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BRIEF ARTICLE

Natural taurine promotes apoptosis of human hepatic stellate cells in proteomics analysis

Xin Deng, Jian Liang, Zhi-Xiu Lin, Fa-Sheng Wu, Ya-Ping Zhang, Zhi-Wei Zhang

Xin Deng, Jian Liang, Fa-Sheng Wu, Ya-Ping Zhang, Zhi-Wei Zhang, The Affiliated Ruikang Hospital of Guangxi Traditional Chinese Medical University, Nanning 530011, Guangxi Zhuang Autonomous Region, China
Zhi-Xiu Lin, School of Chinese Medicine, The Chinese University of Hong Kong, Shatin, Hong Kong, China
Author contributions: Liang J and Deng X designed and performed the research; Wu FS, Zhang YP and Zhang ZW collected and analyzed the data; Lin ZX wrote and revised the paper.
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Correspondence to: Jian Liang, Professor, The Affiliated Ruikang Hospital of Guangxi Traditional Chinese Medical University, Nanning 530011, Guangxi Zhuang Autonomous Region, China. dx8848@126.com
Telephone: +86-771-2238022 Fax: +86-771-2238869
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Abstract

AIM: To study the differential expression of proteins between natural taurine treated hepatic stellate cells and controls, and investigate the underlying regulatory mechanism of natural taurine in inhibiting hepatic fibrosis.

METHODS: A proteomic strategy combining two-dimensional gel electrophoresis and ultra-performance liquid chromatography-electrospray ionization-tandem mass spectrometry (UPLC-ESI-MS/MS) was used to study the differential expression of proteins and Western blotting was used to validate the results. Gene ontology (GO) method was utilized to analyze the functional enrichment of differentially expressed proteins. Flow cytometry was performed to compare the apoptosis rate between taurine-treated and untreated hepatic stellate cells (HSCs).

RESULTS: Nineteen differentially expressed proteins (11 up-regulated and 8 down-regulated) were identified by 2D/MS, and the expression profiles of GLO1 and ANXA1 were validated by Western blotting. GO analysis found that these differentially expressed proteins were enriched within biological processes such as "cellular apoptosis", "oxidation reaction" and "metabolic process" in clusters. Flow cytometric analysis showed that taurine-treated HSCs had a significantly increased apoptosis rate when compared with the control group.

CONCLUSION: Natural taurine can promote HSC apoptosis so as to inhibit hepatic fibrosis.

Key words: Natural taurine; Proteomics; Hepatic stellate cell; Hepatic fibrosis; Apoptosis

Peer reviewers: Zsuzsa Szondy, Professor, Department of Biochemistry and Molecular Biology, University of Debrecen, Nagyerdei krt. 98, Debrecen H-4012, Hungary; Shivendra Shukla, Professor, Department of Medical Pharmacology and Physiology, University of Missouri School of Medicine, 1 Hospital Drive, M530 Medical Sciences Bldg., Columbia, MO 65212, United States

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INTRODUCTION

Hepatic fibrosis (HF) is the excessive accumulation of extracellular matrix (ECM) through which the liver repairs injury[1,2]. HF occurs in most types of chronic liver diseases due to various causes, and approximately 25%-40% of HF cases may ultimately progress to hepatic cirrhosis or even hepatocellular carcinoma. Therefore, prevention of the initiation of HF and interference with or reversal

of the fibrotic process is important for controlling the development of chronic liver diseases, which has become one of the research focuses in China and other countries[3,4].

Hepatic stellate cells (HSCs) are nonparenchymal cells found in the perisinusoidal space of the liver also known as the space of Disse[5]. HSCs contribute significantly to the occurrence of HF because activated HSCs have been found to secrete a great amount of ECM when migrating, proliferating and synthesizing in the injured site of the liver[6,7]. It is generally believed that reversal of the fibrotic process is difficult once HSCs are activated. Some studies, however, have shown that HF may be inhibited to a certain extent by reducing the number of HSCs *via* apoptosis induction[8,9].

Taurine, or 2-aminoethanesulfonic acid ($C_2H_7NO_3S$), is an important anti-injury substance in the body[10]. Taurine has a protective effect on various types of liver injury[11,12] and may mitigate HF by inhibiting the deposition of ECM[13]. The antifibrotic mechanism of taurine may involve its inhibition of the activation and proliferation of HSCs[9,14]. Because the molecular mechanism of taurine-mediated antifibrotic activity has not been fully unveiled and is little studied, it is imperative to use "omics" methods to systematically investigate the molecular mechanism by which taurine inhibits HF.

