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Intergenerational Transmission of Glucose Intolerance and Obesity by In Utero Undernutrition in Mice

Josep C. Jimenez-Chillaron,1 Elvira Isganaitis,1 Marika Charalambous,2 Stephane Gesta,1 Thais Pentinat-Pelegrin,3 Ryan R. Faucette,1 Jessica P. Otis,1 Alice Chow,1 Ruben Diaz,3,4 Anne Ferguson-Smith,2 and Mary-Elizabeth Patti1

OBJECTIVE—Low birth weight (LBW) is associated with increased risk of obesity, diabetes, and cardiovascular disease during adult life. Moreover, this programmed disease risk can progress to subsequent generations. We previously described a mouse model of LBW, produced by maternal caloric undernutrition (UN) during late gestation. LBW offspring (F1-UN generation) develop progressive obesity and impaired glucose tolerance (IGT) with aging. We aimed to determine whether such metabolic phenotypes can be transmitted to subsequent generations in an experimental model, even in the absence of altered nutrition during the second pregnancy.

RESEARCH DESIGN AND METHODS—We intercrossed female and male F1 adult control (C) and UN mice and characterized metabolic phenotypes in F2 offspring.

RESULTS—We demonstrate that 1) reduced birth weight progresses to F2 offspring through the paternal line (C - C = 1.64 g, C - UN = 1.57 g, P < 0.05; UN - C = 1.64 g; UN - UN = 1.60 g, P < 0.05), 2) obesity progresses through the maternal line (percent body fat: C - C = 22.4%, C - UN = 22.9%; UN - C = 25.9%, P < 0.05; UN - UN = 27.5%, P < 0.05), and 3) IGT progresses through both parental lineages (glucose tolerance test area under curve C - C = 100; C - UN = 122, P < 0.05; UN - C = 131, P < 0.05; UN - UN = 151, P < 0.05). Mechanistically, IGT in both F1 and F2 generations is linked to impaired β-cell function, explained, in part, by dysregulation of Sirt1 expression.

CONCLUSIONS—Maternal undernutrition during pregnancy (F0) programs reduced birth weight, IGT, and obesity in both first- and second-generation offspring. Sex-specific transmission of phenotypes implicates complex mechanisms including alterations in the maternal metabolic environment (transmaternal inheritance of obesity), gene expression mediated by developmental and epigenetic pathways (transpaternal inheritance of LBW), or both (IGT). Diabetes 58:460–468, 2009

Human and animal studies have demonstrated a strong association between intrauterine growth retardation/low birth weight (LBW) and increased susceptibility to cardiovascular disease, obesity, and type 2 diabetes during adult life (1–5). This association has been conceptualized by the developmental programming hypothesis, which proposes that environmental stimuli acting during critical windows of development, including fetal and/or early postnatal periods, can induce permanent alterations in cell/tissue structure and function (5).

A growing body of epidemiologic evidence indicates that the effects of developmental programming can be perpetuated to subsequent generations, even in the absence of further environmental stressors during intrauterine and early postnatal life (6,7). For example, offspring of LBW humans also have reduced birth weight (8), increased cardiovascular risk factors (8), and increased susceptibility to metabolic syndrome and type 2 diabetes (7). Similarly, intergenerational effects on birth weight, glucose tolerance, and hypothalamic function have been demonstrated in rat models of fetal programming (9–13). While multiple mechanisms may link nutritional imbalance during early life with transgenerational transmission of metabolic phenotypes, epigenetic mechanisms have gained particular prominence for several reasons (14–16). First, alterations in nutrition during development can alter epigenetic marks, including DNA methylation (12,17–19) and histone modifications (17,20,21) in rodents. Second, epigenetic marks are stable and can be inherited in somatic cells through mitosis or, if occurring in the germ line, through meiosis (22–24). Thus, inheritance of nutritionally induced epigenetic modifications through meiosis may contribute to intergenerational effects.

