Ox-low density lipoprotein (ox-LDL) increased the susceptibility of primary nephrotic syndrome (PNS) by regulating the Treg/Th17 ratio via the MEG3 signaling

Type

Research paper

Keywords

FOXP3, ROR γ t, MEG3, Treg/Th17, miR-125a, primary nephrotic syndrome, ox-low density lipoprotein, miR-17

Abstract

Introduction

Patients with primary nephrotic syndrome (PNS) were reported to exhibit the evident imbalance between the number of Th17 and Treg cells in their peripheral blood monocytes (PBMCs), which might be the immunological basis of the disease.

Material and methods

40 PNS patients and 42 healthy individuals were recruited in this study. FCM assay was used to observe the levels of Treg and Th17 cells.

Results

The Treg/Th17 ratio was evidently decreased in PNS patients. The levels of MEG3 and ROR γ t were increased in the PNS group, while the levels of miR-17, miR-125a and FOXP3 mRNA were reduced in the PNS group. Moreover, the levels of IL-6 and IL-1 β were highly increased in PNS patients. Ox-low density lipoprotein (ox-LDL) treatment significantly increased the levels of MEG3 and ROR γ t mRNA/protein while decreasing the levels of miR-17, miR-125a, and FOXP3 mRNA/protein in THP-1 cells, and the transfection of MEG3 siRNA partly alleviated the dysregulation in the expression of MEG3, relevant miRNAs and relevant mRNAs induced by ox-LDL. Also, the expression of miR-17 and miR-125a was evidently decreased upon the successful transfection of MEG3, but the ROR γ t mRNA/protein levels were promoted while the FOXP3 mRNA/protein levels were inhibited.

Conclusions

Our results demonstrated that ox-LDL could promote the inflammatory response of PNS by decreasing the Treg/Th17 ratio via activating the MEG3 signaling. The activation of MEG3/miR-125a/FOXP3 axis and MEG3/miR-17/ROR γ t axis respectively lead to the Treg/Th17 imbalance, which resulted in up-regulated IL-6 and IL-1 β levels, thus increasing the susceptibility of PNS.

Ox-low density lipoprotein (ox-LDL) increased the susceptibility of primary nephrotic syndrome (PNS) by regulating the Treg/Th17 ratio via the MEG3 signaling

Li Jin¹, Xiaopei Wang¹, Xinfang Xie¹, Ping Lan¹, Shifeng Yang^{1*}

1. Department of Nephrology, Kidney Hospital, The First Affiliated Hospital of Xi'an Jiaotong University, Xi'an 710061, P.R. China

* Correspondence to: Shifeng Yang, Department of Nephrology, Kidney Hospital, The First Affiliated Hospital of Xi'an Jiaotong University, 277 West Yanta Road, Xi'an, Shaanxi Province, People's Republic of China

Email: orthomedical@yeah.net

Tel: 0086-29-85323951

Abstract

Background: Patients with primary nephrotic syndrome (PNS) were reported to exhibit the evident imbalance between the number of Th17 and Treg cells in their peripheral blood monocytes (PBMCs), which might be the immunological basis of the disease. **Method:** 40 PNS patients and 42 healthy individuals were recruited in this study. FCM assay was used to observe the levels of Treg and Th17 cells. **Result:** The Treg/Th17 ratio was evidently decreased in PNS patients. The levels of MEG3 and ROR γ t were increased in the PNS group, while the levels of miR-17, miR-125a and FOXP3 mRNA were reduced in the PNS group. Moreover, the levels of IL-6 and IL-1 β were highly increased in PNS patients. Ox-low density lipoprotein (ox-LDL) treatment significantly increased the levels of MEG3 and ROR γ t mRNA/protein while decreasing the levels of miR-17, miR-125a, and FOXP3 mRNA/protein in THP-1 cells, and the transfection of MEG3 siRNA partly alleviated the dysregulation in the expression of MEG3, relevant miRNAs and relevant mRNAs induced by ox-LDL. Also, the expression of miR-17 and miR-125a was evidently decreased upon the successful transfection of MEG3, but the ROR γ t mRNA/protein levels were promoted while the FOXP3 mRNA/protein levels were inhibited. **Conclusion:** Our results demonstrated that ox-LDL could promote the inflammatory response of PNS by decreasing the Treg/Th17 ratio via activating the MEG3 signaling. The activation of MEG3/miR-125a/FOXP3 axis

and MEG3/miR-17/ROR γ t axis respectively lead to the Treg/Th17 imbalance, which resulted in up-regulated IL-6 and IL-1 β levels, thus increasing the susceptibility of PNS.

