Effects of glutamine supplementation on oxidative stress-related gene expression and antioxidant properties in rats with streptozotocin-induced type 2 diabetes

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Abstract

There are close links among hyperglycaemia, oxidative stress and diabetic complications. Glutamine (GLN) is an amino acid with immunomodulatory properties. The present study investigated the effect of dietary GLN on oxidative stress-relative gene expressions and tissue oxidative damage in diabetes. There were one normal control (NC) and two diabetic groups in the present study. Diabetes was induced by an intraperitoneal injection of nicotinamide followed by streptozotocin (STZ). Rats in the NC group were fed a regular chow diet. In the two diabetic groups, one group (diabetes mellitus, DM) was fed a common semi-purified diet while the other group received a diet in which part of the casein was replaced by GLN (DM-GLN). GLN provided 25 % of total amino acid N. The experimental groups were fed the respective diets for 8 weeks, and then the rats were killed for further analysis. The results showed that blood thioredoxin-interacting protein (Txnip) mRNA expression in the diabetic groups was higher than that in the NC group. Compared with the DM group, the DM-GLN group had lower glutamine fructose-6-phosphate transaminase 1, a receptor of advanced glycation end products, and Txnip gene expressions in blood mononuclear cells. The total antioxidant capacity was lower and antioxidant enzyme activities were altered by the diabetic condition. GLN supplementation increased antioxidant capacity and normalised antioxidant enzyme activities. Also, the renal nitrotyrosine level and Txnip mRNA expression were lower when GLN was administered. These results suggest that dietary GLN supplementation decreases oxidative stress-related gene expression, increases the antioxidant potential and may consequently attenuate renal oxidative damage in rats with STZ-induced diabetes.

Key words: Glutamine; Diabetes; Thioredoxin-interacting protein; Glutamine fructose-6-phosphate transaminase 1; Nitrotyrosine

Diabetes mellitus (DM) is a metabolic disorder characterised by hyperglycaemia, disturbance of macronutrients, and the development of micro- and macrovascular complications. Increasing evidence from both experimental and clinical studies suggests that there are close links among hyperglycaemia, oxidative stress and diabetic complications(1,2). There are four main hypotheses about how hyperglycaemia causes diabetic complications: (1) increased polyol pathway flux; (2) increased hexosamine pathway flux; (3) activation of protein kinase C (PKC) isofoms; (4) increased advanced glycation end-product (AGE) formation. These metabolic pathways are major contributors to reactive oxygen species (ROS) overproduction and high oxidative stress during hyperglycaemia(2–4).

Glutamine (GLN) is the most abundant free amino acid in the circulation. Several studies have demonstrated that GLN has immunomodulating properties and suppresses inflammatory responses(5,6). GLN is required during catabolic processes to manifest optimal tissue responses to catabolism, inflammation and infection. It is considered an essential amino acid during certain diseases(7,8). A previous study has found that supplementing a high-fat diet with GLN attenuated hyperglycaemia in a diabetic rodent model(9). A study by Greenfield et al.(10) demonstrated that GLN improved glycaemic control in type 2 diabetic patients. A recent study performed by our laboratory has also shown that supplemental dietary GLN decreased leucocyte adhesion molecule expression and oxidative stress in organs of mice with type 1 diabetes(11).

Abbreviations: ABTS, 2,2′-azino-di-(3-ethylbenzthiazoline sulphonate); AGE, advanced glycation end product; AR, aldose reductase; BMC, blood mononuclear cell; DM, diabetes mellitus; GFAT, glutamine fructose-6-phosphate transaminase 1; GLN, glutamine; GPx, glutathione peroxidase; GSH, reduced glutathione; GSSG, oxidised glutathione; NC, normal control; PKC, protein kinase C; RAGE, receptor of AGE, ROS, reactive oxygen species; SOD, superoxide dismutase; STZ, streptozotocin; Txnip, thioredoxin-interacting protein.