Therefore, in the present study, we analyzed the differential expression of proteins between taurine-treated HSCs and controls using two-dimensional electrophoresis (2-DE), ultra-performance liquid chromatography-electrospray ionization-tandem mass spectrometry (UPLC-ESI-MS/MS) and bioinformatics method to identify proteins associated with the inhibition of HF by taurine. Moreover, we aimed to understand better the molecular mechanism underlying taurine's protection against HF and thereby provide new targets for the management of HF and drug development.

MATERIALS AND METHODS

Materials

Human HSCs (LX-2) were purchased from XiangYa Central Experiment Laboratory, Central South University, Changsha, Hunan Province, China. Natural taurine was provided by Yuanlong Pearl Co. Ltd., Beihai, Guangxi Zhuang Autonomous Region, China. Acrylamide, bisacrylamide, glycine and HRP-ECL luminescent substrate were purchased from Sigma (USA). Immobilized pH gradient (IPG) strips (immobiline™ DryStrip, pH3-10, nonline, 18 cm) and image analysis software (ImageMaster 2D platinum) were purchased from Amersham Pharmacia. Bradford protein assay kit was provided by Beyotime Institute of Biotechnology (China). Primary and secondary antibodies were purchased from Santacruz; Annexin V apoptosis assay kit, from Nan Jing KeyGen Biotech Co., Ltd. (China); vertical electrophoresis apparatus and Trans-Blot system, from Bio-Rad (USA); Epics XL Ⅱ flow cytometer, from Beckman Coulter (USA); inverted light microscope, from Olympus (Japan); IPGphor IEF System and ImageScanner, from Amersham Pharmacia. Vertical slab electrophoresis apparatus (PROTEAN Ⅱ xi Cell) was bought from Bio-Rad (USA) and UPLC-ESI-MS/MS system was provided by Micromass (UK).

Methods

Incubation and treatment of HSCs (LX-2): The cells were incubated in DMEM containing 100 U/mL penicillin, 100 U/mL streptomycin and 10% fetal bovine serum at 37℃, 50 mL/L CO_2 and saturated humidity. The medium was replaced every other day. When the cell density achieved 80%-90%, trypsin was used for digestion and the cell concentration was adjusted to be 1×10^5/mL. The supernatant was discarded and then reaction was maintained for 48 h after the addition of 2% DMEM containing 40 mmol/L taurine. HSCs were randomized equally to receive treatment with or without taurine.

Protein extraction and quantification: The cells were collected after centrifugation and washed in PBS twice. After 10 μL of RNAase and 10 μL of DNAase, were added respectively, the solution was placed in ice bath at 4℃ for 20 min and then centrifuged at 14000 × *g* for 30 min and the supernatant was collected. Protein quantification was performed by the Bradford method. In the same way, 1 μL of the sample was collected and 99 μL of water was added followed by supplementation with 1 mL of Bradford working solution. After shaking for 5 min, measurement was conducted. The absorbance of the test sample was measured at 595 nm.

2-DE: The first-dimension isoelectric focusing (IEF) electrophoresis was performed on an IPGphor IEF System. Proteins were centrifuged for 2 min before loading. A loading amount of 150 μg was dissolved in rehydration solution containing 8 mol/L urea, 0.02% Chaps, 0.02 mol/L dithiothreitol (DTT) and 0.05% IPG buffer and then 800 μL of cover fluid was added. The focused gel strips were equilibrated twice in sodium dodecyl sulfate (SDS) equilibration buffer (1.5 mol/L tris-Cl, pH 8.8, 50 mmol/L, 30% Glycerol, 6 mol/L Urea, 2% SDS, Bromophenol blue trace) and rotated on a shaking table for 15 min × 2. The first equilibration buffer was supplemented with 20 mmol/L DTT and the second equilibration buffer was added with 100 mmol/L iodoacetamide. Gel strips were taken out and then the vertical second-dimension sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) was run on a PROTEIN Ⅱ xi Cell system. Polyacrylamide gels (13%) were used for separation. Electrophoresis was run at a constant current of 40 mA for 40 min and at 60 mA for 5 h until the bromophenol blue front reached the bottom of the gel. Rapid silver staining was performed in accordance with the manufacturer's manual. Gels were stained with 0.1% Coomassie brilliant blue R350 at 100℃ for 10 min and then de-stained in 10% acetic acid overnight.

Gel image analysis: Stained 2-DE gels were scanned in transmission scan mode using an Image-scanner™. Then,

matching of protein spots and differential expression analyses between the treatment group and the control group were performed using ImageMaster 2D Platinum 5.0 software.

Mass spectrometry and database query: In-gel digestion was done for 19 differentially expressed protein spots whose concentrations met the requirement of mass spectrometry (MS). In-gel digested products were analyzed by UPLC-ESI-MS/MS (Micromass Company). The mass spectral data obtained after processing with the data analysis software PLGS v2.3 were used to search through the NCBInr database with a MS/MS ion strategy using Mascot software (http://www.matrixscience.co.uk). The search parameters included trypsin digestion, M oxidation and iodoacetamide alkylation (variable modifications), and 1 missed cleavage. The mass error tolerance in both the MS and MSMS data was 0.2-Da.