Abbreviation list

HC: healthy control

PNS: primary nephrotic syndrome

PBMC: peripheral blood monocyte

MCNS: minimal change nephritic syndrome;

MN: membranous nephropathy;

MsPGN: mesangial proliferative glomerulonephritis;

FSGS: focal segmental glomerulosclerosis

Running title: ox-LDL affects MEG3 signaling in primary nephrotic syndrome

Key words: primary nephrotic syndrome, ox-low density lipoprotein, Treg/Th17, MEG3, FOXP3, miR-125a, miR-17, ROR γ t

Introduction

As one of the most widespread renal ailment in child patients, primary nephrotic syndrome (PNS) has been deemed as a major cause of chronic renal failures among Chinese children [1]. The features of PNS include elevated permeability of the barrier of glomerular filtration and resulting oedema, hypoalbuminaemia as well as proteinuria. So far, the mechanism underlying the PNS pathogenesis is still mostly unknown. Some scholars assume that the PNS is actually caused by the deregulation of T cells or the abnormality in T cell responses [2-4]. It was also suggested that the imbalance between the number of Th1 and Th2 cells as well as the imbalance between the number of Th17 and Treg cells lead to PNS [4, 5]. It was additionally found that ox-LDL plays a stronger role in reducing the count of Treg cells than in reducing the count of Th17 cells, and the discrepancy between the count of Th17 and Treg cells might be responsible for inducing the pathogenesis of the PNS condition in children. Th17 as well as Treg cells, both of which are

differentiated from naïve CD4⁺ T-cells, participate in the control of inflammatory responses. In particular, the effector T-cells drive the immunity while promoting inflammation, and the inhibitory Treg cells exert an opposing effect by reducing the activity of effector T-cells while reducing the level of inflammatory responses [6]. The equilibrium between the number of immuno-suppressive Foxp3⁺ Treg cells and the number of pro-inflammatory Th17 cells exemplifies a critical factor in regulating the homeostasis of the immune system. Furthermore, a decline in the number of Treg cells can cause immune reactions dominated by Th2 cells, resulting in their increased infiltration into eosinophilic tissues [7]. In addition, Th17 and IL -17 were shown to play an essential role in the PNS pathogenesis in children by lowering the expression of podocalyxin as well as by causing the apoptosis of podocytes [4].

LncRNAs are associated with the progression of many diseases, such as asthma, via post-transcriptional or transcriptional regulation of protein expression by means of various mechanisms [8, 9]. Some of such mechanisms could be explained via the function of competing endogenous RNAs (ceRNAs), i.e., lncRNAs may act as ceRNAs to competitively bind to certain miRNAs via base pair complementation, thus reducing the binding of such microRNAs to target genes, so as lead directly to the changes in target gene expression [10]. It was found that the abnormalities in lncRNA-MEG3 in CD4⁺ T cells could regulate the Treg/Th17 imbalance in asthma patients by functioning as a competing endogenous RNA of microRNA-17/ RORγt [11]. Also, it was shown that the highly-expressed MEG3 could directly suppress expression of miR-125a-5p. Alternatively, it was likewise noticed that the overexpression of miR-125a-5p triggered the rise of Foxp3 expression as well as the decrease in RORγt expression in the CD4⁺ cells isolated from ITP patients, indicating that miR-125a-5p actually participated in the pathogenesis of ITP partially via the regulation of Tregs as well as also Th17 cells [12].