We have previously described a mouse model of intrauterine growth restriction induced by maternal global caloric restriction during pregnancy (25,26). LBW males develop severe glucose intolerance with aging (25), with major contributions from both obesity and impaired β-cell function. To assess intergenerational effects in this model, we intercrossed F1 males and females to 1) evaluate adiposity and β-cell function in second-generation offspring and 2) to determine whether intergenerational inheritance is transmitted through the maternal and/or paternal line. Finally, we assessed expression of candidate genes potentially regulated by epigenetic mechanisms which might contribute to metabolic phenotypes in first- and second-generation offspring.

From the 1Research Division, Joslin Diabetes Center, Harvard Medical School, Boston, Massachusetts; 2Cambridge University, Cambridge, U.K.; 3Hospital Sant Joan de Deu, Universitat de Barcelona, Barcelona, Spain; and the 4Division of Endocrinology, Children’s Hospital Boston, Harvard Medical School, Boston, Massachusetts.

Corresponding author: Mary-Elizabeth Patti, mary.elizabeth.patti@joslin.harvard.edu.

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J.C.J.-C. is currently affiliated with Hospital Sant Joan de Deu, Universitat de Barcelona, Barcelona, Spain.

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RESEARCH DESIGN AND METHODS

Protocols were approved by the Joslin Diabetes Center Institutional Animal Care and Use Committee. Virgin ICR females (6–8 weeks old, parental generation F₀) were caged with ICR males (Fig. 1A). Pregnancy was dated by vaginal plug (day 0.5). F₁ females were housed individually with ad libitum access to Purina 5F chow. On pregnancy day 12.5, F₂ females were assigned to either control (C) or undernutrition (UN) groups randomly. Food intake of F₂-UN dams was restricted from day 12.5 until delivery by 50% compared with that consumed by F₂ controls (25). Litters were equalized to eight pups per dam by removing both the heaviest and lightest mice in the litter, thus retaining those with birth weight closest to the median for each litter. Offspring of F₂ mice were designated as first-generation offspring (F₁) (Fig. 1A). After delivery, all F₂ mothers received chow ad libitum. F₂ pups nursed freely and were weaned at 3 weeks onto 9F chow, provided ad libitum. C and UN females from the F₁ generation were mated at age 2 months with C and UN males from the F₀ generation (Fig. 1A). After confirmation of pregnancy, females were caged individually and fed ad libitum with no dietary manipulation during pregnancy. Pups were designated as second-generation offspring (F₂; C™C™ or UN™UN™; both parents are controls); C™UN™ (female UN, male control); and UN™UN™ (both parents UN). F₂ mice were weaned at 3 weeks onto 9F chow ad libitum; only males were followed for metabolic analysis given the higher prevalence of diabetes in UN-F₁ males (100 vs. 30% in females, as described previously, 50% global caloric restriction of F₀ dams during the last week of gestation blunted feto-maternal growth and resulted in 15% decrease in offspring birth weight (F₂-UN) (25)). In pregnancies of F₁ mice, both maternal food intake and feto-maternal weight gain (supplementary Table 2) were similar among the four experimental groups. Despite this, birth weight was modestly, but significantly, reduced in C™UN™ and UN™UN™ offspring compared with C™C™ (Fig. 1B); UN™UN™ mice had normal birth weight compared with controls. Litter size and length of gestation were similar in all groups (supplementary Table 2). After delivery, all four F₂ groups had similar weights to 40 weeks (Fig. 1C).

Since feto-maternal nutritional status during pregnancy might account for observed differences in birth weight, we determined both maternal and fetal serum concentrations of major macronutrients contributing to fetal growth. In F₀-UN females, caloric restriction resulted in 34% reduction in serum glucose and 80% reduction in triglycerides by day 16.5 of gestation (P < 0.05, Table 1). Likewise, serum insulin and leptin were reduced in F₀-UN dams by 77 and 94%, respectively (P < 0.05) (Table 1). Maternal dysregulation of fuel metabolism was also accompanied by alterations in fetal metabolism. Fetal glucose and leptin levels were decreased by 45 and 65%, respectively, in ED16.5 F₁-UN fetuses (P < 0.05) (Table 2), while triglycerides, free fatty acids (FFAs), glycerol, and insulin did not differ from controls (not shown).

