

Original Paper

# Nmnat 1: a Security Guard of Retinal Ganglion Cells (RGCs) in Response to High Glucose Stress

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## Key Words

Diabetic retinopathy • Nmnat1 • Retinal ganglion cell • MAPK signaling

## Abstract

**Background/Aims:** Retinal neurodegeneration is an early event in the pathological process of diabetic retinopathy (DR). Retinal ganglion cell (RGC) injury is an important pathological feature during neurodegenerative process. Protecting RGCs from high glucose-induced injury is a promising strategy for delaying or hindering diabetes mellitus-related retinal neuropathy. This study aims to investigate the role of Nmnat1, an enzyme which catalyzes a key step in the biosynthesis of nicotinamide adenine dinucleotide (NAD), in high glucose-induced RGC injury. **Methods:** Western blot and immunofluorescence analysis was conducted to detect Nmnat1 expression pattern in the retina and RGC-5 cell. MTT assay, Hoechst staining, trypan blue staining, and calcein-AM/ propidium iodide (PI) staining was conducted to determine the effect of Nmnat1 knockdown on RGC-5 cell function. Microarray and bioinformatics analysis was conducted to identify potential signaling pathways affected by Nmnat1 knockdown. Pharmacological intervention, molecular intervention, and *in vitro* experiments were conducted to reveal molecular mechanism of Nmnat1-mediated protective effect on RGC-5 cell function. **Results:** Nmnat1 is constitutively expressed in retina and RGC-5 cells. Nmnat1 knockdown aggravates RGC injury, and accelerates the development of RGC-5 cell apoptosis upon high glucose stress. MAPK signaling is the primary signaling pathway affected by Nmnat1 knockdown. Under high glucose stress, Nmnat1 knockdown leads to p38-MAPK signaling inactivation. p38-MAPK pathway inhibitor strongly blocks Nmnat1-mediated protective effect on RGC-5 cell function. **Conclusion:** Nmnat1 protects RGC against high glucose-induced injury via p38-MAPK signaling pathway. Nmnat1 may serve as a neuroprotective target for diabetes mellitus-related retinal neuropathy.

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## Introduction

Diabetic retinopathy (DR) is the leading cause of vision impairment and blindness in both developing and developed countries [1]. Microvascular dysfunction is an important hallmark of DR. Thus, DR is often considered as a microcirculatory disease of retina [2]. Recently, increasing studies have revealed that retinal neurodegeneration is also involved in the pathogenesis of DR, which contributes to the development of microvascular abnormalities [3-5]. Understanding the mechanism of retinal neurodegeneration contributes to the development of new prevention and treatment strategies for DR.

Neural apoptosis and reactive gliosis are the important features of retinal neurodegeneration during DR [6]. Retinal ganglion cells (RGCs) located in the inner retina are the retinal neurons in which apoptotic process related to diabetes is first detected [7, 8]. RGC loss leads to a marked reduction in the thickness of retinal nerve fiber layer, which has been reported in rats with streptozotocin (STZ)-induced diabetes, and diabetic patients without or with only minimal DR [8, 9]. Thus, protecting RGCs from high glucose-induced injury could delay or hinder DR-related retinal neurodegeneration.

Nicotinamide mononucleotide adenylyltransferase (Nmnat) constitutes an NAD<sup>+</sup> salvage/recycling pathway using NAM as the precursor in mammalian cells. To date, three different Nmnat enzymes have been identified, including Nmnat1, Nmnat2, and Nmnat3. The function of Nmnat1 was first identified in Wallerian degeneration slow (Wld<sup>s</sup>) mouse model. Overexpression of a chimeric nuclear protein Wld<sup>s</sup> with Nmnat1 activity leads to axonal protective phenotype in these mice [10, 11]. Both mammalian Nmnat1 and *Drosophila* Nmnat1 show neuronal protective activity, although in some studies with reduced efficacy compared to Wld<sup>s</sup> protein [12-14]. In some experimental systems, Nmnat enzymatic activity is critical for neuronal protection phenotype [12, 15]. However, the role of Nmnat1 in DR-related retinal neurodegeneration is still unclear.

In this study, we show that Nmnat1 is constitutively expressed in retina and RGC-5 cell. Nmnat1 knockdown could aggravate RGC damage, and accelerate the development of RGC apoptosis. Under high glucose stress, Nmnat1-mediated protective effect on RGC function is mainly mediated through p38-MAPK signaling pathway. Nmnat1 may become a promising therapeutic target for the treatment of DR-related retinal neurodegeneration.

## Materials and Methods

### *Cell culture and transfection*

Retinal ganglion cell line, RGC-5 cells, were maintained in Dulbecco's modified Eagle's medium (DMEM; Life Technologies) containing 2 mM glutamine, 10 IU/mL penicillin, 10 µg/mL streptomycin, and 10% fetal bovine serum (FBS, Gibco). They were incubated with a humidified atmosphere of 5% CO<sub>2</sub>-95% air at 37°C. Nmnat1 siRNAs were designed and synthesized by Shanghai GenePharma Co. Ltd (Shanghai, China). Lipofectamine 2000 (Invitrogen) was used to transfect siRNAs into RGC-5 cells according to the manufacturer's instruction.