It has been reported that patients with PNS exhibited the evident imbalance between the number of Th17 and Treg cells in their PBMCs, which might be the immunological basis of the disease [13]. The ox-low density lipoprotein (ox-LDL) was proved to alter the dynamic profile of Th17 and Treg cells [14, 15]. The MEG3/miRNA-17/RORγt axis and MEG3/miR-125a-5p axis were involved in asthma and immune thrombocytopenic purpura, respectively [11, 12]. In this study, we hypothesized that the activation of MEG3 signaling could influence the imbalance of

Th17/Treg cells in PNS patients. And the administration of ox-LDL might influence the susceptibility of PNS by influencing the expression of MEG3 and its subsequent target genes and proteins. Therefore, we recruited PNS patients to study the effect of ox-LDL on the imbalance of Th17/Treg cells. We also performed Western blot, RT-qPCR and ELISA assays to study the molecular mechanisms underlying the role of ox-LDL in the pathogenesis of PNS.

Materials and Methods

Patient recruitment and patient characteristics

In this study, 40 PNS patients were recruited as the PNS group, while 42 healthy individuals were recruited as the healthy control (HC) group. Peripheral blood samples as well as demographic and clinical characteristics were collected from all patients in both groups, and then compared using the Student's t tests. In addition, Th17 cells were isolated from the peripheral blood samples and then assayed for target gene expression. Institutional ethical committee has approved the protocol of this study.

Assay of Th17 cells by utilizing flow cytometry

5 mL of peripheral venous blood samples were collected from each of the subjects in the two groups under fasting conditions. In the next step, the samples were centrifugally to isolate 3×10^9 /L of mononuclear cells from each sample. Then, roughly 2 mL of each blood sample were moved into a 24-well cell culture plate and then added with 1.0 μ M per well of Monensin, 60 μ g/L per well of Buddha wave ester, as well as 100 μ M per well of streptin. Subsequently, the plate was incubated in a 5% CO₂ incubator for 5 h at 37 °C before the cell suspension was moved into a sterile 2 mL centrifuge tube, which was then centrifuged at for 6 minutes at 3000 rpm to collect the cell pellet. In the next step, the cell pellet was cleaned with PBS to get rid of the residue liquid before 15 μ L of CD4 as well as 15 μ L of IL17a antibodies were added into each tube. After 30 minutes of incubation in the dark, the cells were fixed in a fixation buffer at 5°C for 10 min in the dark, centrifuged, permeabilized in 1 mL of permeabilization buffer, rinsed with PBS, and respectively stained using PE-tagged anti-IL-17 antibodies as well as PE-tagged anti-IgG1 antibodies for flow cytometry.

Assay of Treg cells by utilizing flow cytometry

2 mL of peripheral venous blood samples were collected from each of the subjects in the two groups under fasting conditions. In the next step, each sample was stained using 15 μ L of CD4 as well as 15 μ L of CD25 antibodies for 30 minutes of incubation in the dark before the cells were fixed in 50 μ L/tube of the fixation buffer at 5°C for 10 min in the dark, centrifuged, permeabilized in 1 mL of permeabilization buffer, rinsed with PBS, and respectively stained using PE-tagged anti-Foxp3 antibodies as well as PE-tagged anti-IgG1 antibodies for flow cytometry.

Evaluation of the Th17/Treg population in total peripheral blood mononuclear cells

5 mL of peripheral venous blood samples were collected from each of the subjects in the two groups under fasting conditions. In the next step, the samples were centrifugally to isolate mononuclear cells, which were seeded into a 24-well cell culture plate at 1×10^6 cells per well. In the next step, the cells were randomly divided into four groups, i.e., a blank group of mononuclear cells treated with ox-LDL at a 0.0 μ g/mL concentration, a 0.1 μ g/mL ox-LDL group of mononuclear cells treated with ox-LDL at a concentration of 0.1 μ g/mL, a 1.0 μ g/mL ox-LDL group of mononuclear cells treated with ox-LDL at a concentration of 1.0 μ g/mL, and a 10.0 μ g/mL ox-LDL group of mononuclear cells treated with ox-LDL at a concentration of 10.0 μ g/mL. Subsequently, the plate was incubated in a 5% CO₂ incubator for 24 h at 37 ° C and the cells were collected for flow cytometry to determine the number of Th17 and Treg cells in each sample.