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GLN is the precursor for the synthesis of glutathione (GSH). There is a significant correlation between GLN supply and intracellular GSH content[12]. There is increasing evidence that GLN supplementation enhances antioxidant capacity in various diseases[13,14]. Because interruption of the production of superoxide would normalise the polyol pathway flux, AGE formation, PKC and NF-κB activation in diabetes[14], we hypothesised that GLN supplementation reduces oxidative stress and thus decreases the associated pathway flux. Therefore, erythrocyte antioxidant enzyme activities and the total antioxidant capacity were measured. On the other hand, we analysed gene expressions of proteins in blood mononuclear cells (BMC) including aldose reductase (AR), glutamine fructose-6-phosphate transaminase 1 (GFAT) and PKC. AR is the first enzyme in the polyol pathway. It catalyses the NADPH-dependent reduction of various carbonyl compounds. GFAT is the rate-limiting enzyme in the hexosamine pathway that converts glucose to glucosamine[5,4]. Abnormal activation of PKC was implicated in decreased glomerular production of NO induced by diabetes[15]. Also, the receptor of AGE (RAGE) and thioredoxin-interacting protein (Txnip) gene expressions were measured in the present study. The RAGE is a multi-ligand receptor of cell surface molecules. Binding of AGE to the RAGE activates a number of pathways implicated in chronic inflammation and the development of diabetic complications[16]. Thioredoxin is a highly conserved thiol reductase that interacts with the endogenous inhibitor Txnip[17,18]. Hyperglycaemia inhibits thioredoxin’s ROS-scavenging function by inducing Txnip[19]. A previous report has found that Txnip expression significantly increases in diabetic animals, and may have implications in the development of end-stage organ damage in diabetics[17]. The present study was designed to investigate the effects of dietary GLN on oxidative stress-related gene expressions and its antioxidant properties. Because the kidneys are the major site of AGE clearance[20], and diabetic nephropathy is a complication that usually occurs in patients with poorly controlled disease, we evaluated oxidative damage to the kidneys in this streptozotocin (STZ)-induced diabetic model.

Materials and methods

Animals

Male Wistar rats, 6-weeks old, weighing 180–200 g at the beginning of the experiment were used in the present study. All rats were housed in a temperature- and humidity-controlled room and were allowed free access to a standard chow diet for 1 week before the study. Care of the laboratory animals was in full compliance with the Guide for the Care and Use of Laboratory Animals (National Research Council, 1996), and the protocols were approved by the Institutional Animal Care and Use Committee at Taipei Medical University.

Study protocols

Rats were assigned to one normal control (NC, n 8) group and two diabetic groups (n 10, each). Diabetes was induced by an injection of 150 mg nicotinamide/kg (Sigma Chemical, St Louis, MO, USA) followed by STZ (Sigma) at a dose of 65 mg/kg after 15 min via an intraperitoneal route. The induction procedure was repeated 1 d later. Nicotinamide was dissolved in 0·9 % saline, and STZ was dissolved immediately before use in sodium citrate (0·05 mol/l; pH 4·5). This is a well-established animal model to imitate type 2 diabetes[21]. Nicotinamide was used to protect pancreatic β-cells against STZ toxicity in order to build up a relative insulin-deficient state in rats that mimic type 2 diabetes[22]. Animals were allowed to eat laboratory chow ad libitum for 1 week. Rats with 12 h fasting blood glucose levels exceeding 2000 mg/l were considered diabetic. Rats in the NC group were fed a regular chow diet. In the two diabetic groups, one group (DM) was fed a common semi-purified diet, while the other group (DM-GLN) was provided an identical diet except that part of the casein was replaced by GLN, which provided 25% of total amino acid N. This amount of GLN was found to have beneficial effects on DM rodents[11]. The experimental diets were isonitrogenous and identical in energy and nutrient distributions (Table 1). After feeding the respective diets for 8 weeks, all rats were anaesthetised and killed by drawing arterial blood from the aorta of the abdomen. Blood samples were collected in tubes containing K2-EDTA (Sigma) and immediately centrifuged at 1500 g for 10 min to separate the plasma. Packed erythrocytes were washed three times with isotonic saline. The kidneys were rapidly excised. All samples were stored at −80°C until further analysed.

Measurement of plasma biochemical parameters

Plasma glucose concentrations at the end of the study were determined by colorimetric methods after an enzymatic reaction with peroxidase (Randox, Antrim, Ireland). TAG, total cholesterol, HDL-cholesterol and LDL-cholesterol, creatinine and blood urea N were analysed by an autoanalyser (Hitachi 7170, Hitachi Limited, Tokyo, Japan). The procedures followed the manufacturers’ instructions.

