Research Article

Investigation of the Protective Effects of Phlorizin on Diabetic Cardiomyopathy in \textit{db/db} Mice by Quantitative Proteomics

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Patients with diabetes often develop hypertension and atherosclerosis leading to cardiovascular disease. However, some diabetic patients develop heart failure without hypertension and coronary artery disease [2]. This phenomenon was first described by Rubler et al. and was termed “diabetic cardiomyopathy” [3]. Diabetic cardiomyopathy is characterized by structural and functional changes in the heart, such as elevated left ventricular (LV) mass, myocardial fibrosis, and abnormal diastolic function [4, 5]. However, the mechanistic details of diabetic cardiomyopathy remain unclear, and this disease has not yet been sufficiently studied.

Phlorizin (phloretin-2'-O-glucoside), a dihydrochalcone derived from apple peels, is a known antioxidant [6]. The main pharmacological property of phlorizin is to produce renal glycosuria and block intestinal glucose absorption through inhibition of sodium/glucose cotransporters in the kidney and intestine [7]. Although cardioprotective benefits of phlorizin have been reported, little is known about the effect of phlorizin on cardiac damage in type 2 diabetes mellitus (T2DM).

In this study, we used phlorizin to treat T2DM in \textit{db/db} mice. These mice exhibit symptoms such as hyperglycemia, obesity, insulin resistance, and renal damage, which occurs after 10–20 weeks of sustained hyperglycemia [8, 9]. Additionally, we used a quantitative proteomic assay, isobaric tag for relative and absolute quantitation (iTRAQ), combined with liquid chromatography-tandem mass spectrometry (LC-MS/MS) to identify and characterize the protein profiles of phlorizin-treated and untreated \textit{db/db} mice. The iTRAQ technique has been widely used to tag peptides

1. Introduction

The prevalence of diabetes mellitus is rapidly increasing worldwide [1]. Patients with diabetes often develop hypertension and atherosclerosis leading to cardiovascular complications. However, some diabetic patients develop heart failure without hypertension and coronary artery disease [2]. This phenomenon was first described by Rubler et al. and was termed “diabetic cardiomyopathy” [3]. Diabetic cardiomyopathy is characterized by structural and functional changes in the heart, such as elevated left ventricular (LV) mass, myocardial fibrosis, and abnormal diastolic function [4, 5]. However, the mechanistic details of diabetic cardiomyopathy remain unclear, and this disease has not yet been sufficiently studied.

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Materials and Methods

2.1. Experimental Animal Treatment. Male C57BLKS/J db/db and db/m mice (n = 24, 7 weeks old) were purchased from the Model Animal Research Center at Nanjing University (Jiangsu, China). All mice were housed in wire-bottomed cages and received laboratory pellet chow and tap water ad libitum in a constant environment (room temperature 22 ± 1.6°C, room humidity 55 ± 5%) with a 12 h-light, 12 h-dark cycle. All experimental protocols were verified and approved by the Animal Ethics Committee of Shandong University. C57BLKS/J db/m mice were used as a control group, which were administered normal saline solution (n = 8). The db/db mice were randomly divided into two groups: the vehicle-treated diabetic group (DM, n = 8), which were administered normal saline solution, and the phlorizintreated diabetic group (DMT, n = 8), which were treated with 20 mg/kg phlorizin. Phlorizin (purity >98%, Jianfeng Biotechnology, Tianjin, China) was dissolved in normal saline solution and administered intragastrically from week 8 to week 18 without hypoglycemic therapy. Animals were weighed each week. At the end of the study, all mice were fasted overnight. Fasting blood was collected before sacrifice to measure fasting blood glucose (FBG), blood triglycerides (TG), and blood total cholesterol (TC) using an Automatic Biochemistry and Blood Glucose (FBG), Blood Triglycerides (TG), and Blood Total Cholesterol (TC) using an Automatic Biochemistry and Blood Glucose Analyzer Instrument (DVI-1650, Bayer, Germany). Specific fluorescence determinations of serum advanced glycation end products (AGEs) were performed using a fluorescence spectrophotometer (Hitachi F-2500, Japan) by measuring 440 nm emissions after excitation at 370 nm. The hearts of the mice were immediately dissected. Tissue and sera were kept at −80°C until further analysis.

2.2. Histological Examination and Ultrastructure Observation. The LV myocardium was fixed in 4% paraformaldehyde and embedded in paraffin. Five-millimeter-thick sections were cut, stained with hematoxylin-eosin (H&E), and examined by light microscopy. Additionally, part of the LV free wall was fixed in 3% glutaraldehyde. Ultrathin sections cut from embedded blocks were stained with uranyl acetate and lead citrate and examined with an H-800 electron microscope (Hitachi, Japan).