Cell culture

THP-1 cells were acquired from ATCC and then cultured in a DMEM medium containing 10% of fetal bovine serum and appropriate penicillin and streptomycin antibiotics (Gibco, Thermo Fisher Scientific, Waltham, MA). The cell culture conditions were at 37 ° C and 5% CO₂ in a fully humidified incubator. After reaching 80% confluence, the cells were divided into several cellular models. In cell model 1, the THP-1 cells were divided into 3 groups, i.e., 1. PBS group (THP-1 cells treated with PBS only); 2. ox-LDL + NC siRNA group (THP-1 cells treated with ox-LDL and then transfected with a NC siRNA); and 3. ox-LDL+ MEG3 siRNA group (THP-1 cells treated with ox-LDL and then transfected with MEG3 siRNA). In cell model 2, the THP-1 cells were divided into 2

groups, i.e., 1. NC group (THP-1 cells transfected with a NC plasmid); and 2. p-MEG3 group (THP-1 cells transfected with the p-MEG3 plasmid). All cell treatment and transfection lasted 48 h, and the transfection was carried out using Lipofectamine 2000 (Invitrogen, Carlsbad, CA) in accordance with the protocol provided by the reagent manufacturer. After 48 h of transfection, the transfected cells were harvested to assay the expression of target genes.

Real time PCR

The collected cell samples were processed by using a Trizol kit (Ambion, Foster City, CA) in accordance with the protocol provided by the assay kit manufacturer to isolate the total RNA content. In the next step, the isolated RNA pellet was resuspended in RNase free water and subject to reverse transcription to generate cDNA. In particular, the synthesis of cDNA using isolated miRNA samples was carried out by using a miScript II RT assay kit (Qiagen, Hilden, Germany) in accordance with the protocol provided by the assay kit manufacturer. On the other hand, the synthesis of cDNA using isolated mRNA samples was carried out by using a GScript First-Strand cDNA Synthesis kit (GeneDirex, New Taipei, Taiwan) in accordance with the protocol provided by the kit manufacturer. In the next step, the expression of MEG3, relevant miRNAs and relevant mRNAs in each sample was determined by real time PCR, which was carried out on a Light Cycler 480 real-time PCR machine (Roche, Basel, Switzerland) by using a miScript SYBR Green PCR assay kit (Qiagen, Germantown, MD) in accordance with the protocol provided by the assay kit manufacturer. Finally, the relative expression of MEG3, relevant miRNAs and relevant mRNAs in each sample was determined by using the $\Delta\Delta C_t$ approach [16].

Vector construction, mutagenesis and dual luciferase assay

Our preliminary bioinformatic analysis predicted a putative binding site of miR-17 on MEG3, as well as a miR-17 putative binding site in the 3'UTR of RORyt mRNA. Therefore, subsequent luciferase assays were carried out to validate regulatory relationship between miR-17 and MEG3 as well as between miR-17 and RORyt mRNA. In brief, wild type sequences of MEG3 as well as RORyt mRNA containing the miR-17 putative binding sites were inserted into pcDNA (Promega, Madison, WI) luciferase reporting vectors, respectively, to generate wild type vectors of MEG3 as well as RORyt mRNA, respectively. At the same time, site-directed mutagenesis was carried

out by using a Quick Change Mutagenesis assay kit (Stratagene, San Diego, CA) in accordance with the protocol provided by the assay kit manufacturer to generate site-directed mutations in the miR-17 putative binding sites on MEG3 as well as RORyt mRNA, respectively, and the mutant sequences of MEG3 as well as RORyt mRNA containing the miR-17 putative binding sites were also inserted into pcDNA luciferase reporting vectors, respectively, to generate mutant type vectors of MEG3 as well as RORyt mRNA. In the next step, THP-1 cells were transfected with wild type/mutant sequences of MEG3 or RORyt mRNA in conjunction with miR-17 mimics or a scramble control using Lipofectamine 2000 (Invitrogen, Carlsbad, CA) in accordance with the protocol provided by the reagent manufacturer. After 48 h of transfection, the luciferase activity of transfected cells was measured by using a Dual-Luciferase assay kit (Promega, Madison, WI) in accordance with the protocol provided by the assay kit manufacturer on a Lumat 9507 LB (Berthold Technologies, Oak Ridge, TN) luminometer.

