Male Men1 heterozygous mice exhibit fasting hyperglycemia in the early stage of MEN1

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Abstract

Multiple endocrine neoplasia type 1 (MEN1) is an autosomal dominant inherited syndrome characterized by multiple tumors in the parathyroid glands, endocrine pancreas and anterior pituitary. Recent clinical studies have revealed a strong association between MEN1 syndrome and the risk of developing diabetes mellitus; however, the underlying mechanisms remain unknown. In this study, heterozygous Men1 knockout (Men1+/-) mice were used as MEN1 models to investigate MEN1-associated glucose metabolic phenotypes and mechanisms. Heterozygous deficiency of Men1 in 12-month-old male mice induced fasting hyperglycemia, along with increased serum insulin levels. However, male Men1+/- mice did not show insulin resistance, as evidenced by Akt activation in hepatic tissues and an insulin tolerance test. Increased glucose levels following pyruvate challenge and expression of key gluconeogenic genes suggested increased hepatic glucose output in the male Men1+/- mice. This effect could be partly due to higher basal serum glucagon levels, which resulted from pancreatic islet cell proliferation induced by heterozygous loss of Men1. Taken together, our results indicate that fasted male Men1+/- mice, in the early stage of development of MEN1, display glucose metabolic disorders. These disorders are caused not by direct induction of insulin resistance, but via increased glucagon secretion and the consequent stimulation of hepatic glucose production.

Introduction

Multiple endocrine neoplasia type 1 (MEN1) is an autosomal dominant inherited syndrome characterized by multiple occurrences of endocrine tumors affecting the parathyroid glands, endocrine pancreas and anterior pituitary (Thakker et al. 2012). Menin, encoded by MEN1, is a tumor suppressor, and its loss of function causes MEN1 syndrome (Marx 2005). It is widely expressed in various tissues, including metabolic tissues such as the pancreas and liver (Guru et al. 1999). In their study on preventing gestational diabetes in pregnant mice, Karnik and coworkers reported that menin expression in the islets is physiologically suppressed by prolactin (Karnik et al. 2007). Furthermore, acute ablation of Men1 in β-cells could prevent and/or treat hyperglycemia in diabetic mice (Yang et al. 2010a,b). Cheng and coworkers (2011) and Cao and coworkers (2013) demonstrated that hepatocyte-specific
knockout of Men1 in mice does not affect glucose metabolism during aging and under a high-fat diet (HFD). However, Wuescher and coworkers reported that liver-specific heterozygous deletion of Men1 leads to glucose intolerance in HFD-fed mice rather than standard diet-fed mice (Wuescher et al. 2011, 2012). These studies suggest that menin plays an important role in glucose metabolism.

MEN1 patients exhibit higher prevalence of impaired fasting glucose levels and diabetes mellitus (DM) (Wagner et al. 2005, McCallum et al. 2006, van Wijk et al. 2012). Clinical studies based on homeostasis model assessment (HOMA) have revealed that patients with MEN1 are insulin resistant (Wagner et al. 2005, McCallum et al. 2006, van Wijk et al. 2012). Heterozygous Men1 knockout (Men1+/-) mice develop endocrine tumors similar to those observed in MEN1 patients (Crabtree et al. 2001, Bertolino et al. 2003, Loffler et al. 2007). However, it is currently unknown whether these mice show abnormalities in glucose homeostasis, similar to MEN1 patients. To investigate MEN1-associated glucose metabolic phenotypes and mechanisms and to better understand the clinical manifestations of MEN1, Men1+/- mice were used as MEN1 models in this study.

Our data showed that heterozygous deletion of Men1 resulted in impairment of glucose metabolism in 12-month-old male mice; however, it did not induce insulin resistance. Instead, it promoted glucagon production and increased hepatic glucose output (HGO), which together contributed to increased glucose levels in Men1+/- males.