2.3. iTRAQ Proteomic Analysis. Heart tissue (50 mg) from each of four mice per group was prepared and digested with trypsin, as previously described [12]. A total of 60 μg of peptides from each group were labeled with iTRAQ reagents following the manufacturer’s instructions (Applied Biosystems). The control group peptides were labeled with Reagent 114; the DMT group, Reagent 116; and the DM group, Reagent 117. The labeled samples were then separated into 10 fractions using PolySULFOETHYL A strong cation-exchange (SCX) columns (4.6 × 100 mm 5μ, 200 Å, PolyLC). Mass spectrometric analysis was performed using a micro-liquid chromatography system (MDLC, GE Healthcare, Pittsburgh, PA, USA) and an LTQ Velos ion trap mass spectrometer (ThermoFinnigan, San Jose, CA, USA).

2.4. Protein Pathway Analysis. Differentially expressed genes were analyzed using Ingenuity Pathway Analysis (IPA, Ingenuity Systems, http://www.ingenuity.com/). The data packet containing the differentially expressed proteins identified in the iTRAQ experiment was converted by IPA to “fold change” and uploaded into IPA. Each identifier was mapped to its corresponding gene object in the Ingenuity Pathways Knowledge Base.

2.5. Western Blotting Analysis. Proteins were separated by SDS-polyacrylamide gel electrophoresis and transferred onto polyvinylidene difluoride membranes as previously described [13]. Membranes were subsequently probed with antibodies against calnexin (1:500 dilution, Abcam), integrin-linked protein kinase (1:1000 dilution, Santa Cruz Biotechnology), or GAPDH (1:5000 dilution, Santa Cruz Biotechnology) overnight at 4°C, which was then followed by incubation with secondary antibody for 2 h. The band intensity was quantified using VisionWorks LS image acquisition and analysis software (UVP, Upland, CA, USA).

2.6. Statistical Analysis. The data are presented as the mean ± standard deviation. Statistical comparisons among the three experimental groups were made using the unpaired Student’s t-test and one-way ANOVA. A value of P < 0.05 was considered statistically significant.

3. Results

3.1. General Metabolic Parameters and AGEs. During the observation period, the DM and DMT groups gained substantially more weight than the control group. Nevertheless, phlorizin treatment significantly reduced body weight gain in db/db mice at the second week after phlorizin administration (Figure 1(a)). After 10 weeks, serum FBG, TG, and TC levels in the DM group were significantly higher than those in the control group. However, phlorizin treatment dramatically reduced these values in the DMT group compared with the DM group (Figures 1(b), 1(c), and 1(d)). In addition, db/db mice had significantly elevated serum AGE levels. After phlorizin treatment, AGE levels in db/db mice were reduced (Figure 2).

3.2. Histological and Ultrastructural Observation. On H&E-stained sections, the DM group exhibited significant myocardial hypertrophy and myofiber disarray accompanied by damaged nuclei and increased degeneration. However, phlorizin treatment attenuated this cardiomyocyte hypertrophy to a level similar to the control group (Figures 3(a), 3(b), and 3(c)). Myocardial ultrastructure could be visualized by electron microscopy (Figures 4(a), 4(b), and 4(c)). In the control group, the myofibrils were arranged in a striated pattern, and the mitochondria were positioned in rows along
Figure 1: General metabolic parameters. (a) Body weight change of mice in the control, DM, and DMT groups. ((b), (c), (d)) Serum FBG, TG, and TC were measured after 10 weeks. * $P < 0.05$ and indicates a significant difference between the control and DM group; # $P < 0.05$ and indicates a significant difference between the DMT and DM group ($n = 8$). DM: vehicle-treated diabetic group; DMT: diabetic group treated with 20 mg/kg phlorizin; FBG: fasting blood glucose; TG: triglycerides; TC: total cholesterol.

Figure 2: The effect of phlorizin on AGE levels in blood. * $P < 0.05$, and indicates a significant difference between the control and DM group; # $P < 0.05$, and indicates a significant difference between the DMT and DM group ($n = 8$). DM: vehicle-treated diabetic group; DMT: diabetic group treated with 20 mg/kg phlorizin; AGEs: advanced glycation end products.