Cell proliferation

The proliferation status of cell samples was measured by using a xCELLigence RTCA DP assay kit (ACEA Biosciences, San Diego, CA) in accordance with the protocol provided by the assay kit manufacturer.

Statistical analysis

All data were expressed as mean $\pm$ SD, and all statistical analyses were carried out by utilizing R Statistical Software. A p-value of lower than 0.05 was considered to be statistically significant. All inter group comparisons were done by using Student's t tests.

Results

Patient recruitment and patient characteristics

In this study, 40 PNS patients were recruited into the PNS group, while 42 healthy individuals were recruited into the healthy control (HC) group. The demographic and clinical characteristics were collected and recorded in Table 1. No obvious differences were found between the PNS group and the HC group.

Percentage of Th17 and Treg cells in the PNS and HC groups

The FCM analysis was performed to observe the percentage of Th17 and Treg cells in the patient groups. As shown in Fig.1, the percentage of Th17 cells in the PNS group was significantly increased compared with that in the HC group (Fig.1A), whereas the percentage of Treg cells in the PNS group was markedly reduced (Fig.1B).

Expression of MEG3, miR-17, miR-125a, RORyt mRNA and FOXP3 mRNA in PNS and HC groups

RT-qPCR results of PMBCs collected from the patient groups showed an increased MEG3 level (Fig.2A) in the PNS group, while the expression of miRNAs including miR-17 (Fig.2B) and miR-125a (Fig.2D) was significantly reduced in patients with PNS. The expression of mRNAs including RORyt mRNA and FOXP3 mRNA showed a different tendency. Compared with the HC group, the PNS group showed an increased RORyt mRNA level (Fig.2C) and reduced FOXP3 mRNA level (Fig.2E). Moreover, the plasma level of MEG3 (Fig.3A) was also increased while the plasma levels of miR-17 (Fig.3B) and miR-125a (Fig.3C) were both decreased in PNS patients.

Levels of IL-6 and IL-1 β in PNS and HC groups

ELISA assay was conducted to observe the levels of pro-inflammatory cytokines including IL-6 and IL-1 β in the patient groups. Accordingly, both the levels of IL-6 (Fig.4A) and IL-1 β (Fig.4B) were highly increased in PNS patients.

Ox-LDL participated in the signaling of MEG3

In this study, three groups of THP-1 cells were set up: 1. PBS group in which the cells were treated with PBS only; 2. Ox-LDL+NC siRNA group in which the cells transfected with NC siRNA were treated with ox-LDL; 3. Ox-LDL+MEG3 siRNA group in which the cells transfected with MEG3 siRNA were treated with ox-LDL. RT-qPCR results indicated that, compared with the PBS group, the expression levels of MEG3 (Fig.5A) and RORyt mRNA (Fig.5C) and protein (Fig.5F) were evidently higher while the expression levels of miR-17 (Fig.5B), miR-125a (Fig.5D), and FOXP3 mRNA (Fig.5E) and protein (Fig.5G) were markedly reduced by the ox-LDL treatment of NC siRNA-transfected THP-1 cells. Moreover, the transfection of MEG3 siRNA not only reduced the

expression of MEG3 up-regulated by ox-LDL, but also partly recovered the dysregulation of relevant miRNAs and mRNAs induced by ox-LDL.

The signaling of MEG3

THP-1 cells were transfected with plasmids carrying MEG3. Then, the expression levels of MEG3, relevant miRNAs, relevant mRNAs and relevant proteins were observed. Accordingly, upon the successful transfection of MEG3 (Fig.6A), the expression of miRNAs including miR-17 (Fig.6B) and miR-125a (Fig.6D) was evidently decreased, while the expression of ROR γ t mRNA (Fig.6C) and protein (Fig.6F) was promoted. The expression of FOXP3 mRNA (Fig.6E) and protein (Fig.6G) was also inhibited in the presence of MEG3.