Table 1. Composition of the experimental diets (g/kg)

<table>
<thead>
<tr>
<th>Components</th>
<th>DM</th>
<th>DM-GLN</th>
</tr>
</thead>
<tbody>
<tr>
<td>Soyabean oil</td>
<td>100</td>
<td>100</td>
</tr>
<tr>
<td>Casein</td>
<td>200</td>
<td>150</td>
</tr>
<tr>
<td>GLN</td>
<td>0</td>
<td>41·7</td>
</tr>
<tr>
<td>Salt mixture†</td>
<td>35</td>
<td>35</td>
</tr>
<tr>
<td>Vitamin mixture†</td>
<td>10</td>
<td>10</td>
</tr>
<tr>
<td>Methyl cellulose</td>
<td>31</td>
<td>31</td>
</tr>
<tr>
<td>Choline bitartrate</td>
<td>2·5</td>
<td>2·5</td>
</tr>
<tr>
<td>Met</td>
<td>3</td>
<td>3</td>
</tr>
<tr>
<td>Maize starch</td>
<td>618·5</td>
<td>626·8</td>
</tr>
</tbody>
</table>

DM, diabetes without glutamine; DM-GLN, diabetes with glutamine; GLN, glutamine.

† The vitamin mixture contained the following (mg/g): thiamin hydrochloride, 0·6; riboflavin, 0·6; pyridoxine hydrochloride, 0·7; nicotinic acid, 3; calcium pantothenate, 1·6; biotin, 0·05; cyanocobalamin, 0·001; retinyl palmitate, 1·6; d–α-tocopherol acetate, 20; cholecalciferol, 0·25; menaquinone, 0·005.
Measurement of the plasma total antioxidant capacity

The total antioxidant capacity was measured using an antioxidant assay kit (Cayman Chemical, Ann Arbor, MI, USA). The principle of the assay is the ability of aqueous and lipid antioxidants in the sample to inhibit the oxidation of 2,2′-azino-di-3-ethylbenzthiazoline sulphonate (ABTS) to $\text{ABTS}^+$ by metmyoglobin. The capacity of the antioxidants present in the sample to prevent ABTS oxidation was compared with that of standard Trolox, a water-soluble tocopherol analogue. All samples were diluted 1:30 with the assay buffer before being assayed. Trolox standards and reagent were prepared according to the manufacturer’s instructions. Then, 10 μl of Trolox standard and samples were loaded onto a ninety-six-well plate. Also, 10 μl of Trolox standard and samples were loaded onto a ninety-six-well plate. Also, 10 μl of Trolox standard and samples were loaded onto a ninety-six-well plate. Also, 10 μl of metmyoglobin and 150 μl of chromogen were added to the wells. The reaction was initiated by adding 40 μl H$_2$O$_2$ as quickly as possible. The plate was covered and incubated for 5 min at room temperature and was monitored at an absorbance of 750 nm in a spectrophotometer. Samples and Trolox standards were assayed in duplicate. Results are presented as nm Trolox equivalents.

Measurement of erythrocyte antioxidant enzyme activities, and reduced and oxidised glutathione contents

To 100 μl of packed erythrocytes, 300 μl of cold distilled water were added to lyse the cells. Then, the lysed erythrocytes were centrifuged at 15 000 g for 10 min. The supernatants were used to analyse the antioxidant enzyme activities including those of catalase, glutathione peroxidase (GPx), glutathione reductase and superoxide dismutase (SOD; Randox). Total glutathione and oxidised glutathione (GSSG) were measured by a previously described enzymatic method. The content of GSH was calculated as the difference between total glutathione and GSSG. To assay GSSG, we added 4 μl of 10 mM-1-methyl-2-vinylpyridinium (Sigma) to 70 μl of packed erythrocytes (derivatised sample), mixed them and kept at room temperature for 1 h. After that, buffer A (200 μM-NADPH, 2 units/ml glutathionine reductase and 2 mM-EDTA in 50 mM-phosphate buffer) and buffer B (10 mM-5,5′-dithiobis-2-nitrobenzoic acid in 50 mM-phosphate buffer) were immediately added to 10 μl of the derivatised sample. The change in the optical density at 5 min was measured with a spectrophotometer at 405 nm. To determine total glutathione, buffers A and B were added to erythrocytes, and absorption was measured at 405 nm. The glutathione content was calculated on the basis of a standard curve generated with a known concentration of glutathione. Enzyme activities, and GSH and GSSG contents are expressed per mg Hb. Hb was determined by an autoanalyzer (Hitachi).