By contrast, during the F₁ generation pregnancy, maternal glucose, triglycerides, FFAs, insulin, and leptin did not differ between groups at pregnancy day 16.5 (Table 1). However, serum glycerol was increased by 49 and 59% in dams of C™C™ and UN™UN™ pregnancies, respectively (P < 0.05) compared with C™C™ (Table 1). Despite no major differences in maternal metabolism, we observed some differences in ED16.5 F₂ fetuses. Glucose levels were increased by 66% in UN™UN™ fetuses (P < 0.05), and insulin increased by 41% in UN™UN™ fetuses (P < 0.05) (Table 2). There were no significant differences in UN™C™ fetuses.

Intergenerational inheritance of glucose intolerance.

Glucose levels in F₂ males did not differ in either fed (Fig. 2A) or fasting conditions (supplementary Fig. 1A) up to 10

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FIG. 1. Experimental design, birth weight, and growth curves. A: Experimental design, including breeding scheme for second-generation (F₂) offspring. Circles designate females and squares designate males. Note that mating pairs were nonsiblings. Metabolic analysis was performed in males only. B: Body weight at birth for F₂ offspring. C: Postnatal growth curves for F₂ male mice. For all panels, values are means ± SE (n = 15 mice/group). *P < 0.05; **P < 0.01 vs. C™C™ (ANOVA).
reduced glucose-stimulated insulin secretion may also
be explained in part by a 23% reduction in Kir6.2 expression in
F1-UN islets (Fig. 4B). In contrast, Kir6.2 expression was normal in both F1 and F2
control male and UN-UN female × control male.

<table>
<thead>
<tr>
<th></th>
<th>Control</th>
<th>Undernourished</th>
<th>Control female × control male</th>
<th>Undernourished female × control male</th>
<th>Undernourished female × undernourished male</th>
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<tr>
<td>Blood glucose (mg/dl)</td>
<td>99 ± 3</td>
<td>65 ± 4*</td>
<td>111 ± 6</td>
<td>103 ± 5</td>
<td>105 ± 4</td>
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<tr>
<td>Serum insulin (ng/ml)</td>
<td>0.84 ± 0.33</td>
<td>0.19 ± 0.13*</td>
<td>1.6 ± 0.36</td>
<td>1.7 ± 0.22</td>
<td>2.0 ± 0.41</td>
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<tr>
<td>Serum leptin (ng/ml)</td>
<td>7.2 ± 1.9</td>
<td>0.42 ± 0.22*</td>
<td>32.9 ± 0.6</td>
<td>34.3 ± 0.5</td>
<td>38.7 ± 14</td>
</tr>
<tr>
<td>Serum TG (mg/dl)</td>
<td>218 ± 29</td>
<td>44 ± 27*</td>
<td>156 ± 47</td>
<td>202 ± 15</td>
<td>210 ± 47</td>
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<tr>
<td>Serum glycerol (mg/dl)</td>
<td>41.8 ± 5.7</td>
<td>32.4 ± 5.9</td>
<td>37 ± 5.1</td>
<td>55 ± 10.5*</td>
<td>59 ± 6.8*</td>
</tr>
<tr>
<td>Serum FFAs (mmol/l)</td>
<td>1.2 ± 0.17</td>
<td>1.0 ± 0.13</td>
<td>1.2 ± 0.20</td>
<td>1.5 ± 0.19</td>
<td>1.6 ± 0.23</td>
</tr>
</tbody>
</table>

Data are means ± SE. Maternal serum levels of hormones and nutrients at pregnancy day 16.5. *P < 0.05 vs. controls. Significance was determined by Student’s t test in F1 dams and ANOVA in F2 dams. TG, triglycerides.