Materials and methods

Animal model

All animal protocols were approved by the Animal Ethics Committee of the Xiamen University. Men1+/−/− (C57BL/6) mice heterozygous for the Men1 locus (Men1+) were a gift from Francis Collins (National Human Genome Research Institute, Bethesda, MD, USA). They were housed in a pathogen-free environment in a 12h light:12h darkness cycle and given free access to water and standard chow diet. Studies were conducted using the Men1+/- mice as a model for MEN1, with age-matched wild-type (Men1+/-) mice as controls. Because mice developed multiple endocrine tumors late in life (Crabtree et al. 2001, Bertolino et al. 2003, Loffler et al. 2007), Men1+/- mice at the age of 12 months (the early stage of development of MEN1) and 18 months (the middle-advanced stage of development of MEN1) were used in this study. Mice were fasted for 24 h, anesthetized with 1.2% avertin (240 mg/kg body weight) and then their blood was collected by cardiac puncture. One hour before administration of the anesthetic, the mice were weighed and injected intraperitoneally with bromodeoxyuridine (BrdU; Sigma-Aldrich) in phosphate-buffered saline (PBS) at a dose of 50 mg/kg body weight. The whole pancreas and liver were harvested for histological and molecular biological analyses, respectively. Concentrations of fasting serum hormones, including insulin, glucagon, glucose-dependent insulinotropic polypeptide (GIP), glucagon-like peptide-1 (GLP-1), ghrelin, leptin, plasminogen activator inhibitor-1 (PAI-1) and resistin, were estimated with the Bio-Plex Pro Mouse Diabetes Standard 8-Plex Assay (Bio-Rad).

Glucose tolerance test

After an overnight fast, mice were weighed and injected intraperitoneally with a bolus of glucose (2 g/kg body weight). Blood glucose levels were determined from tail blood before and, at the indicated time points, after glucose injection with a OneTouch UltraEasy glucometer (LifeScan, Milpitas, CA, USA).

Insulin tolerance test

Mice were fasted for 5 h before receiving an intraperitoneal injection of insulin (0.75 U/kg) in PBS. Blood glucose concentrations were estimated in tail blood before and, at the indicated time points, after insulin injection.

Pyruvate tolerance test

Overnight fasted mice were injected intraperitoneally with sodium pyruvate (2 g/kg body weight). Blood glucose values were tested from tail blood before and, at the indicated time points, after sodium pyruvate injection.

Western blotting analysis

After the indicated animal experiments, liver tissues were lysed in ice-cold radioimmunoprecipitation assay buffer (Beyotime Institute of Biotechnology, Nantong, China). Protein concentrations were determined with a BCA Protein Assay Kit (Pierce). Tissue lysates (50 µg protein) were separated by 10% sodium dodecyl sulfate-polyacrylamide gel electrophoresis and electrophoretically transferred onto a polyvinylidene difluoride membrane. After blocking for 60 min at room temperature in Tris-buffered saline containing 0.1% Tween 20 and 5% nonfat milk, the membranes were incubated overnight at 4°C with anti-pAkt

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(Ser473) antibody (Cell Signaling, #9271), anti-Akt antibody (Cell Signaling, #9272), anti-pIRS-1 (Tyr632) antibody (Santa Cruz, sc-17196), or anti-GAPDH antibody (Epitomics, P04406). The membranes were washed thrice with Tris-buffered saline containing 0.1% Tween 2 and incubated with horseradish peroxidase-conjugated secondary antibodies, and then the protein levels were detected using an enhanced chemiluminescence kit (Millipore).

Quantitative polymerase chain reaction analysis

Total RNA was extracted from frozen liver tissues using TRIzol reagent (Invitrogen). One microgram of total RNA was reverse transcribed into cDNA using the PrimeScript RT Reagent Kit with gDNA Eraser (TaKaRa, Dalian, China) according to the manufacturer’s instructions. Quantitative polymerase chain reaction (qPCR) was performed as described previously (Xu et al. 2013) using an ABI StepOne detection system (Applied Biosystems) with the primer sequences, which are listed in Table 1. Mouse Gapdh was used as an internal control.

