IGF2)* gene, which has a role in growth and development, compared
311 with their unexposed, same-sex siblings [81]. The same authors went on to further
312 characterize DNA methylation, from whole blood, at 15 genomic loci harboring genes
313 implicated in growth, development, and metabolic disease [82]. Again, adults who
314 had been exposed to prenatal famine, exhibited altered methylation levels in the
315 promoters of six of the chosen genes: DNA methylation of the *interleukin 10 (IL10)*,
316 *leptin (LEP)*, *ATP-binding cassette, sub-family A, member 1 (ABCA1)*, *guanine*
317 *nucleotide binding protein, alpha stimulating-antisense RNA (GNAS-AS)*, and
318 *maternally expressed 3 (MEG3)* gene promoters was higher among individuals
319 prenatally exposed to Dutch famine in comparison with their unexposed same-sex
320 siblings [82]. Another report demonstrated an association between macrosomic
321 babies and an increased placental methylation of the *glucocorticoid receptor* gene,
322 which is a well-known candidate gene for obesity [83]. This study not only associates
323 perinatal growth as a measure of the intrauterine environment with epigenetic
324 alterations of the *glucocorticoid receptor* gene but also suggests a critical role for
325 DNA methylation in determining placental function [83].

326 Recent studies have explored the role of epigenetics in offspring exposed to GDM.
327 For instance, two candidate-gene studies of placental tissue, maternal circulating
328 blood cells and cord blood cells from women with and without GDM, revealed that
329 maternal glucose levels were associated with placental *LEP* [84], and adiponectin

330 [85] methylation providing a potential link between maternal hyperglycemia, fetal
331 programming and long-term risk of obesity. Another study compared the methylation
332 pattern in peripheral blood leukocytes from non-diabetic adolescent Pima Indians
333 who were either offspring of diabetic mothers or offspring of non-diabetic mothers.
334 Using a methylated DNA immunoprecipitation (Me-DIP-chip) assay differential
335 methylated regions were assayed and subsequent *in silico* pathway analysis
336 identified maturity onset diabetes of the young (MODY), T2D and Notch signaling as
337 the top 3 enriched pathways with differentially methylated genes. These pathways
338 include genes which are important in pancreatic development, β -cell response to
339 glucose as well as insulin secretion [86], highlighting the potential impact of
340 intrauterine hyperglycemia on methylation of genes implicated in β -cell function,
341 thereby predisposing the offspring to increased risk of diabetes. Recently, a study
342 using the 2-step epigenetic Mendelian randomization approach found that maternal
343 glycemia is part of the causal pathways leading to higher leptin levels in cord blood
344 with DNA methylation as a mediator of this association [87]. This study supports that
345 maternal glycemia leads to epigenetic adaptations in the *LEP* region of the offspring,
346 potentially contributing to long-term programming of excessive adiposity later in life.
347 Although these studies provide exciting insights into possible epigenetic signatures
348 that may contribute to long-term programming of obesity and metabolic disorders,
349 one has to bear in mind that small samplings were included and these studies also
350 lack of independent replication, hence the methylation changes detected often do not
351 reach biological levels of significance.

352 It is relevant to mention that children whose mothers had diabetes during pregnancy
353 are at increased risk of becoming obese and developing diabetes at young ages.
354 Furthermore, many of these female offspring already have diabetes or abnormal

355 glucose tolerance by the time they reach their reproduction age, prolonging the cycle
356 of diabetes [88]. There is some evidence that epigenetic and phenotypic traits
357 induced by early life environment can be passed from one generation to the next
358 [89], however, there is no evidence that it is the case for GDM.

359 **3. Clinical aspects**

360 As stated before, GDM is associated with short and long term complications, both for
361 the mother and for the child. Fetal and newborn short-term complications include
362 respiratory distress syndrome [90], prematurity, breech presentation [91],
363 hypoglycemia, hyperbilirubinemia, macrosomia and death [92]. Macrosomia, defined
364 as fetal weight over 4000g, is the most common fetal complication, and is associated
365 with several perinatal adverse outcomes, such as acute fetal distress, birth trauma
366 and emergency cesarean section [92]. In addition to these immediate risks, there are
367 significant long-term risks of later life obesity, glucose intolerance, hypertension and
368 cardiovascular disease in children of diabetic mothers [49].

369 The HAPO study has firmly established that maternal hyperglycemia, even at levels
370 that do not meet the definition of GDM, is closely linked to macrosomia and
371 excessive fetal growth [49] and also establishes a directly proportional relationship
372 between maternal glycaemia and primary cesarean-section and neonatal
373 hypoglycemia [72]. Also, treating milder hyperglycemia with lifestyle interventions
374 and/or drug therapy, reduces mean blood sugar levels and improves outcomes. Two
375 randomized trials using insulin have shown that glucose lowering strategies reduce
376 birth weight, the proportion of large for gestational age infants, cesarean-section and
377 perinatal morbidity [93,94]. Moreover, several publications about the use of oral

378 hypoglycemic agents, such as glibenclamide and metformin for the treatment of
379 GDM [95-97], have shown the same results in terms of glycemic control or
380 pregnancy outcomes compared with insulin. Even though, treatment of GDM,
381 whether with diet or with pharmacologic intervention, has shown to improve maternal
382 and infant outcome in the short term, no long-term studies evaluating the impact of
383 maternal glycemic control on the child's future metabolic complications are available.
384 The current diagnosis of GDM is made during the late second trimester, which
385 means the pathological state has already been established influencing the
386 programming of the fetus.