months of age. Likewise, serum levels of triglycerides, glycerol, and FFAs were also similar among the four F2 groups at 2 and 4 months (not shown). However, UN-UN offspring had lower serum insulin and 30 min after a glucose load compared with C-C mice, developed hyperinsulinemia in the fed state between 4 and 8 months of age (P < 0.05) (Fig. 2B). Fasting insulin was similar in all F2 groups (supplementary Fig. 1B). To better define glucose homeostasis, we performed intraperitoneal glucose tolerance testing in all F2 mice. Strikingly, glucose tolerance was impaired (relative to C-C) in C-UN and UN-UN mice, and UN-UN mice between 4 and 6 months of age (P = 0.03, P = 0.003, and P = 0.007, respectively) (Fig. 3A).

We next explored potential mechanisms responsible for glucose intolerance in F2 offspring of UN parents. UN-UN mice were clearly insulin resistant (assessed by insulin tolerance) by age 6 months (P < 0.001) (Fig. 3B). By contrast, C-C and UN-NE mice exhibited normal insulin sensitivity.

Since glucose intolerance may also reflect dysregulation of insulin secretion, we assessed glucose-stimulated insulin secretion in vivo and ex vivo. We first measured serum insulin with fasting and 30 min after a glucose load (glucose tolerance test) (Fig. 4A); glucose-stimulated insulin secretion was reduced in F2 offspring from F1-UN parents compared with C-C mice at age 4 months (P < 0.05 for all comparisons) (Fig. 4A). Likewise, ex vivo glucose-stimulated insulin secretion was also impaired in islets from 4-month-old UN-UN mice (P < 0.05 for both) but not C-UN mice (Fig. 4B). Thus, reduced glucose-stimulated insulin secretion may also contribute to impaired glucose tolerance (IGT) in F2 mice.

One potential candidate underlying insulin secretory dysfunction in F2 mice is altered expression and/or function of the β-cell ATP-dependent K+ channel, composed of Sur1/Kir6.2 subunits. We assessed the functional capacity of this complex using in vivo challenge with the sulfonylurea tolbutamide (1 mg/kg i.p.). Tolbutamide induced a 15% increase in serum insulin after 30 min in C-C mice (P < 0.05) (Fig. 4C) (supplementary Fig. 2A). In contrast, F2 offspring from UN parents had impaired tolbutamide response (Fig. 4C) (supplementary Fig. 2A). Paralleling in vivo data, tolbutamide stimulated insulin release from freshly isolated C-C islets by fivefold (Fig. 4D), while responses in all other groups were significantly reduced, with only minor increases in C-UN and UN-UN islets and no effect in UN-C mice (Fig. 4D). We also incubated islets with diazoxide, a potassium channel stimulator. Diazoxide tended to reduce insulin release from C-C islets (>50%, P = 0.1) (supplementary Fig. 2B). Interestingly, response in C-C islets was nearly normal, but diazoxide had only minimal effect in C-UN and UN-UN islets (5–10% decrease) (supplementary Fig. 2B). Together, these data suggest that dysfunctional potassium channel activity may contribute to impaired insulin secretion in F2 mice.

To determine whether alterations in expression might contribute to dysfunction of potassium channels, we assessed Sur1 and Kir6.2 expression in isolated islets. Sur1 expression was reduced by 23% (P < 0.05) in F1-UN islets (Fig. 4E). Likewise, Sur1 expression was reduced by 33% in C-UN islets (P < 0.05), by 50% in UN-UN islets (P < 0.05), and by 38% in UN-UN islets (P < 0.05) (Fig. 4E). By contrast, Kir6.2 expression was normal in both F1 and F2 islets (Fig. 4F).

Since epigenetic regulation at the Sur1 locus might be mechanistically linked to differential expression in F2 offspring of LBW mice, we assessed DNA methylation...
within CpG islands at the Sur1 promoter using methylation-sensitive PCR (27); we did not detect differential methylation in either F1 (Supplementary Fig. 3) or F2 islets (not shown).