3.3. iTRAQ Proteomics Profiling. Using the iTRAQ approach, we analyzed the effect of phlorizin on the myocardial protein profile of db/db mice. A total of 1627 proteins were identified. Of the 113 differentially expressed proteins, 29 were elevated in the DM group compared with the control group but were still decreased by phlorizin treatment. An additional 84 proteins were decreased in the DM group compared with the control group, but these were restored by the phlorizin treatment (see Supplementary Material available online at http://dx.doi.org/10.1155/2013/263845).
Figure 3: H&E staining of LV myocardium after 10 weeks: (a) control group, (b) DM group, and (c) DMT group. Magnification, 400x. Arrows indicate the hypertrophic cardiomyocytes with enlarged nuclei.

Figure 4: Electron microscopic examination of nuclei, mitochondria, sarcomeres, and myofibrils in the LV myocardium after 10 weeks: (a) control group, (b) DM group, and (c) DMT group. N: nuclei; Mi: mitochondria; Z: sarcomere; MF: myofibrils.

Figure 5: Top biofunctional processes associated with the differentially expressed proteins generated by IPA.

We used IPA software to conduct gene ontology analysis and to classify the molecular functions of significantly altered proteins. Figure 5 shows the top-ranked biological functions, including lipid metabolism and energy production, which are biological processes altered during diabetic cardiomyopathy. The top protein network was generated by pathway analysis of differentially expressed proteins (Figure 6). There was a cluster of 35 proteins in the network, of which 24 are included on our list. These proteins are likely to be involved in biological processes such as lipid metabolism, mitochondrial function, and cardiomyopathy.

3.4. Functional Classification of Proteins Involved in Metabolic Disorders in db/db Mice Detected by iTRAQ

3.4.1. Altered Proteins in Cardiac Lipid Metabolism. Lipotoxicity occurring with T2DM and obesity impairs cardiac lipid metabolism [14]. The identified proteins associated with cardiac lipid metabolism are listed in Table 1. Proteins upregulated after phlorizin treatment included microsomal triglyceride transfer protein (Mttp), nicotinamide phosphoribosyltransferase (Nampt), tyrosine-protein phosphatase nonreceptor type II (Ptpn11), low-density lipoprotein receptor (LDLr), protein-tyrosine phosphatase-like member B (Ptplb), and sorbin and SH3 domain-containing protein 1 (Sorbs1). However, glycosylphosphatidylinositol-anchored high-density lipoprotein-binding protein 1 (Gphbp1), which was initially identified as an HDL-binding protein involved in reversing cholesterol transport, was downregulated in the DMT group compared with the DM group.

3.4.2. Altered Proteins Related to Myocardial Mitochondria. Diabetic cardiomyopathy is usually associated with abnormal energy production due to impaired mitochondrial function. We detected several proteins related to myocardial mitochondria (Table 1). Proteins that were significantly upregulated in the DMT group compared with the DM group include the following: 5’-AMP-activated protein kinase catalytic subunit alpha-2 (Prkaa2), endonuclease G (EndoG), and NADH
dehydrogenase (ubiquinone) iron-sulfur protein 6 (Ndufs6). Other proteins such as apoptosis-inducing factor 2 (Atpaf2), ATP synthase mitochondrial F1 complex assembly factor 2 (Aifm2), and lipoic acid synthetase (Lias) were significantly downregulated in the DMT group compared with the DM group.

3.4.3. Altered Proteins Involved in Cardiomyopathy. Several factors contribute to diabetic cardiomyopathy, including myocardial hypertrophy, elevated wall-thickness-to-chamber ratios, and increased stiffness of the LV wall [15]. We found that several proteins associated with cardiac contraction and diastolic function were decreased in the DM group and reversed after phlorizin treatment (Table 1). For example, the cytoskeletal protein titin (Ttn) and death-associated protein kinase 3 (DAPK3 or ZIPK) were upregulated in the DMT group compared with the DM group.

There were also some differentially expressed proteins on this list. Missense mutations or small deletions in some genes, for example, desmin (Des), integrin-linked protein kinase (Ilk), myosin regulatory light chain 2 (My12), dystrophin (Dmd), gelsolin (Gsn), lamin A/C (Lmna), and laminin subunit α-2 (Lama2), have been linked to cardiomyopathy. These proteins were upregulated in the DMT group compared with the DM group, indicating that diabetic cardiomyopathy improved after phlorizin treatment. We also listed the differentially expressed proteins involved in cardiac hypertrophy, including glutaredoxin-3 (Glrx3) and collagen alpha-2(I) chain (Colla2). These proteins were upregulated in the DMT group compared with the DM group. Other important proteins involved in heart development and disease that were altered in db/db mice and reversed after phlorizin treatment include adenomatous polyposis coli (Apc), calnexin (Canx), myomesin-1 (Myom1), and voltage-dependent L-type calcium channel subunit beta-2 (Cacnb2).