Immunohistochemistry

Four-micrometer-thick sections of formalin-fixed, paraffin-embedded mouse pancreatic tissues were cut and placed consecutively onto silanized glass slides, and were routinely dewaxed and rehydrated. After rinsing with PBS, the sections were immersed in 3% hydrogen peroxide solution for 10 min to block endogenous peroxidase activity. For DNA denaturation, sections were placed in 2M HCl for 30 min. Antigens were retrieved in 0.1% trypsin solution for 20 min at 37°C. Nonspecific binding was prevented by incubation in 5% normal goat serum for 15 min in a humidified chamber. The sections were

Table 1 Primers used for qPCR analysis.

<table>
<thead>
<tr>
<th>Sequence name</th>
<th>Primers</th>
<th>Temperature (°C)</th>
<th>Size (bp)</th>
</tr>
</thead>
<tbody>
<tr>
<td>mG6pc-F</td>
<td>5′-GTGCACTGAAAGCTGTCTGTG-3′</td>
<td>63</td>
<td>139</td>
</tr>
<tr>
<td>mG6pc-R</td>
<td>5′-TCCGGAGGCTGGATTGTG-3′</td>
<td>61</td>
<td>139</td>
</tr>
<tr>
<td>mPck1-F</td>
<td>5′-GAACTGACAGACTGCCCCTATGT-3′</td>
<td>62</td>
<td>165</td>
</tr>
<tr>
<td>mPck1-R</td>
<td>5′-GTGCAAGGCCCCAGTTTG-3′</td>
<td>60</td>
<td>165</td>
</tr>
<tr>
<td>mGapdh-F</td>
<td>5′-AACAGAAACTCCACTCTCTC-3′</td>
<td>58</td>
<td>111</td>
</tr>
<tr>
<td>mGapdh-R</td>
<td>5′-CCTTTGCTGTAGCGTGTT-3′</td>
<td>58</td>
<td>111</td>
</tr>
</tbody>
</table>

Figure 1

Male Men1<sup>−/−</sup> mice exhibit fasting hyperglycemia. (A) Blood glucose levels after 24 h of fasting in 12-month-old and 18-month-old mice (n=20 and 6, respectively). (B) Serum insulin levels 24 h after fasting in 12-month-old Men1<sup>+/+</sup> and Men1<sup>−/−</sup> mice (n=10). (C) Glucose tolerance test in 12-month-old vs 18-month-old male mice (n=6). Data are presented as the mean ± S.E.M. *P<0.05, **P<0.01.

Figure 2

Insulin resistance is not induced in male Men1<sup>−/−</sup> mice. (A) Body weights of 12-month-old Men1<sup>+/+</sup> and Men1<sup>−/−</sup> mice (n=20). (B) The activity (phosphorylated serine 473 on Akt) and total levels of Akt and the tyrosine phosphorylation of IRS-1 in the liver were evaluated after 24 h of fasting (n=10). (C) An insulin tolerance test was performed (n=6), in 12-month-old Men1<sup>−/−</sup> vs Men1<sup>−/−</sup> male mice. Data are presented as the mean ± S.E.M. *P<0.05, **P<0.01, ***P<0.001.

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then incubated with anti-BrdU antibody (Sigma, B2531) overnight at 4°C. After washing with PBS, antibody binding was detected with horseradish peroxidase-conjugated secondary antibody (Fuzhou Maixin Biotechnology Co, Ltd, Fuzhou, China) at 37°C. The sections were visualized with diaminobenzidine solution, and then lightly counterstained with hematoxylin. As DNA denaturation is not required for anti-glucagon antibody (Abcam, ab10988), the antigens were retrieved in 10mM citrate buffer (pH 6.0) for 15 min in a pressure cooker.

**Statistical analysis**

Data are presented as the mean ± standard error of the mean (s.e.m.). For data at single time point, statistical differences were evaluated by unpaired Student’s t-test or one-way analysis of variance (ANOVA), as appropriate. Datasets with multiple time points (e.g., GTT, ITT and PTT) were analyzed by repeated-measures ANOVA. A P value of < 0.05 was considered significant.