GO functional analysis: GO is a stratified tree structure for analysis of gene and protein functions[15]. We used the BinGO plugin in the Cytoscape platform to analyze functions of 19 differentially expressed proteins, with special focus on the enrichment of these proteins in biological process[16,17]. Then, we classified the significantly enriched GO terms according to functional similarity. Finally, we visualized the significantly enriched GO terms and their parent/child items in a tree structure in the Cytoscape platform and indicated the classification of the GO terms in the diagram.

Apoptosis detection: HSCs were incubated in the presence of 40 mmol/L taurine for 48 h, washed in PBS twice and then re-suspended in 100 μL of buffer containing calcium ion. After this, staining was carried out for 20-30 min by adding 5 μL of Annexin V-FITC dye and then for 5 min by supplementation with 5 μL of PI dye. The cell concentration was adjusted to be about 1×10^5/mL by adding a proper amount of calcium ion-containing buffer. The cells were detected on a flow cytometer within 1 h, with the excitation wavelength and the emission wavelength of 488 nm and 530 nm, respectively. The experiment was repeated in triplicate for each sample.

Western blotting: Total proteins in HSCs were extracted as described in the section of protein extraction and quantification, quantified by the Bradford method, isolated by SDS-PAGE and then transferred onto a nitrocellulose membrane with a Trans-Blot SD apparatus. The membrane was blocked in a blocking buffer (TBST solution containing 5% skim milk) at room temperature (RT) for 2 h. Primary antibodies were added at a dilution of 1:500 and the membrane facing down was incubated at RT for 1 h with slight shaking. After incubation with primary antibodies, the membrane was washed and incubated at RT for 1 h with mild shaking in the presence of horseradish peroxidase (HRP) conjugated goat anti-mouse secondary antibodies (1:5000). After this, the membrane was washed. *Visualization* of *protein bands* was achieved by the chemiluminescence method and the films were developed and fixed. GAPDH was used as an internal reference. The experiment was repeated in quadruple for each protein.

Statistical analysis

Data were expressed as mean ± SD. Difference in the relative content of differentially expressed protein spots was analyzed by *t* test for statistical significance ($P < 0.05$) and *t* test was also performed to determine whether treatment with taurine caused a statistically significant change in apoptosis of HSCs ($P < 0.05$). Hypergeometric test was used to test the enrichment of GO terms. A multiple testing procedure controlling false discovery rate (FDR) was performed as described by Benjamini and Hochberg, with the threshold for enrichment significance set to be FDR < 0.01[18]. All statistics were performed on R software.

RESULTS

2-DE and image analysis

Under the same experimental conditions, the 2-DE experiment was repeated 3 times separately for 2 groups of protein samples. Three pieces of parallel gels with high resolution and good reproducibility were obtained for each group. The mean number of protein spots from 3 pieces of gels was 745 ± 32 in the taurine treatment group *vs* 748 ± 25 in the control group, with a match rate of 86.08% between groups. Six hundred and forty-three differential protein spots were screened from both groups. Of these protein spots, 19 spots (11 up-regulated and 8 down-regulated) showed more than three-fold differential expression (Figure 1) following treatment with taurine. Figure 2 is a local amplification of 4 pairs of up-regulated or down-regulated protein spots, which clearly demonstrates changes in protein expression between taurine-treated HSCs and controls.

Identification of differentially expressed proteins by UPLC-ESI-MS/MS

Identification by UPLC-ESI-MS/MS was performed for the 19 differentially expressed proteins following in-gel digestion and peptide extraction. The resulting peptide fragments were used to search through the NCBInr database using Mascot software and these 19 differentially expressed proteins were successfully identified (ions scores > 38, $P < 0.05$). Table 1 summarizes the code, name, relative molecular weight, isoelectric point and peptide fragment coverage for the differentially expressed proteins. The most significantly up-regulated expression was observed in GLO1, a glyoxylase capable of catalyzing and forming lactoylglutathione, which has been reported to be linked to inflammatory reactions and tumors[19,20]. In contrast, AKR1A1, an aldehyde reductase important for both glucose metabolism and oxidative reactions[21], showed the most markedly down-regulated expression.