3.5. Validation of iTRAQ Data for Selected Candidate Proteins. We selected two proteins for Western blot analysis to validate the iTRAQ data. As shown in Figure 7(a), calnexin was found to be decreased, whereas integrin-linked protein kinase was increased in the DMT group compared with the DM group. Quantification of band intensity showed that the results from density of bands are almost consistent with the iTRAQ data (Figure 7(b)). This indicates that the iTRAQ data are reliable.

4. Discussion

Diabetic cardiomyopathy accompanying T2DM is a complicated disorder caused by multifactorial pathology including...
Table 1: Functional classification of altered proteins related to cardiac lipid metabolism, mitochondrial function, and cardiomyopathy.

| Accession no. | Symbol | Protein name | Molecular weight (Da) | PI | iTRAQ ratio (DM/C) | iTRAQ ratio (DMT/DM) |
|---------------|--------|--------------|-----------------------|----|-------------------|---------------------|
| Cardiac lipid metabolism | | | | | | |
| IPI00785217 | LDLr | Low-density lipoprotein receptor | 94947.38 | 4.82 | 0.22 | 3.05 |
| IPI00943405 | Mttp | Microsomal triglyceride transfer protein large subunit | 100750.94 | 7.51 | 0.4 | 1.83 |
| IPI00655029 | Sorbsl | Sorbin and SH3 domain-containing protein 1 | 103977.89 | 5.65 | 0.46 | 1.83 |
| IPI00320188 | Nampt | Nicotinamide phosphoribosyltransferase | 55446.82 | 6.69 | 0.53 | 1.78 |
| IPI00133956 | Gpihbp1 | Glycosylphosphatidylinositol-anchored high density lipoprotein-binding protein 1 | 24566.22 | 4.81 | 5.71 | 0.19 |
| IPI00124411 | Ptplb | Protein-tyrosine phosphatase-like member B | 28402.43 | 9.59 | 0.23 | 3.95 |
| IPI0036479 | Ptpn11 | Tyrosine-protein phosphatase nonreceptor type II | 68034.75 | 6.87 | 0.16 | 2.95 |
| Mitochondrial components and function | | | | | | |
| IPI00882331 | Lias | Lipoyl synthase, mitochondrial | 32173.8 | 8.48 | 2.63 | 0.49 |
| IPI00128345 | Ndufs6 | NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial | 13019.78 | 8.86 | 0.59 | 1.55 |
| IPI00114840 | Endog | Endonuclease G, mitochondrial | 32190.74 | 9.56 | 0.39 | 1.78 |
| IPI00336348 | Atpaf2 | ATP synthase mitochondrial F1 complex assembly factor 2 | 34287.29 | 6.35 | 1.68 | 0.65 |
| IPI00276157 | Aifm2 | Apoptosis-inducing factor 2 | 41355.63 | 8.16 | 2.58 | 0.45 |
| IPI00929796 | Prkaa2 | 5'-AMP-activated protein kinase catalytic subunit alpha-2 | 62022.37 | 7.94 | 0.43 | 1.81 |
| Cardiomyopathy | | | | | | |
| IPI00896736 | Apc | Adenomatosis polyposis coli | 310880.6 | 7.44 | 2.39 | 0.45 |
| IPI00351550 | Glrx3 | Glutaredoxin-3 | 37778.42 | 5.42 | 0.35 | 1.61 |
| IPI00130102 | Des | Desmin | 53497.99 | 5.21 | 0.3 | 1.7 |
| IPI00116668 | Ilk | Integrin-linked protein kinase | 51373.15 | 8 | 0.18 | 3.15 |
| IPI00756257 | Ttn | Titin | 3906489.35 | 5.91 | 0.34 | 1.69 |
| IPI00555015 | Myl2 | Myosin regulatory light chain 2, ventricular/cardiac muscle isoform | 18864.35 | 4.86 | 0.38 | 1.73 |
| IPI00117846 | Dapk3 | Death-associated protein kinase 3 | 51421.9 | 8.91 | 0.33 | 2.45 |
| IPI00828253 | Dmd | Dystrophin | 425831.77 | 5.66 | 0.46 | 1.88 |
| IPI00759994 | Gsn | Gelsolin | 80762.65 | 5.52 | 0.41 | 2.33 |
| IPI00222188 | Colla2 | Collagen alpha-2(I) chain | 129556.97 | 9.27 | 0.17 | 2.05 |
| IPI00620256 | Lmna | Isoform A of Lamin-A/C | 74237.82 | 6.54 | 0.18 | 2.05 |
| IPI00874362 | Lama2 | Laminin subunit alpha-2 | 342781.06 | 5.78 | 0.32 | 1.51 |
| IPI0019618 | Canx | Calnexin | 67278.1 | 4.5 | 1.77 | 0.64 |
| IPI00626655 | Myomi | Myomesin-1 | 185464.52 | 5.83 | 0.48 | 1.54 |
| IPI00420996 | Cacnb2 | Voltage-dependent L-type calcium channel subunit beta-2 | 64714.53 | 9.17 | 0.59 | 1.69 |