### *Pharmacological intervention*

RGC-5 cells were transfected with Nmnat1 siRNA or Nmnat1 plasmid to change Nmnat1 expression levels. After that, RGC-5 cells were pretreated with MAPK inhibitors (U0126, 10 µM; SB203580, 10 µM; SP600125, 10 µM) for 1 h to inhibit MAPK signaling, and then exposed to high glucose (30 mM) for 48 h. U0126 (ERK inhibitor), SB203580 (p38 inhibitor), and SP600125 (JNK inhibitor) were purchased from Sigma Chemical.

### *Western blot analysis*

RGC-5 cells were incubated with high glucose for 48 h (30 mM) with or without Nmnat1 siRNA transfection, and then washed with ice-cold PBS. These cells were homogenized in lysis buffer, and centrifuged at 12,000×g for 15 min. Protein concentration was detected using BCA assay. Protein (30 µg)

was separated by 8-10% SDS-PAGE, and then transferred to polyvinylidene difluoride membranes. The membranes were blocked with 5% non-fat dry milk for 1 h at room temperature. The membranes were subsequently incubated with primary antibody and horseradish-conjugated secondary antibody. The blots were detected using the enhanced chemiluminescence (ECL) kit.

#### *Cell viability assay*

Cell viability was determined using 3-(4, 5-dimethylthiazol-2-yl)-2, 5-diphenyltetrazolium bromide (MTT) assay. Briefly, MTT solution (Sigma, 0.5 mg/ml) was added into each well of a 96-well plate, and incubated at 37°C for 3 h. The plates were then removed. Dimethyl sulfoxide (DMSO) was added to dissolve the purple formazan product. The absorbance at the wavelength of 570 nm was detected using a Multi-Mode microplate reader (Molecular Device).

#### *Hoechst staining assay*

Hoechst 33258 fluorescent dye was used to detect DNA condensation and nuclear fragmentation. In brief, RGC-5 cells were ( $2 \times 10^5$  cells/well) were seeded onto 6-well plates for the required treatment. These cells were washed with PBS, and fixed with 4% paraformaldehyde for 15 min. They were then washed with PBS, and stained with Hoechst 33258 (mg/ml) for 15 min. Finally, these cells were observed using an Olympus IX-73 microscope.

#### *Trypan blue staining*

RGC-5 cells were seeded onto 12-well plates at the density of  $5 \times 10^4$  cells/well. After the required treatment, these cells were trypsinized. 4% trypan blue solution (Gibico) was added for 10 min staining. The stained cells were observed using an Olympus IX-73 microscope.

#### *Calcein-AM/propidium iodide (PI) staining*

Calcein-AM and PI double staining was used to discriminate viable and dead cells. Briefly, RGC-5 cells were fixed with 4% paraformaldehyde for 15 min after the required treatment, and then stained with Calcein-AM solution (Molecular Probes, 10  $\mu$ mol/L) for additional 15 min. After washing with PBS for three times, these cells were then stained with PI (Molecular Probes, 10  $\mu$ mol/L) for 10 min. Viable cells were observed using a 490 nm excitation filter; while dead cells were observed using a 545 nm excitation filter.

#### *Immunofluorescence analysis*

Retina tissue was fixed in 4% paraformaldehyde for 1 h, immersed in 30% sucrose for 4 h, embedded in optimal cutting temperature (OCT) compound (Tissue-Tek; Sakura Finetek, Torrance, CA), and sectioned at 30  $\mu$ m. Retinal slices were then incubated in 1% Triton X-100 in 0.1% citrate for 1 h and stained with Nmnat1 antibody conjugated with Cy-3 at 4°C overnight. Immunofluorescence labeling was then observed using an Olympus IX-73 microscope.

#### *Microarray analysis*

Total RNAs were isolated from Nmnat1-knockdown RGC-5 cells and scrambled siRNA-transfected RGC-5 cells. The cDNAs were labeled using the Superscript Plus Direct cDNA labeling system (Invitrogen), and then hybridized to the chip. Hybridization images were collected using an Agilent Microarray Scanner G2565BA. Data was first analyzed using the Agilent Feature Extraction software. Further analysis was performed using the GeneSpring GX v11.5.1 software package (Agilent Technologies). Differentially expressed mRNAs were input into the Database for Annotation, Visualization and Integrated Discovery (DAVID, <http://david.abcc.ncifcrf.gov>) for the annotation and functional analysis, including gene set enrichment analysis and mapping gene sets to KEGG pathway.