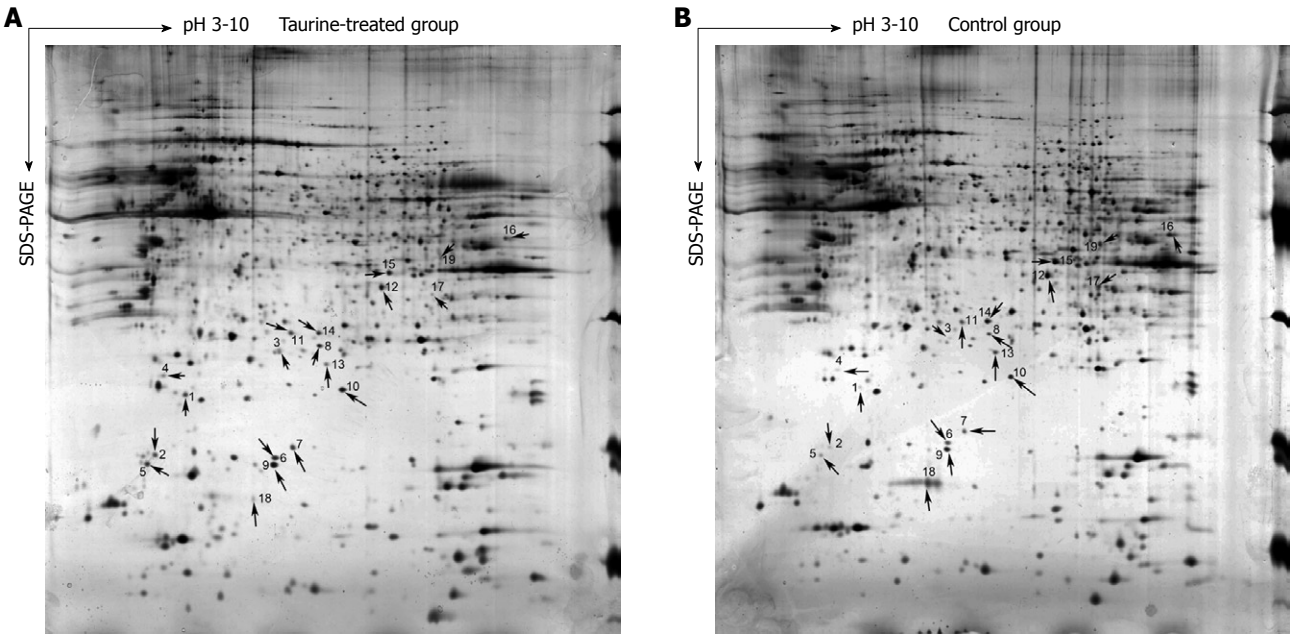

Figure 1 Two-dimensional gel electrophoresis (2-DE) images of taurine-treated hepatic stellate cells (HSCs) and controls. A: Taurine-treated group; B: Control group. In both images, transverse arrows represent isoelectric focusing and longitudinal ones represent sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE).

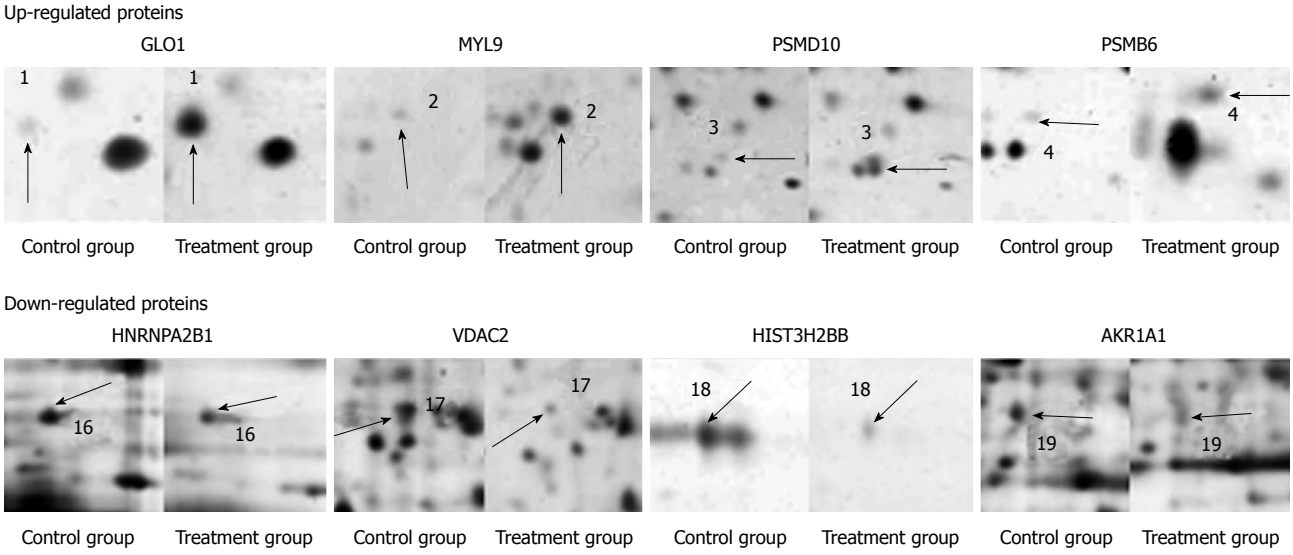

Figure 2 Local amplification of some differentially expressed protein spots (arrows). Up-regulated: GLO1, MYL9, PSMD10 and PSMB6, and down-regulated: HNRNPA2B1, VDAC2, HIST2H2BB and AKR1A1.