Altered cardiac energy metabolism and increased oxidative stress [16]. Obesity is associated with high levels of circulating fatty acids, which result in increased fatty acid uptake and TG accumulation in the myocardium. Furthermore, increased oxygen damage and generation of reactive oxygen species (ROS) augment cardiac damage [17]. Thus, the normalization of cardiac energy metabolism and reduction in oxidative stress may be important factors in the treatment of diabetic cardiomyopathy.

Phlorizin has been reported to have an antidiabetic effect due to its antioxidant properties [18]. In this study, we observed that the levels of serum FBG, TG, and TC in the DM group were dramatically elevated compared with the control group and that the oral administration of phlorizin significantly reduced these levels. These results suggest that phlorizin may be able to prevent diabetes and its complications by lowering blood FBG, TG, and TC levels.

Based on the iTRAQ data and the IPA results, protein expression involved in cardiac lipid metabolism seems to be markedly stimulated by phlorizin. In diabetic patients, elevated circulating fatty acids and TG, together with hyper-insulinemia, augment cardiac uptake of fatty acids and


Figure 7: (a) Western blot validation of the differentially expressed proteins integrin-linked protein kinase (ILK) and Calnexin. (b) Quantification of band intensity using VisionWorks LS image acquisition and analysis software.

In a diabetic heart, glucose utilization is diminished. Instead, the heart relies almost exclusively on fatty acids for ATP generation. Increased fatty acid uptake by the heart reduces energy efficiency by inducing mitochondrial damage [16]. In this study, we identified several important proteins connected to mitochondrial structure and function. The altered expression of these proteins may cause deleterious effects on cells, resulting in cardiac energy deficit and cardiomyopathy. Here, we found that the phlorizin treatment reversed the expression of these proteins, suggesting a correlation between the cardioprotective effect of phlorizin and proteins involved in mitochondrial energy production.

Oxidative stress has been implicated in the pathogenesis of diabetes. A high rate of fatty acid oxidation also causes a pathological ROS accumulation, which leads to mitochondrial damage in cardiomyocytes [17]. Several factors contribute to ROS production in T2DM, such as AGEs [24]. In this study, we found that phlorizin treatment can significantly lower plasma AGE levels in db/db mice, which is consistent with its antioxidative ability to decrease ROS generation.

The development of diabetic cardiomyopathy has been divided into two phases: early metabolic alterations and later myocardial degenerative changes [25]. These irreversible pathological alterations include an increased stiffness of the LV wall, the accumulation of connective tissue and insoluble collagen, and abnormalities of various proteins [26]. Among the identified proteins that are involved in cardiac remodeling, titin was upregulated in the DMT group compared with the DM group. Recent observations have shown that the intrasarcomeric protein titin can alter myocardial diastolic stiffness through a number of different mechanisms such as isoform shifts, phosphorylation by protein kinase G or protein kinase A and titin-actin interactions at the Z-disc [27]. Another upregulated protein was Dapk3, also called ZIPK. Recent studies have identified smooth muscle myosin regulatory light chain and the regulatory subunit of the smooth muscle myosin light chain phosphatase as substrates for ZIPK [28]. This evidence suggests a key role for ZIPK in the regulation of cardiac contractility [29]. Here, our results demonstrate a cardioprotective role for phlorizin through the regulation of genes modulating cardiac contraction and diastolic function.

In conclusion, for the first time, the present study has established the quantitative iTRAQ profile of global cardiac proteins using a db/db diabetic mouse model treated with or without phlorizin. We found that phlorizin treatment may protect against diabetic cardiomyopathy by modulating cardiac lipid and energy metabolism and altering the expression of a set of proteins involved in cardiac damage. We
also observed that phlorizin treatment significantly decreased body weight, blood glucose, blood TG, and blood TC. These findings suggest that, in the future, phlorizin may be utilized as a novel effective therapeutic approach for the treatment of diabetic cardiomyopathy.

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