#### *Statistical analysis*

Statistical analysis was performed using SPSS 13.0 software. Data was shown as mean  $\pm$  SEM. Differences between different groups were analyzed by Student's *t* test or one-way ANOVA. *P* < 0.05 was considered statistically significant.

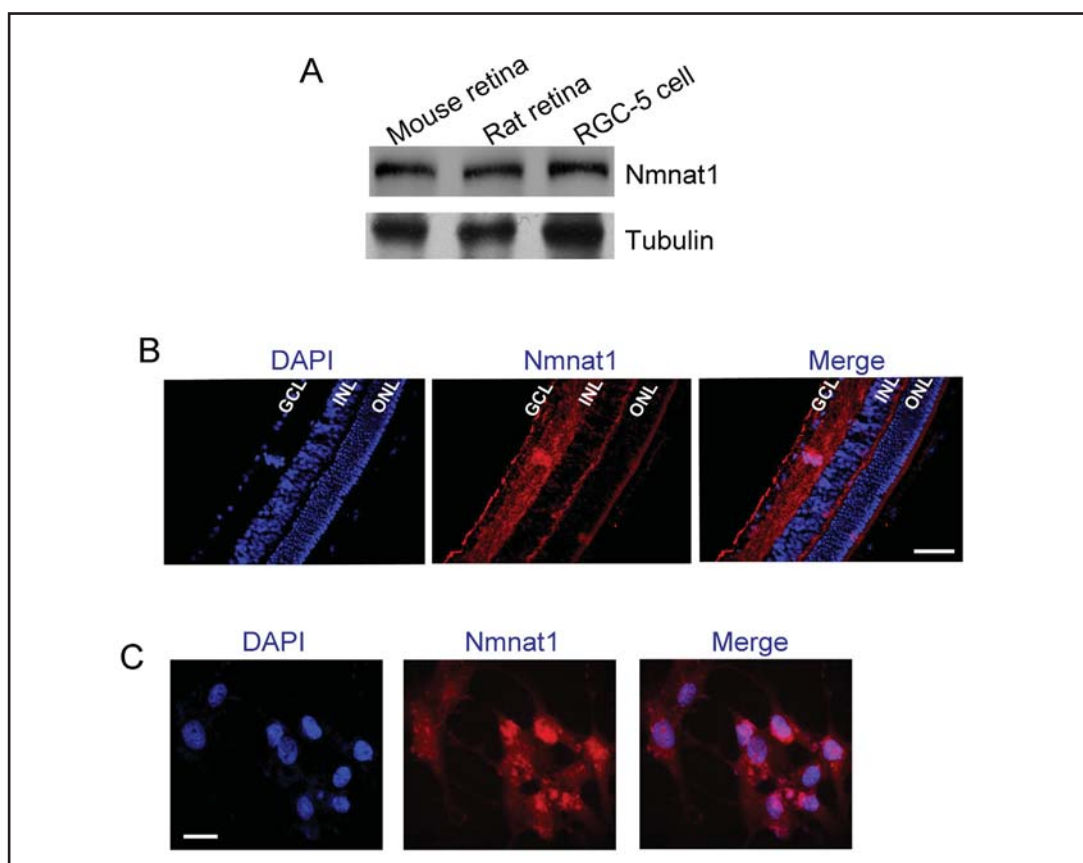
## Results

### *Detection of Nmnat1 expression pattern in retina and RGC-5 cell*

Nmnat1 is a protein involved in mammalian NAD<sup>+</sup> salvage/recycling signaling. Its expression is regulated by nutrient and stress in a number of human cell lines and primary rat tissues [16, 17]. Although several studies have shown that the Nmnat1 is expressed in many tissues [18-21], it is still unknown whether it is expressed in retina and RGC-5 cell. Western blot analysis showed that Nmnat1 was expressed in RGC-5 cell and in the retina of mouse and rat (Fig. 1A). Immunofluorescence experiments revealed that Nmnat1 was expressed in the inner plexiform layer, outer plexiform layer, and ganglion cell layer of mouse retina (Fig. 1B). We also found that Nmnat1 was localized in both the nucleus and cytoplasm of RGC-5 cell (Fig. 1C).