**Intergenerational inheritance of obesity.** We have previously shown that F1-UN males develop increased adiposity as early as 2 months of age (26). In the F2 generation, both maternal lineage offspring groups developed increased adiposity by 4 months (P < 0.05) (Fig. 5A). Interestingly, adiposity in UN♀-UN♂ mice is largely visceral in location (Fig. 5A). In parallel, serum leptin is increased in UN♀-UN♂ mice (P < 0.05) (Fig. 5B). We observed no differences in epididymal adipocyte size distribution or histology (not shown) or in adipose expression of genes regulating differentiation and/or metabolic function, including peroxisome proliferator–activated receptor γ, CCAAT/enhancer binding protein α, fatty acid binding protein 4, and Glut4, from any F2 group at 4 months of age (supplementary Table 3).

Since obesity in UN♀-UN♂ mice implicates a contribution from epigenetic factors, we determined expression of imprinted genes known to regulate adipocyte development and/or function and thus potentially contributing to obesity, including preadipocyte factor 1 (Pref1) (30), Necdin (31), and paternally expressed gene 1 (Peg1) (32). Pref1, an inhibitor of adipogenesis expressed from the paternally inherited chromosome, was reduced in epididymal fat from F1-UN males (P < 0.05) and from both paternal F2 lineages, C♀-UN♂ and UN♀-UN♂ (P < 0.01) (Figs. 5C and D). This effect appeared restricted to Pref1 since expression of Necdin and Peg1, also paternally expressed, was not statistically different from controls in either F1 or F2 offspring (Figs. 5C and D). In addition, expression of retrotransposon-like 1 (Rtl1) and mater-
nally expressed 2 (Gtl2), two genes also regulated by the same imprinting signals as Pref1 (28), did not differ among groups in F1 and F2 offspring (not shown).

To determine whether changes in Pref1 gene expression were related to differential methylation at this imprinted locus, we assessed DNA methylation by Southern blotting. We did not detect any alterations in DNA methylation at the Pref1 differentially methylated region, the intergenic
differentially methylated region, or the *Gtl2* promoter region (supplementary Fig. 4A and B).

**DISCUSSION**

Human data indicate that metabolic phenotypes associated with exposure to maternal undernutrition can also be observed in second-generation offspring. Conceptually, transgenerational inheritance of disease risk may be mediated by nongenomic mechanisms, including either 1) epigenetic mechanisms (16) or 2) other broader indirect mechanisms associated with parental physiology (rev. in 6). First, alterations in nutrition during development can alter epigenetic marks, thus regulating gene expression through DNA methylation (12,17–19) and/or histone modifications (17,20,21). Interestingly, such epigenetic modifications may progress with aging during postnatal life, in association with metabolic phenotypes, as recently observed at the pancreatic duodenal homeobox-1 and GLUT4 locus in rodent models of intrauterine programming (33–35). If these epigenetic changes occur in the germ line, they can be inherited through meiosis (22–24), thus providing a plausible explanation for intergenerational effects, transmitted via either maternal or paternal lines.

In addition, other indirect biological processes may influence phenotypes in subsequent generations. For example, uterine size is reduced in girls that are born small (F1) and remain short (36); this may influence fetal growth and reduce weight in their progeny (F2) (rev. in 6). Therefore, physical constraints may alter birth size through the maternal lineage. Furthermore, maternal metabolism may also influence cross-generational phenotypes (37). Maternal undernutrition during pregnancy (F0) increases risk for developing diabetes and obesity in her offspring (F1). When these high-risk adult F1 females become pregnant, the metabolic stress of pregnancy may result in hyperglycemia and/or overt gestational diabetes that may, in turn, contribute to fetal hyperinsulinemia, obesity, and increased diabetes risk in F2 offspring (37).

**FIG. 5.** Characterization of the obese phenotype. A: Total and visceral fat mass by dual-energy X-ray absorptiometry in 4-month-old males (*n* ≥ 6 mice/group). B: Serum leptin levels in 4-month-old males (*n* ≥ 6/group). C and D: Expression of imprinted genes assessed by quantitative PCR in epidydimal fat from 4-month-old F1 males (*n* = 6/group) and 4-month-old F2 males (*n* = 6/group). Results are expressed as means ± SE. *P* < 0.05 vs. C♀-C♂; **P** < 0.01 vs. C♀-C♂ (ANOVA).
For these two examples, intergenerational transmission of phenotypes would occur exclusively through the maternal lineage, as opposed to epigenetic mechanisms.