Validation of differentially expressed proteins by Western blotting

Among the differentially expressed proteins identified successfully by mass spectrometry, the protein GLO1 and ANXA1 were selected and subjected to Western blotting detection. Taurine treatment caused a significantly up-regulated expression of GLO1 and ANXA1 in HSCs (Figure 3). These expression profiles were completely consistent with the locally amplified 2-D electrophoretogram in Figure 2. Therefore, Western blotting detection of the differentially expressed proteins confirmed the reliability and validity of the proteomic high throughput experiments.

GO functional analysis of differentially expressed proteins

We entered the names of the differentially expressed proteins into the BinGO plugin in the Cytoscape platform to perform GO functional enrichment analysis, with special focus on the changes in the biological process of HSCs after taurine treatment. Table 2 lists 9 significantly enriched GO terms and relevant proteins identified after screening with a threshold of FDR < 0.01. Functional categorization of the GO terms revealed that these differentially expressed proteins were enriched within biological processes such as "cellular apoptosis", "oxidation reaction" and "metabolic process" in clusters. Figure 4 provides

Table 1 MS identification of differentially expressed proteins in taurine-treated and control groups

Code	Protein spot ID	Record number of protein	Name of protein	Description	log_2 (differential ratio)	Relative molecular weight (kDa)	Isoelectric point	Score	Coverage (%)
Up-regulated proteins									
1	1394	gi|2392338	GLO1	Chain a, human glyoxalase i with benzyl-glutathione inhibitor	4.25	20.6	5.12	408	51
2	1431	gi|29568111	MYL9	Myosin regulatory light chain 9 isoform a	3.30	19.8	4.80	631	62
3	1330	gi|4506217	PSMD10	Proteasome 26S non-ATPase subunit 10 isoform 1	3.24	24.4	5.71	279	35
4	1380	gi|558528	PSMB6	Proteasome subunit Y	2.62	25.3	4.80	403	26
5	1438	gi|4507669	TPT1	Tumor protein, translationally-controlled 1	2.48	19.6	4.84	375	61
6	1428	gi|4502101	ANXA1	Annexin I	1.48	38.7	6.57	1069	53
7	1419	gi|5174539	MDH1	Cytosolic malate dehydrogenase	1.18	36.4	6.91	223	17
8	1321	gi|4504517	HSPB1	Heat shock protein beta-1	0.99	22.8	5.98	567	49
9	1432	gi|5453710	LASP1	LIM and SH3 protein 1	0.95	29.7	6.61	362	34
10	1385	gi|31543380	PARK7	Parkinson disease protein 7	0.70	19.9	6.33	128	50
11	1285	gi|2982080	SOD1	Chain a, familial als mutant g37r cuznsod	0.50	15.9	5.87	292	45
Down-regulated proteins									
12	1130	gi|5453559	ATP5H	ATP synthase, H+ transporting, Mitochondrial F0 complex, subunit d isoform a	-0.66	18.5	5.21	277	47
13	1355	gi|5802974	PRDX3	Peroxiredoxin 3 isoform a precursor	-0.70	27.7	7.67	128	16
14	1284	gi|194097323	ECHS1	Mitochondrial short-chain enoyl-coenzyme A hydratase 1 precursor	-0.83	31.4	8.34	481	30
15	1067	gi|9955007	PRDX2	Chain a, thioredoxin peroxidase b from red blood cells	-1.14	21.8	5.44	446	38
16	953	gi|14043072	HNRNPA2B1	Heterogeneous nuclear ribonucleoprotein A2/B1 isoform B1	-1.86	37.4	8.97	181	15
17	1165	gi|190200	VDAC2	Porin	-2.81	38.1	6.32	281	22
18	1464	gi|1568551	HIST3H2BB	Histone H2B	-3.19	13.9	10.31	270	35
19	980	gi|5174391	AKR1A1	Aldo-keto reductase family 1, member A1	-3.55	36.6	6.32	306	22

MS: Mass spectrometry.