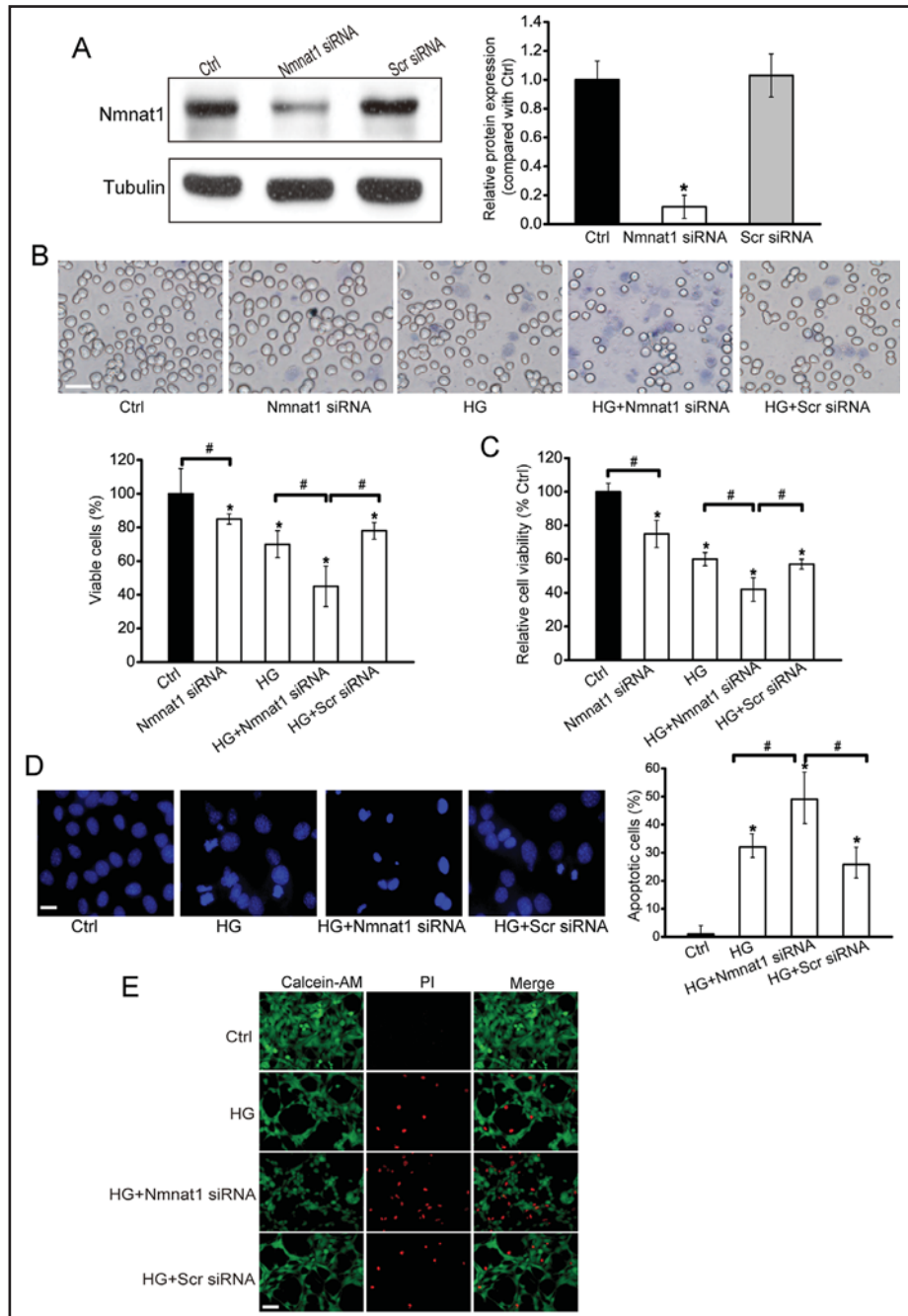
### *Nmnat1 knockdown affects RGC-5 cell function in vitro*

To reveal the functional relevance of Nmnat1 in response to high glucose stress, we determined the effect of Nmnat1 knockdown on RGC function *in vitro*. Western blot analysis showed that Nmnat1 expression was significantly reduced after Nmnat1 siRNA transfection (Fig. 2A). High glucose significantly decreased the number of viable cells (Fig. 2B) and reduced RGC-5 cell viability (Fig. 2C) as detected by trypan blue staining and MTT assay. Nmnat1 knockdown could further reduce the viability of RGC-5 cells (Fig. 2B and 2C).



**Fig. 1.** Detection of Nmnat1 expression pattern in retina and RGC-5 cell. (A) Total proteins were extracted from mouse retinas, rat retinas, and RGC-5 cells. Western blots were performed to detect Nmnat1 expression. Tubulin was detected as the internal control. A representative immunoblot was shown. (B) Immunofluorescence experiments were conducted to detect Nmnat1 expression in mouse retina. Scale bar, 100  $\mu$ m. (C) Immunofluorescence experiments were conducted to detect Nmnat1 expression in RGC-5 cells. Scale bar, 20  $\mu$ m.