Since it is difficult to dissect the relative parental contributions and the molecular mechanisms that lead to $F_2$ offspring outcomes in humans, we have utilized our mouse model of maternal undernutrition during pregnancy to address these important questions. We have previously shown that global caloric restriction during the last week of gestation in pregnant females ($F_0$) impairs fetal growth, resulting in 15–20% reduction in birth weight, and the development of both obesity and glucose intolerance in $F_1$ offspring (25,26). These alterations are multifactorial in origin, with glucose intolerance mediated, in part, by impaired glucose-stimulated insulin secretion (25). We now demonstrate that metabolic phenotypes are also observed in the $F_2$ generation: 1) reduced birth weight progresses from $F_1$ to $F_2$ through the paternal, but not the maternal, line (Fig. 1B); 2) $F_2$ offspring of both $F_1$-UN males and females develop IGT with aging, in parallel with β-cell dysfunction (Figs. 3A and 4A and B) and, in $\text{UN}^-\text{UN}^\pm$, insulin resistance (Figs. 2B and 3B); and 3) obesity progresses through the maternal, but not the paternal, lineage (Fig. 5A).

**Intergenerational transmission of LBW.** Maternal undernutrition ($F_0$) during the last week of gestation results in reduced birth weight in both $F_1$ (25) and $F_2$ offspring of $F_1$-UN males ($\text{C}^-\text{UN}^\pm$ and $\text{UN}^-\text{UN}^\pm$) but not offspring of $F_1$-UN females ($\text{UN}^\pm\text{C}^-$) (Fig. 1B). Such patrilineal inheritance of reduced birth weight may be attributed to alterations in fetoplacental gene expression and/or function, most likely mediated by epigenetic modifications. While we did not detect major metabolic dysregulation in $\text{C}^-\text{UN}^\pm$ and $\text{UN}^-\text{UN}^\pm$ mice at embryonic day 16.5 (Tables 1 and 2), it is likely that more subtle or time-dependent effects on placental function account for paternally mediated reductions in birth weight in this setting.

While experimental (9,11,38,39) and human (40,41) data show similar paternal transmission patterns of birth weight, population-based studies also indicate that intergenerational aggregation of LBW can also occur through maternal lineages (40,41). Such results may reflect species differences and complex influences on human birth weight (e.g., genetics, maternal size). Furthermore, human population data generally exclude complicated pregnancies (e.g., gestational diabetes) and thus may also exclude the impact of fetal “overgrowth” due to increased nutrient supply in the context of previous maternal LBW.

**Intergenerational transmission of glucose intolerance.** $F_1$-UN males exhibit moderate hyperglycemia and IGT with aging and dysregulated glucose-stimulated insulin secretion (25). Additionally, all $F_2$ offspring of $F_1$-UN parents develop glucose intolerance by age 4 months (Fig. 3A). Therefore, intergenerational progression of glucose intolerance can derive from both the maternal and paternal lines. While maternal and grandmaternal inheritance of diabetes has been demonstrated in rats (9,11,38,39), here we present the first experimental evidence for transgenerational transmission of IGT also through the paternal lineage. In agreement, paternal LBW in humans has recently been linked to risk of metabolic syndrome in both offspring and grandoffspring (7).