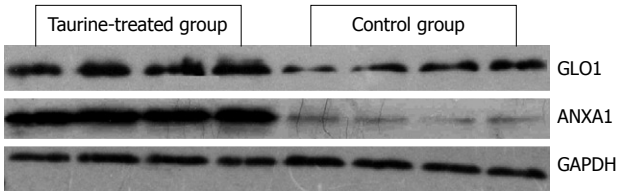

Figure 3 Results of validation by Western blotting for differentially expressed proteins. GAPDH was used as an internal reference. The experiment was repeated 4 times for each protein. Four columns in the right side represent the control group and the other 4 columns in the left side are from the taurine-treated group.

a visualized network of the 9 significantly enriched GO terms and their parent/children items. We can see that Cluster 1, 2 and 3 correspond to the category of "cellular apoptosis", "oxidation reaction" and "metabolic process" in Table 2, respectively. The consistency between these two dimensions suggests an important role of these biological processes in taurine-treated HSCs.

Results of apoptosis detection

To further confirm the functional findings from proteome data, we detected apoptosis of HSCs treated with or without taurine. Figure 5 shows that taurine treatment resulted in a significant increase in the apoptosis rate of HSCs (13.6% ± 3.3% *vs* 4.65% ± 1.1% in the control group, $P < 0.05$). Thus, proteome data and results of apoptosis detection consistently suggest that taurine may have an inhibitory effect on HF by promoting HSC apoptosis.

DISCUSSION

In the present study, we employed a proteomics strategy combining 2-DE and UPLC-ESI-MS/MS to investigate difference in protein expression between natural taurine-treated and untreated HSCs. Nineteen differentially expressed proteins (11 up-regulated and 8 down-regulated) were identified. The protein GLO1 and ANXA1 were then selected and subjected to validation by Western blotting, yielding expression profiles in full agreement with results obtained by 2-DE. GO functional analysis showed that these differentially expressed proteins were enriched within biological processes - "cellular apoptosis", "oxidation reaction" and "metabolic process" in clusters. Flow cytometric analysis showed that taurine-treated HSCs had a significantly increased apoptosis rate compared with the control group. Our comparative proteomic analysis revealed that taurine may inhibit HF by promoting HSC apoptosis.

The apoptosis mechanism of HSCs is complex where various apoptotic pathways are not only inter-independent but also interconnected. For instance, the iron chelator deferoxamine, which may increase the activity of caspase 3 when inducing the release of mitochondrial cytochrome C (cyt-c), induces HSC apoptosis *via* both the mitoch-

Table 2 Functional categorization of differentially expressed proteins

GO number	Functional description	Proportion (%)	Protein	*P* value	FDR value
Apoptosis-related					
51093	Negative regulation of developmental process	32	TPT1|ANXA1|HSPB1|GLO1|PRDX2|SOD1	2.20E-6	2.61E-4
42981	Regulation of apoptosis	32	TPT1|ANXA1|HSPB1|GLO1|PRDX2|SOD1	3.19E-5	1.49E-3
43067	Regulation of programmed cell death	32	TPT1|ANXA1|HSPB1|GLO1|PRDX2|SOD1	3.45E-5	1.49E-3
Oxidation reaction-related					
42542	Response to hydrogen peroxide	16	PRDX3|SOD1|PARK7	4.28E-6	4.07E-4
6979	Response to oxidative stress	21	PRDX2|PRDX3|SOD1|PARK7	8.18E-6	5.65E-4
302	Response to reactive oxygen species	16	PRDX3|SOD1|PARK7	8.33E-6	5.65E-4
Metabolism-related					
44248	Cellular catabolic process	37	PSMB6|AKR1A1|PSMD10|ECHS1|PRDX3|SOD1|MDH1	9.67E-6	5.74E-4
9056	Catabolic process	37	PSMB6|AKR1A1|PSMD10|ECHS1|PRDX3|SOD1|MDH1	3.12E-5	1.49E-3
42743	Hydrogen peroxide metabolic process	11	PRDX3|SOD1	2.45E-4	9.69E-3

Hypergeometric test, FDR < 0.01. GO: Gene ontology.