**Fig. 2.** Nmnat1 knockdown affects RGC-5 cell function *in vitro*. (A) RGC-5 cells were transfected with Nmnat1 siRNA, scrambled (Scr) siRNA, or left untreated (Ctrl) for 48 h. Western blot was conducted to detect Nmnat1 expression. Tubulin was detected as the internal control. A representative immunoblot was shown along with the densitometric quantitative result. (B-E) RGC-5 cells were transfected with scrambled siRNA (Scr), Nmnat1 siRNA, or left untreated (Ctrl), and then exposed with or without high glucose (30 mM) for 48 h. Viable cells were assessed



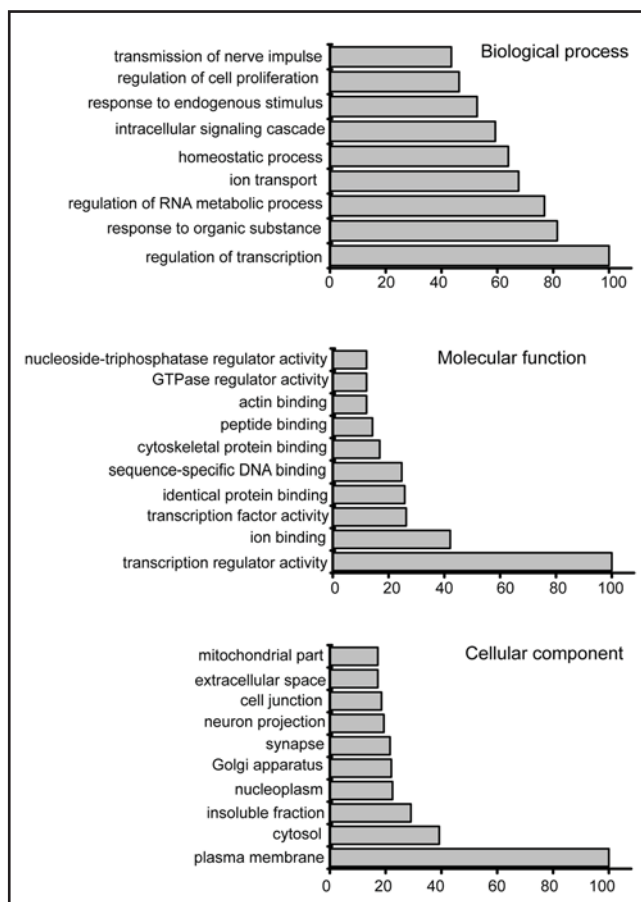
by cell counting after trypan blue exclusion. Scale bar: 50  $\mu$ m. (B) Cell viability was detected using MTT method (C). The data was expressed as the relative change compared with Ctrl group without high glucose treatment. (D) Apoptotic cells were analyzed using Hoechst staining and quantitated. The data was shown as means $\pm$ S.E.M. and represented four independent experiments in which >300 cells were counted. Scale bar: 20  $\mu$ m. (E) Apoptotic cells were analyzed using PI/calcein-AM double staining. Scale bar: 50  $\mu$ m. "\*" indicated a significant difference compared with the corresponding control group. "#" indicated a significant difference between the marked groups.

To determine whether Nmnat1 regulates the development of high glucose-induced apoptosis, RGC-5 cells were treated with Nmnat1 siRNA, scrambled siRNA, or left untreated, followed by high glucose treatment. Compared with high glucose-treated group, the combination of Nmnat1 knockdown and high glucose treatment resulted in higher apoptotic





**Fig. 3.** Genome-wide analysis of differentially expressed genes between Nmnat1 knockdown cells and wild-type RGC-5 cells. Microarray analysis was conducted to compare gene expression difference between Nmnat1 siRNA-transfected RGC-5 cells and scrambled siRNA-transfected RGC-5 cells. Gene enrichment (GO) analysis was used to reveal the biological modules of differentially expressed mRNAs, including biological process, cellular component, and molecular function.