**Results**

**Male Men1<sup>+/−</sup> mice exhibit fasting hyperglycemia**

Because the association between MEN1 and DM risk was primarily established by measuring fasting plasma glucose levels, we first evaluated the fasting glucose and insulin levels in mice at 12 months of age. As shown in Fig. 1A and B, relative to wild-type controls, female Men1<sup>+/−</sup> mice showed normal glucose regulation, whereas both fasting blood glucose and serum insulin levels were significantly increased in male Men1<sup>+/−</sup> mice. Nevertheless, heterozygous loss of Men1 in male mice did not induce significant impairment in the ability to clear a glucose load during GTT (Fig. 1C). To confirm impaired glucose metabolism in the middle-advanced MEN1 mouse model, we estimated blood glucose levels in the mice at 18 months of age. Surprisingly, fasting blood glucose level in the Men1<sup>+/−</sup> male was similar to that in the Men1<sup>+/+</sup> controls (Fig. 1A). A small but significant improvement in glucose tolerance was observed in Men1<sup>+/−</sup> male mice during GTT (Fig. 1C).

**Insulin resistance is not induced in male Men1<sup>+/−</sup> mice**

The increased fasting blood glucose and serum insulin levels observed in humans with MEN1 is classically interpreted to be a consequence of insulin resistance. Obesity is known to cause insulin resistance and alterations in glucose metabolism (Kahn et al. 2006). In this study, no significant difference in body weight was observed between male Men1<sup>+/−</sup> mice and the Men1<sup>+/+</sup> control group, and female Men1<sup>+/−</sup> mice weighed even less than their controls (Fig. 2A). These findings suggest that the effect of heterozygous lack of Men1 on metabolism is not mediated by obesity.

Insulin resistance affects multiple tissues, including the liver and muscle (Bajaj & Defronzo 2003). Overproduction of glucose by the liver, despite the presence of hyperinsulinemia, is primarily responsible for fasting hyperglycemia (Rodan & Bernroider 2003). Therefore, we examined insulin signaling in the liver by using the phosphorylation of Akt on serine 473 as a marker of insulin action. Relative to wild-type controls, the phosphorylation of serine 473 on Akt in the liver of Men1<sup>+/−</sup> males is found to be significantly increased (Fig. 2B). No change in total Akt level was observed. Thus, the activity of Akt, a downstream target of insulin, is not inhibited in Men1<sup>+/−</sup> males. Consistent with this, we observed a significant increase in the tyrosine phosphorylation of insulin receptor substrate 1 (IRS-1), which is another crucial target of insulin signaling (Fig. 2B). These data demonstrate that the heterozygous absence of Men1 does not cause direct impairment of insulin signaling in mice. To further investigate the effect of heterozygous ablation of Men1 on insulin sensitivity, we performed ITT in male mice. Insulin sensitivity was significantly enhanced in male Men1<sup>+/−</sup> mice (Fig. 2C). These data suggest that the increased glucose and insulin levels observed in the male Men1<sup>+/−</sup> mice are not caused by the underlying insulin resistance.

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**Figure 3**

Male Men1<sup>+/−</sup> mice display increased hepatic glucose output. (A) Pyruvate tolerance test was performed (n = 6), and (B and C) the expression levels of gluconeogenic genes (mG6pc and mPck1) in the liver were analyzed after 24 h of fasting (n = 10), in 12-month-old Men1<sup>+/+</sup> vs Men1<sup>+/−</sup> male mice. Data are presented as the mean ± s.e.m. *P < 0.05, **P < 0.01.
Male \( \text{Men}^{1/-} \) mice display increased HGO

The heterozygous deficiency of \( \text{Men}1 \) does not induce insulin resistance, but causes an increase in glucose and insulin levels. An obvious reason for this increase is that heterozygous knockout of \( \text{Men}1 \) in males promotes HGO, which is primarily derived from gluconeogenesis under fasting conditions (Wahren & Ekberg 2007). Pyruvate is a major substrate for gluconeogenesis; therefore, to determine if the male \( \text{Men}^{1/-} \) mice exhibited increased glucose production, we performed PTT. As expected, \( \text{Men}^{1/-} \) mice exhibited higher blood glucose levels upon pyruvate administration, suggesting increased hepatic glucose production (Fig. 3A). The gluconeogenesis pathway is catalyzed by several key enzymes, including phosphoenolpyruvate carboxykinase (PCK1) and glucose-6-phosphatase (G6PC), which are the first and last rate-limiting enzymes of the process, respectively (Zhang et al. 2014). Consistent with the results of the PTT, hepatic mRNA levels of G6pc were significantly higher in fasted \( \text{Men}^{1/-} \) mice than those in fasted \( \text{Men}^{1/+} \) mice (Fig. 3B). Although Pck1 mRNA was also slightly increased...
Men1+/− mice exhibit fasting hyperglycemia