We previously demonstrated that impaired glucose-stimulated insulin secretion is an early key phenotype in $F_1$-UN males (25). Multiple metabolic adaptations lead to β-cell dysfunction in $F_1$-UN mice, including altered glucokinase, hexokinase-1, and ATP-dependent K$^+$ channel activities (25) (J.C.J.-C., unpublished data). We now find that glucose-stimulated insulin secretion is also impaired in islets of $F_1$ mice from UN parents and is likely a major contributor to glucose intolerance (Fig. 4A and B). Additionally, we show that potassium channel activity is also altered in islets from $F_2$-UN offspring both in vivo and in vitro (Fig. 4C and D; supplementary Fig. 2A and B). Thus, it is interesting that expression of $\text{Sur}1$ is reduced by 30% in islets from both $F_1$-UN mice and islets from $F_2$ C$^-\text{UN}^\pm$, $\text{UN}^-\text{UN}^\pm$, and $\text{UN}^\pm\text{UN}^\pm$ mice (Fig. 4E), indicating that dysregulation of $\text{Sur}1$ gene expression and function can be transmitted to $F_2$ through both maternal and paternal lines. This effect was specific to $\text{Sur}1$, since Kir6.2 gene expression was normal in both $F_1$ and $F_2$ islets (Fig. 4F). Together, these data suggest that dysregulation of $\text{Sur}1$ expression may alter potassium channel function (42) and ultimately contribute to whole-body glucose intolerance in our model. In agreement, genetic ablation of $\text{Sur}1$ results in metabolic phenotypes similar to those of our mouse model. $\text{Sur}1^{-/-}$ mice remain euglycemic for the majority of their lifespan, displaying moderate glucose intolerance with aging (43,44). Isolated islets from $\text{Sur}1^-/-$ mice show impaired glucose-stimulated insulin secretion and lack of responsiveness to tolbutamide in vitro (43).

Which mechanism(s) is responsible for reduced $\text{Sur}1$ expression in both $F_1$ and $F_2$ islets? Since decreased $\text{Sur}1$ gene expression progresses to $F_2$ offspring through the paternal lineage, we hypothesized that reductions in $\text{Sur}1$ expression would be mediated, in part, by altered DNA methylation; however, we did not observe differences in methylation of the $\text{Sur}1$ proximal promoter region (supplementary Fig. 2). A potential limitation of our approach is that we utilized DNA from islets (a mixture of β-, α-, δ-, and PP cells), potentially masking β-cell–specific differences. Alternatively, reduced expression of $\text{Sur}1$ in islets from $F_1$ and $F_2$ mice might also be due to 1) altered methylation of another genomic region(s), 2) altered histone modification, or 3) changes in binding/expression of other transcription factors regulating $\text{Sur}1$. Future experiments will focus on potential mechanisms mediating decreased expression of $\text{Sur}1$.

An additional factor likely to contribute to impaired glucose tolerance in $\text{UN}^-\text{UN}^\pm$ mice is insulin resistance, observed by age 6 months (Figs. 2B and 3B). Of note, insulin resistance arises when both parents were growth restricted in utero, suggesting that interface between these two lineages is necessary and sufficient to induce insulin resistance. While the specific mechanisms underlying insulin resistance in $\text{UN}^-\text{UN}^\pm$ mice remain under investigation, it is interesting to note that $\text{UN}^-\text{UN}^\pm$ mice also display increased visceral fat by age 4 months (Fig. 5A). Therefore, it is tempting to speculate that insulin resistance may develop secondary to progressive accumulation of visceral fat in $\text{UN}^-\text{UN}^\pm$.

**Intergenerational transmission of obesity.** Childhood obesity is linked to parental obesity (45). Although it is difficult to dissect the relative contribution of shared environmental factors to these phenotypes in humans, maternal metabolic dysregulation during pregnancy may be a key contributor (46,47). We similarly demonstrate that adiposity phenotypes progress to $F_0$ offspring through the maternal lineage (Fig. 5A), implicating subtle maternal metabolic dysfunction during pregnancy and/or maternal epigenetic effects. It is important to note that despite
increased adiposity in these groups, body weight remained similar to that of controls (Fig. 1C). Therefore, offspring of F1-UN females do not have overt obesity but have a shift in body composition (higher fat mass with concomitantly reduced lean body mass) (26). On the other hand, although paternal transmission alone is not sufficient to drive adiposity in C\textsuperscript{2}-UN\textsuperscript{3} mice, paternal effects may contribute to the increased abdominal fat accumulation in UN\textsuperscript{2}-UN\textsuperscript{3} mice as compared with UN\textsuperscript{2}-C\textsuperscript{3} mice.