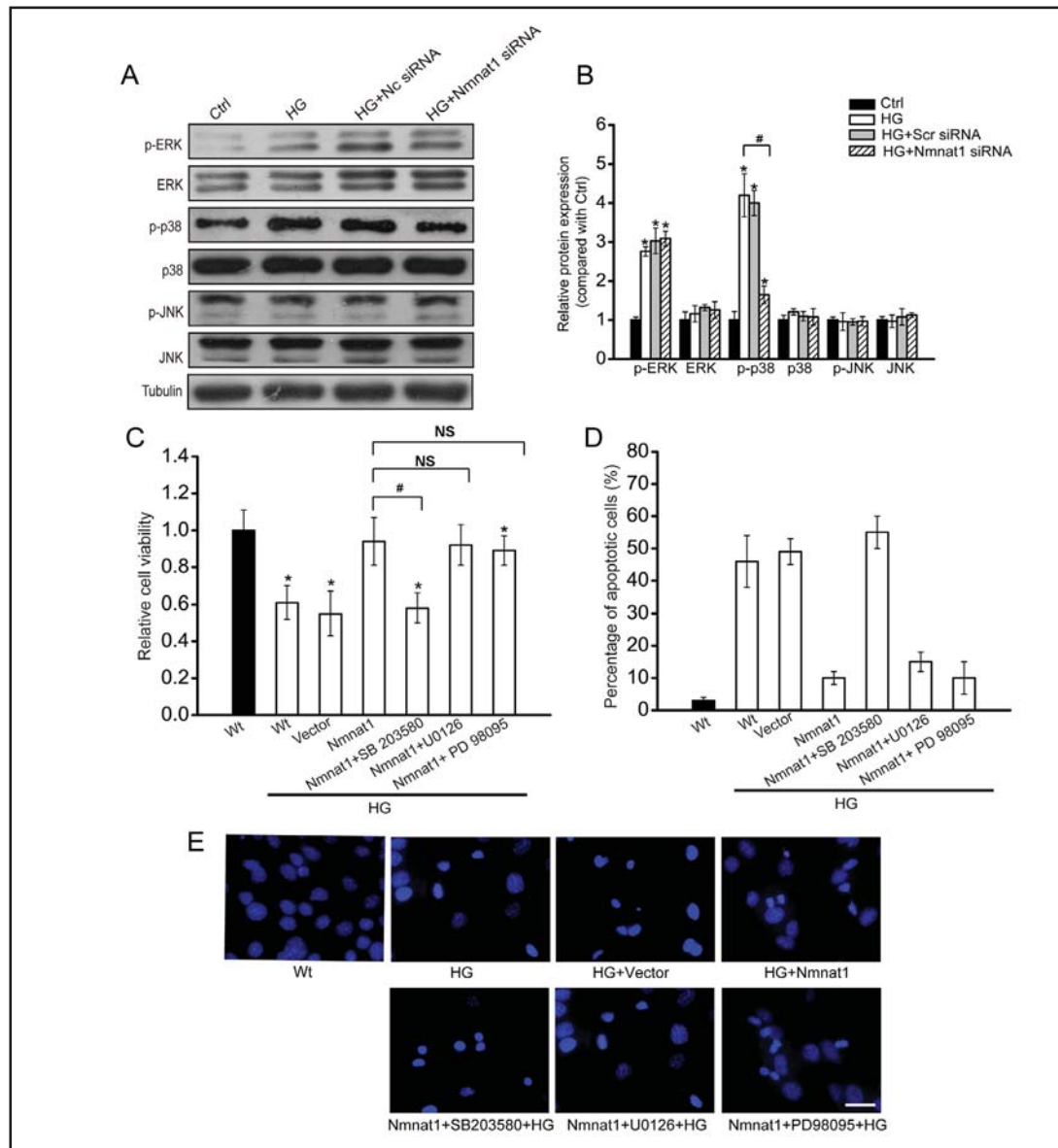


**Table 2.** Top 10 signaling pathways affected by Nmnat1 knockdown

Term	P Value	Fold Enrichment
MAPK signaling pathway	3.48E-13	3.137629097
Neuroactive ligand-receptor interaction	1.15E-06	2.710084034
Calcium signaling pathway	0.002031	2.276470588
Tight junction	0.028798	1.814198783
Wnt signaling pathway	0.029715	4.110294118
Leukocyte transendothelial migration	0.044901	1.858567775
Endocytosis	0.060841	1.554141059
Cell adhesion molecules (CAMs)	0.063781	1.666335453
rno04930:Type II diabetes mellitus	0.07389	2.348739496
rno04060:Cytokine-cytokine receptor interaction	0.087847	1.502239474

ERK1/2 levels. Nmnat1 knockdown significantly reduced phosphorylated p38 levels, but had no effect on the levels of phosphorylated ERK1/2 or JNK1/2 (Fig. 4A and 4B), suggesting that Nmnat1 knockdown leads to inactivation of p38-MAPK signaling. To further examine whether p38 is involved in Nmnat1-mediated protective effect on RGC-5 cell function, Nmnat1 was overexpressed in RGC-5 cells. These cells were pretreated with SB203580, U0126, or SP600125, and then exposed to high glucose for 48 h. MTT assays showed that SB203580, a p38-MAPK signaling inhibitor, strongly blocked Nmnat1-mediated protective effect on RGC-5 cell function, whereas U0126 (ERK inhibitor) or SP600125 (JNK inhibitor) treatment did not affect Nmnat1-mediated protective effect on RGC-5 cell function (Fig. 4C). Hoechst 33342 staining showed that Nmnat1 overexpression decreased high glucose-





**Fig. 4.** Nmnat1 protect RGC-5 cells against high glucose-induced injury through p38-MAPK signaling. (A, B) RGC-5 cells were transfected with Nmnat1 siRNA, scrambled siRNA (Scr), or left untreated, and then exposed to high glucose (30 mM) for 48 h. The untreated group was taken as the control group (Ctrl). Representative immunoblots (A) of total p38, total ERK, total JNK, p-p38, p-ERK, p-JNK, and tubulin were shown along with the densitometric quantitative results (B). (C) RGC-5 cells were transfected with Nmnat1 plasmid or vector (pcDNA3.0), then pretreated with SB203580, U0126, or SP600125 for 1 h, and finally exposed to high glucose (30 mM) for additional 48 h. Cell viability was detected by MTT assay (n = 4). (D, E) RGC-5 cells were treated as shown in Fig. 4C. Apoptotic cells were analyzed using Hoechst staining and quantitated. The data was shown as means  $\pm$  S.E.M. and represented four independent experiments in which > 300 cells were counted. Statistical result was shown in Fig. 4D. A representative image for Hoechst staining was shown Fig. 4E. Scale bar: 20  $\mu$ m. \*indicated a significant difference compared with wild-type (WT) group. #indicated a significant difference between the marked groups. NS: no significant difference.