Total RNA extraction

Blood samples were applied to a Ficoll-Hypaque gradient (Amersham Biosciences, Piscataway, NJ, USA), and BMC were separated by density gradient centrifugation with a density of 1.077 g/ml for 30 min at 650 g and 4°C. BMC were washed twice with sterilised PBS (Sigma) and resuspended in 0.5 ml PBS. Total RNA from BMC was isolated using the Qiagen RNeasy Mini Kit (Qiagen, Crawley, Sussex, UK) according to the manufacturer’s protocol. Total RNA of the kidneys was obtained from 50 mg tissue by the guanidine isothiocyanate extraction method, using the Trizol Reagent (Invitrogen, Carlsbad, CA, USA). Chloroform was added and allowed to stand at room temperature for 10 min. After centrifugation, the aqueous phase with RNA was transferred to a microtube. Cold isopropanol was added to the aqueous phase and precipitated by centrifugation. The RNA pellet was washed twice with 75% ethanol. The pellet was air-dried and dissolved in RNase-free water. The total RNA solution was stored at −80°C for a subsequent assay. The concentration of RNA was determined and quantified by measuring the absorbance at 260 and 280 nm on a spectrophotometer.

Real-time RT-PCR

The primers of the housekeeping gene (β-actin), AR, GFAT, PKC, RAGE and Txnip were purchased from Mission Biotech (Taipei, Taiwan). Primer sequences used for the quantitative RT-PCR assays are listed in Table 2. RNA was reverse-transcribed using an RT system (Fermentas, Vilnius, Lithuania). Briefly, 12 μl water containing 1 μg RNA were mixed with 1 μl oligo (dT) primer (0.5 μg/μl) and incubated for 5 min at 65°C. To the mixture, 4 μl of 5 × RT buffer,
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2 μl deoxyribonucleotide triphosphate mix (10 mmol/l), 1 μl RNase inhibitor and 1 μl MultiScribe-RT (200 U/μl) were added and incubated at 42°C for 60 min, and then the reaction was terminated by heating to 70°C for 5 min. Complementary DNA was used for the real-time PCR assay performed with an ABI 7300 sequence detection system (Applied Biosystems, Foster City, CA, USA) according to the supplied guidelines.

Analysis of nitrotyrosine in kidney homogenates

A 25% kidney homogenate was prepared in ice-cold lysis buffer (10% SDS and 10 mM-Tris base; pH 7.5) containing a protease inhibitor cocktail (Complete, Roche Diagnostics, Mannheim, Germany), using a homogeniser. The homogenates were centrifuged at 22 000g for 20 min to remove cell debris. Supernatants were used for the analysis of nitrotyrosine. Nitrotyrosine concentrations were measured using a commercial ELISA kit (Millipore, Bedford, MA, USA). Nitrobovine serum albumin (Sigma) was coated onto wells of microtitre strips, and nitrotyrosines were quantified using anti-nitrotyrosine antibodies. Competition was accomplished by adding 50 μl organ supernatant samples and 50 μl primary antibodies to the wells. Each competes with the coated nitrated proteins for antibody binding. The amount of antibody that binds to the coated nitro-bovine serum albumin is inversely proportional to the amount of nitrotyrosine present in the samples added to the well of the plate. The procedures followed the manufacturer’s instructions.

Statistical analysis

Data are presented as mean values and standard deviations. All statistical analyses were performed using the SAS software package (SAS, Cary, NC, USA). Differences among different groups were determined by a one-way ANOVA followed by Duncan’s post hoc test. P<0.05 was considered statistically significant.

Results

Body weight and food intake

There were no differences in the initial body weights among the three groups. The food intake (DM group 27.9 (SD 2.4) g/d v. DM-GLN group 28.62 (SD 1.13) g/d; P>0.05) or body weights (DM group 323.7 (SD 74.8) g v. DM-GLN group 332.5 (SD 90.1) g; P>0.05) after feeding the diets for 8 weeks did not differ between the two diabetic groups.

Oxidative stress-related gene expressions by blood mononuclear cells

Txnip mRNA expression was higher in the NC group. Compared with the DM group, the DM-GLN group had lower GFAT, RAGE and Txnip gene expressions. There were no differences in AR or PKC-β mRNA expressions among the three groups (Fig. 1).

Plasma levels of biochemical parameters

Plasma glucose, total cholesterol, HDL-cholesterol, LDL-cholesterol, TAG and creatinine levels were significantly higher in the diabetic groups than in the NC group. There were no differences in glucose, total cholesterol, TAG, HDL-cholesterol, LDL-cholesterol, creatinine or blood urea N levels between the DM and DM-GLN groups (Table 3).

Plasma total antioxidant capacity

The total antioxidant capacity was significantly lower in the diabetic groups than in the NC group. The DM-GLN group had a higher total antioxidant capacity than the DM group (Table 4).