We next evaluated potential mechanisms mediating increased adiposity in UN\textsuperscript{2}-C\textsuperscript{3} and UN\textsuperscript{2}-UN\textsuperscript{3} mice. First, food intake was similar in all groups (not shown). Second, expression of adipocyte differentiation markers, including peroxisome proliferator-activated receptor \(\gamma\), CCAAT/enhancer binding protein \(\alpha\), fatty acid binding protein 4, or Glut4, was similar in all F1 and F2 groups (supplementary Table 3) (E.L., J.C.J.-C., M. Woo, A.C., J. DeCoste, M. Vokes, M. Liu, S. Kasif, A.-M. Zavacki, R. Leshan, M. Myers, M.E.P., unpublished data). Similarly, we observed no major differences in adipocyte size distribution among F2 groups (not shown). Additional studies will be required to determine whether alterations in adipocyte metabolic function or in systemic energy homeostasis also contribute to adiposity.

Since obesity in UN\textsuperscript{2}-UN\textsuperscript{3} mice implicate a partial role for epigenetic factors, it is very interesting that Pref\textsuperscript{1} expression was significantly decreased in F1-UN, C\textsuperscript{2}-UN\textsuperscript{3}, and UN\textsuperscript{2}-UN\textsuperscript{3} mice (Fig. 5C and D). Patrilineal inheritance of Pref\textsuperscript{1} expression may be explained by the fact that it is expressed from the paternally inherited chromosome; altered expression would be predicted to be inherited from F1-UN males but not F1-UN females. Mice lacking functional Pref\textsuperscript{1} have increased adiposity (48); conversely, mice overexpressing Pref\textsuperscript{1} have reduced fat content (49) (A.F.-S., unpublished data). Thus, decreased Pref\textsuperscript{1} expression may contribute, in part, to development of obesity in F1-UN, UN\textsuperscript{2}-C\textsuperscript{3}, and UN\textsuperscript{2}-UN\textsuperscript{3} mice. While our data support a potential role of Pref\textsuperscript{1} in the development of adiposity in our mouse model, it has to be noted that its expression has been determined in epididymal fat, a depot without direct parallel in humans. Thus, although many adipose genes are similarly expressed in both rodents and humans (50), extrapolation of Pref\textsuperscript{1} gene expression data from our model to humans must be undertaken with caution.

Imprinting of Pref\textsuperscript{1} is under complex control by both paternal and maternal alleles (28). We did not detect changes in methylation of the differentially methylated regions that regulate imprinting at this locus in face from 4-month-old mice of either F1 or F2 generations (supplementary Fig. 4). These data suggest that, as with Sut\textsuperscript{1}, altered expression of Pref\textsuperscript{1} is due to either changes in expression or function of an upstream transcription factor, histone modification, or another yet-unknown genomic region that is epigenetically modified. Thus, additional studies are required to define the potential role of epigenetics in adipose development in our model.

In conclusion, we demonstrate that maternal undernutrition during pregnancy programs reduced birth weight, glucose intolerance, and obesity in first- and second-generation offspring, even despite ad libitum feeding during second pregnancy. Different aspects of these phenotypes are transmitted via the maternal lineage (obesity), the paternal lineage (reduced birth weight), or both (glucose intolerance). Sex differences in transmission of phenotypes implicate complex mechanisms: 1) matrilineal inheritance of disease is multifactorial and includes metabolic, epigenetic, and mitochondrial mechanisms; and 2) patrilineal inheritance is primarily due to epigenetic mechanisms. While we do not yet understand the complex array of molecular mechanisms associated with fetal programming of disease, such studies will be of great importance for the design of future therapeutic interventions aimed to prevent and/or modulate adult phenotypes, not only in LBW humans but also in their children and grandchildren.

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