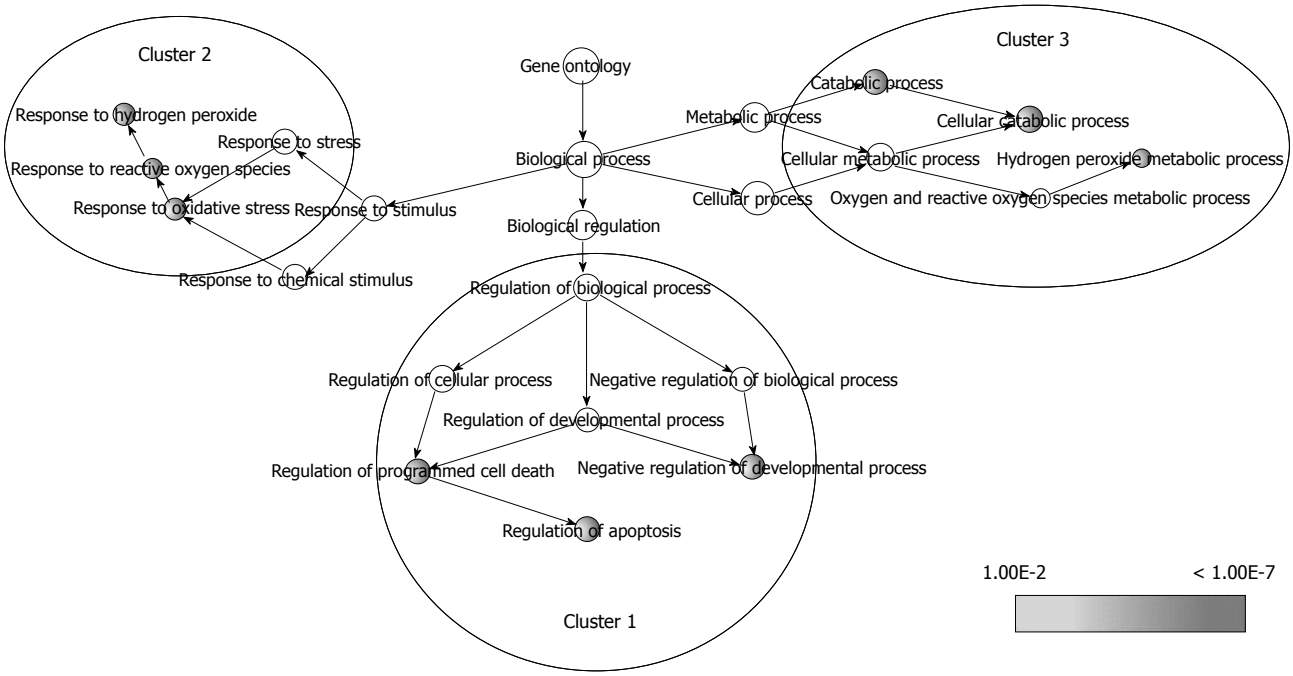

Figure 4 Network diagram of functional categorization of differentially expressed proteins. The categories in this tree structure fully correspond to the 3 categories in Table 2 and the depth of color ranging from light to dark gray indicates the significance level of FDR in Table 2. Gray nodes represent significantly enriched GO terms and white nodes signify GO terms that have a parent/child relationship with gray nodes. Connecting lines between nodes construct a directional hierarchy of the GO terms.

ondrial pathway and the death receptor pathway[22]. Our previous study has also found that natural taurine may regulate the TGF-β1/smad signaling pathway and has an activity against HF[23]. To date, however, the molecular mechanism and relevant pathways responsible for taurine's ability to promote HSC apoptosis have not been well understood. During confirmation of this phenomenon, we found differential expression of proteins including TPT1, ANXA1, HSPB1, GLO1, PRDX2 and SOD1 in taurine-treated HSCs, which was tightly associated with cellular apoptosis. Therefore, we presume that TPT1, ANXA1, HSPB1, GLO1, PRDX2 and SOD1 are important proteins in the taurine-mediated pathway of HSC apoptosis. These proteins may play a role in classical apoptotic pathways. Or they may constitute, on their own, a specific apoptotic pathway for HSCs by interacting with each other and regulating other proteins. We need to analyze taurine-mediated HSC apoptosis based on findings. Our another previous work has shown that natural taurine may protect mitochondria in HF rats by regulating liver lipid peroxidation, indicating an anti-HF effect[24]. Functional analysis of the differentially expressed protein demonstrated the ability of taurine to regulate oxidation reaction in HSCs. In fact, oxidation-related biological processes, such as reactive oxygen species (ROS) in Table 2, are closely associated with apoptosis induction[25]. Among