387 Different testing strategies have been evaluated for diagnosis of GDM to improve
388 maternal and infant health. A recent study by Farrar *et al.* has evaluated and
389 compared different testing strategies for the diagnosis of GDM. For instance, when
390 comparing 75-gram oral glucose tolerance test (OGTT) versus 100-gram OGTT,
391 women given the 75-gram OGTT had a higher relative risk of being diagnosed with
392 GDM, however there was insufficient evidence to allow assessment of which
393 strategy is best for GDM diagnosis [98]. Furthermore, this trial did not evaluate when
394 is the best timing during pregnancy to test women with GDM. The formal diagnostic
395 criteria for GDM involve an OGTT at 24- 28 weeks gestation. Different countries and
396 organizations have different standards and cut-off points to define normal glucose
397 tolerance and to define GDM but the International Association of Diabetes and
398 Pregnancy Study Group (IADPSG) has recently determined new and lower
399 thresholds, in the light of data indicating that glucose lowering strategies improve
400 pregnancy outcomes even in women with mild glucose intolerance [93]. Although a
401 glucose challenge test at 24-28 weeks is diagnostically robust, it has the
402 disadvantage of being time consuming and difficult to extend to the whole

403 population. Another big disadvantage is the time during pregnancy when the test is
404 performed, since it does not facilitate early management of GDM, exposing the fetus
405 to a hyperglycemic environment for the whole of the first and part of the second
406 trimester. This is important because there is evidence that fetuses exposed during
407 early pregnancy to hyperglycemia had accelerated growth patterns from the first
408 trimester onwards [99], highlighting the need for development of diagnostic models
409 for GDM early in pregnancy to better stratify and predict risk of long term GDM-
410 related complications and offer targeted intervention.

411 **4. Conclusion and implications for prevention**

412 Maternal diabetes is strongly linked to adverse pregnancy outcome, with clear
413 evidence that exposure to maternal diabetes *in utero* has long term adverse effects
414 on the offspring. This likely occurs due to epigenetic modifications of the fetal
415 genome, and as such could be averted by therapy applied during pregnancy.
416 Although treatment of extreme maternal hyperglycaemia improves pregnancy
417 outcomes in the short term, the long term effects of treatment, and the threshold of
418 maternal glycemia at which therapy is optimally applied is unknown. Further
419 research is required to address both of these important issues. Possible topics of
420 research that could help improve clinical GDM treatment and prevention of fetal
421 programming are summarised in Table 1.

Table 1. Strategies for improving GDM treatment and prevention of intrauterine programming

Epidemiology Research	Molecular Research
<ul style="list-style-type: none"> • Large, well-designed trials to provide information about the best strategies to identify women with GDM. • Determine whether better glucose control throughout pregnancy would prevent the long-term consequences on the offspring. 	<ul style="list-style-type: none"> • Identification of the mechanisms underlying insulin resistance in human pregnancy. • Identification of non-invasive early-screening tests for GDM. GDM diagnosis need to be accurate, acceptable to pregnant women and affordable.

422

423

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 427 study.

428 6. References

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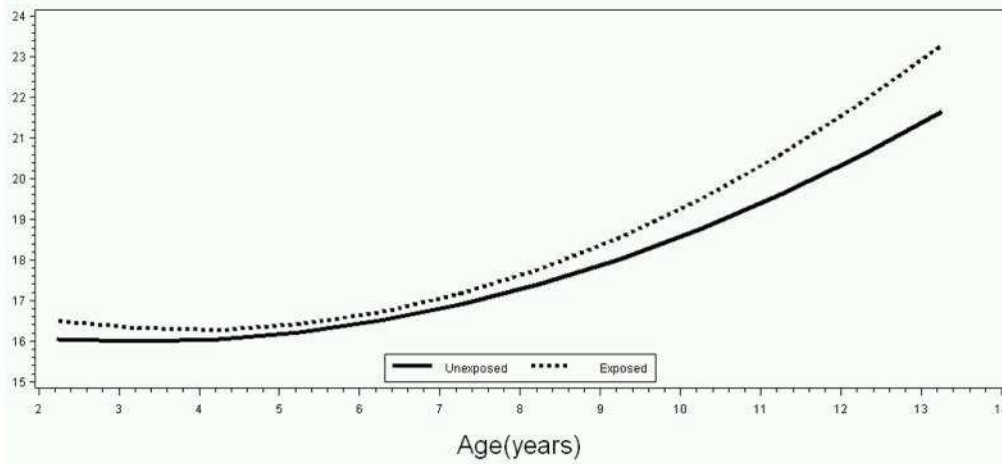
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695 **Figure legend**

696 **Figure 1. Mean BMI curves for youth both exposed and unexposed to maternal**
697 **diabetes *in utero* from 27 months of age to 13 years, adjusted for sex,**
698 **race/ethnicity.** *Reprinted from The Journal of Pediatrics, Volume 158, Issue 6,*
699 *Crume TL, Ogden L, Daniels S, Hamman RF, Norris, JM and Dabelea D, The Impact*
700 *of In Utero Exposure to Diabetes on Childhood Body Mass Index Growth*
701 *Trajectories: The EPOCH Study, Copyright (2011), with permission from Elsevier*
702 *[26].*

703

BMI Growth Trajectory from 27 Months to 13 Years

Adjusted for sex, race/ethnicity

Effect of ExposureAverage BMI: $p=0.01$ BMI trajectory: $p=0.008$

Highlights

- Gestational diabetes prevalence is increasing globally.
- Fetal programming predisposes for future diseases in diabetic mothers and offspring.
- Need to establish perinatal management and postpartum diabetes prevention strategies.
- Long term complications could be predicted by early-pregnancy diagnostic models for GDM.