Erythrocyte antioxidant enzyme activities, and reduced and oxidised glutathione levels

GPx and SOD activities were significantly higher, while catalase activity was lower in the DM group than in the NC and DM-GLN groups. There were no differences in catalase, GPx or SOD activities between the NC and DM-GLN groups. The DM-GLN group had higher glutathione reductase activity than the NC and DM groups. There were no differences in GSH levels among the three groups; however, the GSSG level was significantly higher in the DM group than in the NC and DM-GLN groups (Table 4).
**Txnip gene expression and nitrotyrosine levels in the kidneys**

The DM group had higher Txnip mRNA expression than the NC and DM-GLN groups. The nitrotyrosine level was highest in the DM group. There were no differences in Txnip mRNA expressions or nitrotyrosine levels between the NC and DM-GLN groups (Table 5).

**Discussion**

Increased production of free radicals and/or an impaired antioxidant defence capability in diabetes indicate a central contribution of ROS to the pathological consequences of diabetes\(^{(23)}\). Hyperglycaemia-induced overproduction of superoxide is the causal link between high glucose levels and diabetic complications. In the present study, we investigated the effect of GLN on key enzyme and protein expressions involved in major pathways responsible for hyperglycaemic damage.

The present results demonstrated that DM results in higher plasma glucose, lipid and creatinine levels, indicating that abnormal nutrient metabolism and renal function occurred. We also observed that the HDL-cholesterol level was higher in the DM groups than in the NC group. The rat is a species without endogenous cholesteryl ester or TAG transfer capacity, because its lipid transfer protein activity is relatively low\(^{(24)}\). Therefore, it is reasonable to have higher HDL-cholesterol when total plasma cholesterol is high in a diabetic condition. The findings of the present study did not show a decrease in glucose levels in diabetic rats after supplemental dietary GLN administration. The present results are inconsistent with previous reports which showed that supplementing GLN had positive effects on glucose metabolism by increasing insulin sensitivity which may lead to better glycaemic control\(^{(9,10)}\). However, the present study is consistent with a previous study performed by our laboratory which also showed that dietary GLN did not affect plasma glucose\(^{(11)}\).

Hyperglycaemia results in increased enzymatic conversion of glucose to the polyalcohol sorbitol, with concomitant decreases in NADPH and GSH\(^{(4)}\). A previous study has found that AR inhibition prevented diabetic neuropathy in a 5-year animal study\(^{(25)}\). AGE originally arise from non-enzymatic reactions between extracellular proteins and glucose. Intracellular hyperglycaemia is the primary initiating event in the formation of AGE. AGE bind to the RAGE on endothelial cells, mesangial cells and macrophages, inducing receptor-mediated production of ROS, and activate the transcription factor NF-kB and subsequent gene expressions\(^{(4)}\). Blockade of the RAGE was shown to inhibit the development of diabetic nephropathy\(^{(26,27)}\). Hyperglycaemia may also indirectly activate PKC isoforms.

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**Table 3. Plasma concentrations of glucose, TAG, total cholesterol (TC), HDL-cholesterol (HDL-C) and LDL-cholesterol (LDL-C), creatinine and blood urea nitrogen (BUN) in the various groups at the end of the experiment (Mean values and standard deviations, n 8 for the normal control group (NC) and n 10 for each diabetic group)**

<table>
<thead>
<tr>
<th></th>
<th>NC</th>
<th></th>
<th>DM</th>
<th></th>
<th>DM-GLN</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Glucose (mg/l)</td>
<td>1843(^{a})</td>
<td>137</td>
<td>4572(^{b})</td>
<td>769</td>
<td>4431(^{b})</td>
<td>629</td>
</tr>
<tr>
<td>TAG (mg/l)</td>
<td>409(^{a})</td>
<td>71</td>
<td>806(^{b})</td>
<td>484</td>
<td>756(^{b})</td>
<td>388</td>
</tr>
<tr>
<td>TC (mg/l)</td>
<td>391(^{a})</td>
<td>49</td>
<td>605(^{b})</td>
<td>107</td>
<td>633(^{b})</td>
<td>174</td>
</tr>
<tr>
<td>HDL-C (mg/l)</td>
<td>126(^{a})</td>
<td>10</td>
<td>273(^{b})</td>
<td>86</td>
<td>286(^{b})</td>
<td>96</td>
</tr>
<tr>
<td>LDL-C (mg/l)</td>
<td>164(^{a})</td>
<td>31</td>
<td>222(^{b})</td>
<td>53</td>
<td>254(^{b})</td>
<td>57</td>
</tr>
<tr>
<td>Creatinine (mg/l)</td>
<td>3-5(^{a})</td>
<td>0-2</td>
<td>3-8(^{b})</td>
<td>0-4</td>
<td>3-9(^{b})</td>
<td>0-2</td>
</tr>
<tr>
<td>BUN (mg/l)</td>
<td>195(^{a})</td>
<td>19</td>
<td>244(^{b})</td>
<td>69</td>
<td>238(^{b})</td>
<td>87</td>
</tr>
</tbody>
</table>

DM, diabetes without glutamine; DM-GLN, diabetes with glutamine.