induced RGC-5 cell apoptosis. SB203580 treatment could interrupt this protective effect, whereas U0126 or SP600125 treatment had no effect on this effect (Fig. 4D). Collectively, these results suggest that p38-MAPK signaling is involved in Nmnat1-mediated protective effect on RGC-5 cell function.

## Discussion

Nmnat1 encodes an enzyme which catalyzes a key step in the biosynthesis of nicotinamide adenine dinucleotide (NAD), which is highly conserved from archaeobacteria to human [22]. Studies in *Drosophila* and mice have revealed a neuroprotective role of Nmnat1 in neurodegenerative conditions including tauopathies, Charcot-Marie-Tooth (CMT) disease, Parkinson's disease, and glaucoma. Loss of Nmnat1 could lead to rapid and severe neurodegeneration [23-26]. In this study, we reveal a role of Nmnat1 in diabetes mellitus-related retinal neurodegeneration. Nmnat1 could protect RGCs against high glucose-induced injury *in vitro*.

DR is not only a microvascular disease but also a neurodegenerative disease [27]. Hyperglycemia could lead to the apoptosis of both retinal neurons and vascular cells [28, 29]. RGCs are located in the inner retina, and are easily injured in response to high glucose stress. Nmnat1 knockdown could aggravate RGC injury, and accelerate the development of RGC apoptosis, suggesting a protective role of Nmnat1. A recent study has revealed that cytoplasmic overexpression of Nmnat1 could protect mouse retinal ganglion cell axons and soma against from glaucomatous and ischemic-induced injury [30], also suggesting a protective role of Nmnat1 under stress condition. Taken together, Nmnat1 is emerged as a security guard of RGCs in response to stress.

To understand the mechanism of Nmnat1-mediated protective effect on RGC function, we conducted genome-wide analysis of gene expression through microarray, which can simultaneously detect the expression of thousands of transcripts. We found that the highest enriched GOs targeted by differentially expressed mRNAs were regulation of transcription (ontology: biological process), plasma membrane (ontology: cellular component), and transcription regulator activity (ontology: molecular function), suggesting that Nmnat1 knockdown may affect gene transcription, which in turn affects the expression of genes associated with RGC function. Signaling pathway analysis provides the knowledge about genomes and the relationship to biological system. We show that these differentially expressed mRNAs are most enriched in MAPK signaling pathway. MAPK family is a common participant in mediating growth factor receptor as well as adhesive and tensional signals from the cell surface to the nucleus. They are activated in response to physiological angiogenic stimuli, such as elevated shear stress and mechanical stretch [31, 32]. The activation of MAPK signaling in RGCs may be responsible for diverse downstream actions such as cell proliferation, cell apoptosis, and electrical signal transduction.

Microarray and bioinformatics analysis suggests that Nmnat1 knockdown affects the activity of MAPK signaling. Thus, we investigated the involvement of MAPK signaling in Nmnat1-mediated protective effect on RGC function. MAPKs are a family of serine/threonine kinases, including extracellular signal-regulated kinase (ERK), c-Jun N-terminal protein kinase (JNK), and p38 MAPK [31, 33]. Nmnat1 knockdown leads to the inaction of p38 MAPK signaling. SB203580, a p38 MAPK pathway inhibitor, strongly blocks the effect of Nmnat1-mediated protective effect on RGC function, suggesting that p38-MAPK signaling is mainly involved in Nmnat1-mediated protective effect in RGC function. MAPK signaling activation has been reported to contribute to neuroprotection, and be involved in the development of diabetic retinopathy [34-37]. MAPK signaling could regulate a variety of cellular activities, including proliferation, differentiation, survival, and death. These biological processes may co-regulate to cope with diverse extracellular and intracellular stimuli [31]. In this study, we show novel evidence that MAPK signaling is involved in neuroprotection.

In conclusion, we show that Nmnat1 knockdown could aggravate RGC injury, and accelerate the development of RGC apoptosis in response to high glucose stress. Nmnat1 protects RGC against high glucose-induced injury via p38-MAPK signaling pathway. Nmnat1 may serve as a neuroprotective target for diabetes mellitus-related retinal neuropathy.

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## Disclosure Statement

None declared.