Research

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*Gao and others

Men1+/− mice exhibit fasting hyperglycemia

352

Effects of other serum hormones involved in lipid and glucose metabolism

To enhance our understanding of metabolic phenotypes in Men1+/− mice, we also examined the levels of other serum hormones involved in lipid and glucose metabolism (Fig. 5). Female Men1+/− mice had higher serum leptin and lower serum ghrelin levels than the Men1+/+ controls (Fig. 5C and D). No significant differences were found in the levels of other hormones between the two genotypes.

Discussion

Glucose homeostasis involves the maintenance of a delicate balance between its production and utilization. Failure of glucose homeostasis leads to diseased states, including hyperglycemia and DM. Type 1 diabetes arises from autoimmune-induced β-cell damage (Bluestone et al. 2010), whereas type 2 diabetes develops mainly because of insulin resistance (Kahn et al. 2014). Eventually, insulin production is insufficient for maintaining normal blood glucose levels, leading to hyperglycemia and secondary complications, including cardiovascular disease, kidney dysfunction and blindness (Bluestone et al. 2010, Kahn et al. 2014). In the current animal studies, we observed that, compared with 12-month-old male Men1+/+ mice, male Men1+/− mice had impaired glucose metabolism, characterized by high fasting blood glucose and serum insulin levels. These findings are consistent with previous clinical reports (Wagner et al. 2005, McCallum et al. 2006, van Wijk et al. 2012). Clinical studies based on HOMA have indicated that insulin resistance leads to glucose metabolic disorder in patients with MEN1 (Wagner et al. 2005, McCallum et al. 2006, van Wijk et al. 2012). However, we provide evidence that the effects of heterozygous loss of Men1 on glucose metabolism are not mediated by inducing insulin resistance. In the ITT, male Men1+/− mice displayed significantly enhanced glucose clearance rates. The activation of Akt in the liver also suggested that the Men1+/− males were not insulin resistant.

upregulated, no significant difference between the two genotypes was observed (Fig. 3C). These data suggest that heterozygous loss of Men1 promotes gluconeogenesis and basal glucose production in the liver.

Fasting hyperglycemia is associated with islet proliferation and increased fasting serum glucagon levels in male Men1+/− mice

Glucagon regulates HGO in the fasted state by increasing gluconeogenesis and glycogenolysis in the liver (Hancock et al. 2010, Ramnanan et al. 2011). Men1 is crucial for the development (Fontaniere et al. 2008) and proliferation of pancreatic islets (Karnik et al. 2005, Schnepf et al. 2006), and therefore plays an important role in regulating basal insulin and glucagon secretion in mice. Under the experimental conditions of this study, we observed hyperplasia of pancreatic islets and development of islet tumors in Men1+/− mice (Fig. 4A). Moreover, compared with Men1+/+ controls, male Men1+/− mice displayed a marked increase in pancreatic islet area and cell proliferation (Fig. 4B and C). Higher fasting serum glucagon levels and glucagon immunohistochemical staining were observed in male Men1+/− mice, indicating that the increased glucagon level contributed significantly to the elevated HGO and blood glucose levels in the male Men1+/− mice under fasting conditions (Fig. 4D and E).
The increase in blood glucose levels in the absence of insulin resistance suggests that heterozygous knockout of Men1 in male mice promotes HGO. Excess production of glucose from the liver is achieved by either increasing gluconeogenesis or by stimulating glycolysis (Roden & Bernroider 2003). Under physiological conditions, during prolonged fasting, hepatic gluconeogenesis plays a crucial role in maintaining normal plasma glucose levels (Wahren & Ekberg 2007). Compared with the Men1+/+ controls, male Men1+/- mice displayed increased glucose levels after pyruvate administration. Consistent with the results of the PTT, hepatic mRNA level of the gluconeogenic gene, G6pc, was significantly higher in fasted male Men1+/- mice than in their control male mice, providing further evidence that heterozygous knockout of Men1 promotes gluconeogenesis and hepatic glucose production, leading to an elevation in fasting plasma glucose concentration.