\(^{a,b}\) Mean values within a row with unlike superscript letters were significantly different (\(P<0.05\); one-way ANOVA with Duncan’s post hoc test).

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**Table 4. Plasma total antioxidant capacity and erythrocyte antioxidant enzyme activities, reduced (GSH) and oxidised glutathione (GSSG) at the end of the experiment (Mean values and standard deviations, n 8 for the normal control group (NC) and n 10 for each diabetic group)**

<table>
<thead>
<tr>
<th></th>
<th>NC</th>
<th></th>
<th>DM</th>
<th></th>
<th>DM-GLN</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Trolox equivalents (mM)</td>
<td>1-84(^{a})</td>
<td>0-33</td>
<td>0-98(^{b})</td>
<td>0-36</td>
<td>1-36(^{b})</td>
<td>0-16</td>
</tr>
<tr>
<td>Catalase (U/g Hb)</td>
<td>12.7(^{a})</td>
<td>1.0</td>
<td>10.7(^{b})</td>
<td>1.6</td>
<td>12.8(^{a})</td>
<td>1.5</td>
</tr>
<tr>
<td>GPx (U/g Hb)</td>
<td>606-2(^{a})</td>
<td>83-0</td>
<td>786-2(^{b})</td>
<td>103-3</td>
<td>706-1(^{a})</td>
<td>119-7</td>
</tr>
<tr>
<td>GRd (U/g Hb)</td>
<td>1.1(^{a})</td>
<td>0-2</td>
<td>1.1(^{a})</td>
<td>0-2</td>
<td>1.3(^{b})</td>
<td>0-2</td>
</tr>
<tr>
<td>SOD (U/g Hb)</td>
<td>6123(^{a})</td>
<td>1534</td>
<td>8669(^{b})</td>
<td>1220</td>
<td>6922(^{a})</td>
<td>1871</td>
</tr>
<tr>
<td>GSH ((\mu \text{mol/g Hb}))</td>
<td>1-40</td>
<td>0-13</td>
<td>1-39</td>
<td>0-25</td>
<td>1-31</td>
<td>0-23</td>
</tr>
<tr>
<td>GSSG ((\mu \text{mol/g Hb}))</td>
<td>0-10(^{a})</td>
<td>0-02</td>
<td>2-97(^{b})</td>
<td>0-70</td>
<td>1-19(^{c})</td>
<td>0-27</td>
</tr>
</tbody>
</table>

DM, diabetes without glutamine; DM-GLN, diabetes with glutamine; GPx, glutathione peroxidase; GRd, glutathione reductase; SOD, superoxide dismutase.

\(^{a,b}\) Mean values within a row with unlike superscript letters were significantly different (\(P<0.05\); one-way ANOVA with Duncan’s post hoc test).
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Table 5. Kidney-relative thioredoxin-interacting protein (Txnip) mRNA expression and nitrotyrosine levels in kidney homogenates

<table>
<thead>
<tr>
<th></th>
<th>NC (Mean values and standard deviations, n 4 for Txnip, n 8 for the normal control group (NC) and n 10 for each diabetic group for nitrotyrosine, representative of duplicate measurements)</th>
<th>DM (Mean values and standard deviations)</th>
<th>DM-GLN (Mean values and standard deviations)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Txnip (n-fold)</td>
<td>1.01±1  0.19</td>
<td>1.79±1  0.16</td>
<td>1.22±1  0.39</td>
</tr>
<tr>
<td>Nitrotyrosine (µg/ml)</td>
<td>17.33±3  0.04</td>
<td>22.81±6  3.36</td>
<td>17.80±7  3.00</td>
</tr>
</tbody>
</table>

DM, diabetes without glutamine; DM-GLN, diabetes with glutamine.

**A** Mean values within a row with unlike superscript letters were significantly different (P < 0.05; one-way ANOVA with Duncan’s post hoc test).

References


Acknowledgements

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