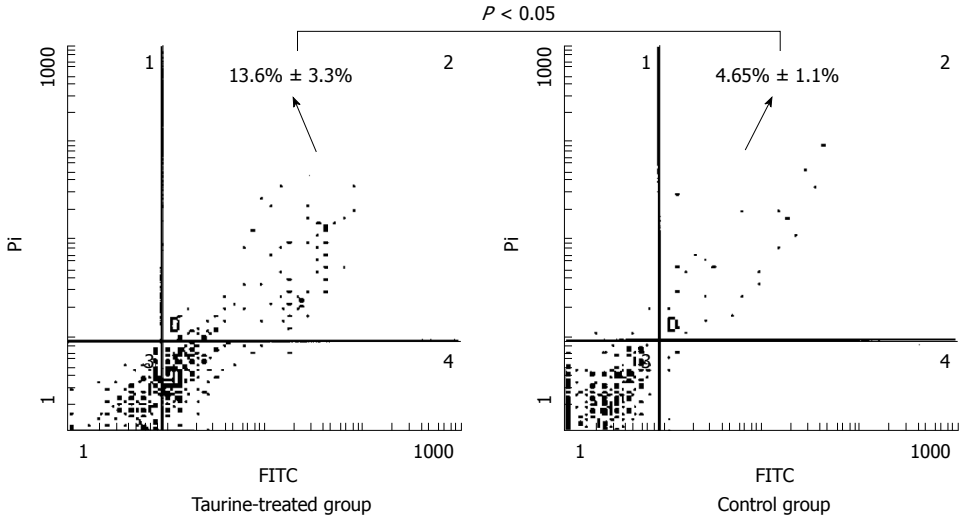

Figure 5 Apoptosis profiles of HSCs treated or untreated with taurine. The experiment was repeated 3 times for each sample (*t* test, $P < 0.05$). Cell count in the second quadrant was used to calculate the apoptosis rate.

the proteins involved in oxidation reaction, some may be engaged in HSC apoptosis as well (SOD1), and some belong to the same protein family (PRDX3 and PRDX2). Moreover, the hydrogen peroxide metabolic process listed in Table 2 is actually one of the basic steps of oxidation reaction[26,27] and this metabolism-related process also involves SOD1 and PRDX3. Thus, it is possible that, in the interconnected process of HSC apoptosis, SOD1 and PRDX3 play a critical mechanism-specific role. For the reasons given above, we presume that natural taurine may facilitate the release of cyt-c from mitochondria and then promote HSC apoptosis by directly or indirectly inducing activation of caspase *via* ROS[25,28] and that SOD1and PRDX3 are two significant functional proteins in the process.

The hepatic parenchyma consists of parenchymal liver cells (PLCs) including hepatocytes and non-parenchymal liver cells (NPLCs) associated with sinusoids including HSCs. It has been demonstrated that the activation of HSCs is the key issue in the pathogenesis of HF[7]. Changes of hepatocytes proliferation may stimulate hepatocyte interaction with HSCs possibly *via* cell adhesion molecules leading to HSC activation and HSC clustering[29,30]. It is obvious that HSCs is the most important HF target cell line in the liver, however, HSC-HSC and hepatocyte-HSC cell adhesion may play a combined role in HF. Therefore, study of the activation and apoptosis of HSC can extensively survey the possible pathological mechanisms of HF, but further investigations on animal models or clinical patients *in vivo* will obtain more exact results for HF in living organisms.

Taurine can either be synthesized chemically or extracted from natural sources. However, natural taurine is more superior to synthetic taurine in promoting HSC apoptosis[31]. The advantage and innovativeness of our present study are reflected in the selection of natural taurine for investigation of its mechanism in regulating HSC apoptosis. In addition, since no studies using proteomic high throughput technologies to investigate the inhibition of HF by taurine have been published in China and other countries, our findings are useful for future systematic studies on biological mechanism.

Life is a vast and complex dynamic network system and the therapeutic mechanism of drug treatment mimics an integrated modulatory chain effect involving a variety of pathways in regulating biological networks[32]. The present study, which systematically investigated how natural taurine may regulate HF-associated biological networks, will help to cast a new light on the action mechanism and targets of taurine.

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COMMENTS

Background

Hepatic fibrosis (HF) occurs in most types of chronic liver diseases and approximately 25%-40% of HF cases may ultimately progress to hepatic cirrhosis. Hepatic stellate cells (HSCs) contribute significantly to the occurrence of HF and the activation of HSC is the key issue in the pathogenesis of HF. It is expected that HSCs are targets for pharmacological or molecular interventions for the treatment of HF.

Research frontiers

Taurine is a kind of important anti-injury substance in the body. Taurine has a protective effect on various types of liver injury. It has been clear that the antifibrotic mechanism of taurine may involve its inhibition of the activation and proliferation of HSCs. However, the molecular mechanism of taurine-mediated antifibrotic activity is largely unknown. Now the research hotspot is to unveil the underlying regulatory mechanisms and accumulate data for drug development.

Innovations and breakthroughs

In the present study, the authors analyzed the differential expression of proteins between taurine-treated HSCs and controls by comparative proteomics technologies. It is the first investigation to study the natural taurine mediated protection effects against HF. Nineteen differentially expressed proteins were identified and functional analysis provided confident evidence of HSC apoptosis promotion by taurine treatment.

Applications

The study results are very helpful to understand better the molecular mechanism underlying taurine's protection against HF and thereby provide new targets for the management of HF and drug development.

Peer review

The authors investigated the effect of taurine on the HSCs by proteomic analysis. They identified 19 differently expressed proteins belonging to the

biological process of apoptosis, cellular oxidation and metabolic processes. They also found an increased rate of apoptosis in taurine exposed cells. Overall, this work is of interest in relation to taurine induced protection in HF and in the underlying alterations in specific proteins in HSC.

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