The increased HGO observed in this study was unexpected, because the male Men1+/- mice displayed increased glucose and insulin levels, which normally act to suppress HGO (Edgerton et al. 2006, Ramnanan et al. 2010). As Akt phosphorylation was activated in the livers of male Men1+/- mice, insulin resistance may not be the reason for the increased HGO. Therefore, the obvious reason for the increased HGO is the increase in glucagon levels in male Men1+/- mice, despite the high levels of glucose and insulin. In 12-month-old male Men1+/- mice, increased fasting glucagon levels were observed as a result of pancreatic islet cell proliferation induced by heterozygous ablation of Men1. In mice, the majority of cells within the islets are insulin-secreting β-cells (approximately 65–75%), whereas glucagon-secreting α-cells represent less than 20% of the individual islet area (Brissova et al. 2005). Therefore, dilatation of α-cells via proliferation would be expected to have a greater physiological impact on glucose homeostasis than dilatation of an equivalent or even greater number of β-cells. This would explain the increase in fasting serum glucagon concentration and, consequently, impaired fasting blood glucose, despite the elevated fasting serum insulin levels.

Male Men1+/- mice exhibited fasting hyperglycemia at the age of 12 months, but demonstrated improved glucose tolerance at the age of 18 months. Previous clinical studies on patients with MEN1 have revealed that most early islet lesions tested positive for glucagon, whereas the advanced hormone-secreting islet tumors detected in the same patients were mainly insulinomas (Anlauf et al. 2006, Perren et al. 2007). These results indicate that glucagon-positive early lesions may be replaced or overtaken by insulinomas and mixed islet tumors during tumorigenesis. This hypothesis is supported by the recent reports that Men1 ablation in α-cells leads to the formation of insulinomas (Lu et al. 2010, Shen et al. 2010), which might provide a possible explanation for the dynamic change in glucose metabolism in Men1+/- males.

Although no difference in body weight was observed between the genotypes in male mice, female Men1+/- mice weighed significantly less than their controls and exhibited higher serum leptin and lower serum ghrelin levels. The reduction in body weight may have been caused by either a decrease in food intake or an increase in energy expenditure. Because leptin and ghrelin can act centrally to decrease and increase feeding, respectively, the higher leptin and lower ghrelin levels in female Men1+/- mice may reflect their lower food intake (Klok et al. 2007, Nogueiras et al. 2008).

In this study, all mice were under fasting condition. Whether higher blood glucose levels emerge in female Men1+/- mice challenged with feeding and whether refeeding alters the metabolic phenotype in male Men1+/- mice remain to be elucidated. Moreover, we noticed differences in glucose metabolic phenotypes and body weight between male and female mice. Currently, the reason(s) underlying the observed sexually dimorphic metabolic phenotypes remain unclear. Furthermore, studies on gonadectomized or ovariectomized mice need to be conducted to eliminate the influence of sex hormones.

In summary, we elucidated the glucose metabolic phenotype of mice exhibiting the early stage of development of MEN1. In male Men1+/- mice, pancreatic islet proliferation induced by heterozygous knockout of Men1 increased fasting basal serum glucagon concentration. It subsequently promoted hepatic gluconeogenesis, resulting in impaired fasting blood glucose levels, despite an increase in insulin concentration and insulin sensitivity.

Declaration of interest
The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of the research reported.

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Author contributions

G-H J and M-Q X designed the experiments and revised the manuscript; Z-X-Z G, I, W-T X, S-Q W, X-R B, Y-L G and H-J Z performed the experiments and acquired the data; Q-Z H, Y C and Z-E W contributed to the separation of the desired tissues; Z-X-Z G, M-Q X and G H-J analyzed the data; and Z-X-Z G wrote the manuscript.

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