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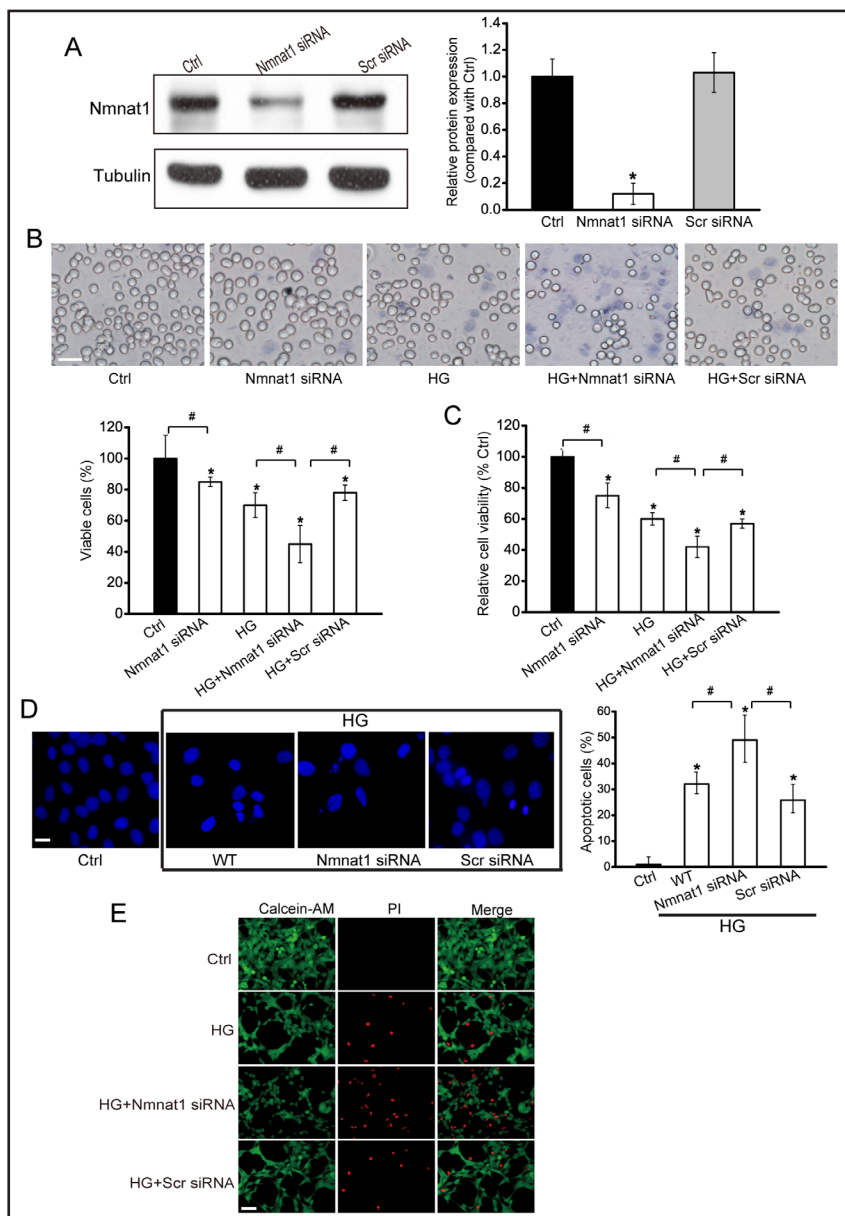
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## Erratum

In the article by Zhou et al., entitled “Nmnat 1: a Security Guard of Retinal Ganglion Cells (RGCs) in Response to High Glucose Stress” [Cell Physiol Biochem 2016;38:2207-2218 (DOI: 10.1159/000445576)] there is an error in Figure 2. The correct figure and the legend is reproduced correctly here. The authors sincerely regret this error due to wrong submission during the review process.

**Fig. 2.** Nmnat1 knockdown affects RGC function *in vitro*. (A) RGCs were transfected with Nmnat1 siRNA, scrambled (Scr) siRNA, or left untreated (Ctrl) for 48 h. Western blots were performed to detect Nmnat1 expression. Tubulin was detected as the internal control. A representative immunoblot was shown along with quantitative result. (B-E) RGCs were transfected with Scr siRNA, Nmnat1 siRNA, or left untreated (Ctrl), and then exposed with or without high glucose (30 mM) for 48 h. Viable cells were detected by cell counting after trypan blue exclusion. Scale bar: 50  $\mu$ m. (B). Cell viability was detected using MTT method (C). The data was expressed as relative change compared with Ctrl group without high glucose treatment. (D) Apoptotic cells were analyzed using Hoechst staining and quantitated. The



data was shown as means $\pm$ S.E.M. and represented four independent experiments in which >300 cells were counted. (E) Apoptotic cells were analyzed using PI/Calcein-AM double staining. Scale bar: 50  $\mu$ m. “\*” indicated significant difference compared with the corresponding control group. “#” indicated significant difference between the marked groups.