Establishment of the MEG3 axis

As shown in Fig.7A, bioinformatic tools predicted a putative binding site of miR-17 on MEG3, and the subsequent luciferase assay validated that the relative luciferase activity was only reduced in THP-1 cells co-transfected with MEG3 and miR-18. Also, a miR-17 putative binding site was observed in the 3'UTR of ROR γ t mRNA (Fig.7B), and the luciferase assay also validated that ROR γ t mRNA was targeted by miR-17, thus establishing the MEG3/miR-17/ROR γ t axis. As shown in Fig.7C, miR-125a could bind to MEG3, and the transfection of miR-125a also reduced the luciferase activity of MEG3 in THP-1 cells, validating the signaling pathway of MEG3/miR-125a/FOXP3.

Discussion

In this study, we enrolled subjects with or without PNS and compared their expression of candidate lncRNAs, miRNAs, and target genes. We found that, in the PNS group, the percentage of Th17 cells was increased whereas the percentage of Treg cells was reduced. In the PBMC and plasma samples collected from the PNS group, an increased MEG3 level was presented with reduced levels of miR-17 and miR-125a. The mRNA level of ROR γ t was increased while the FOXP3 mRNA level was reduced in the PNS group. Moreover, the levels of pro-inflammatory cytokines including IL-6 and IL-1 β were highly increased in PNS patients. A past study revealed that ox-LDL induced a stronger effect on Treg cells as compared to the effect on Th17 cells in children PNS

[14]. It was additionally disclosed that ox-LDL reduced the viability as well as proliferation of cells to promote persistent inflammation as well as apoptosis. It was also disclosed that ox-LDL plays its role through upregulating the expression of MEG3 in Raw264.7 cells [17]. Many studies showed that three cytokines play important roles in coronary heart diseases. For example, IL-5 links natural and adaptive immunity to the epitopes of low-density lipoprotein (LDL) that has been oxidized to induce the growth of cells carrying IgM antibodies that are specific to oxLDL. Furthermore, IL-10 as well as TGF- β are both related to Treg cells by playing critical and non-redundant roles in preventing the formation of atherosclerosis by means of their immunosuppressive, anti-inflammatory, as well as vasculo-protective features [18]. Naive CD4⁺ T cells in mice activated by TGF- β as well as IL-6 result in the activation of retinoic acid-related orphan nuclear receptor γ t (ROR γ t), which controls the differentiation of Th17 cells [19]. It was also discovered that Th17 cells results in pediatric PNS by elevating the expression of IL-23, IL-1 β , IL-6, as well as RORc [4].

Past research has shown that lncRNA-MEG3 regulates the balance between Treg and Th17 cells [12]. For example, qRT-PCR showed the positive lncRNA-MEG3 as well as microRNA-17 expression in the CD4⁺ T cells isolated from the peripheral blood samples of patients with asthma, while the increased expression of lncRNA MEG3 was accompanied by the increased expression of microRNA-17, suggesting that the lncRNA MEG3 may disrupt the equilibrium between Treg and Th17 cells in the patients with asthma [11]. Bioinformatic analysis also illustrated the presence of 4 binding sites between miR-125a-5p and MEG3, and MEG3 inhibited the expression of miR-125a-5p by interacting with it directly, so as to induce the imbalance between the number of Treg and Th17 cells in ITP [12]. Another research also revealed that lncRNA MEG3 can work as a ceRNA to suppress the expression of microRNA-17 while upregulating the expression of ROR γ t, causing the hyperfunction of Th17 as well as a reduced Treg/Th17 ratio [11]. In this study, we also performed bioinformatic and luciferase assays to validate that MEG3 can sponge miR-17 and miR-125a expression, and that ROR γ t mRNA was targeted by miR-17, thus establishing the MEG3/miR-125a/FOXP3 axis and MEG3/miR-17/ROR γ t axis.

Interesting, the depletion in the number of Foxp3⁺ CD4⁺ Treg cells causes severe auto-immunity, immuno-pathology, as well as allergy [20]. It was also shown that the number of Treg cells was

significantly reduced in PNS patients, suggesting that the Treg cells play a key protective role in the onset of proteinuria as well as PNS [21, 22]. It was also shown that the effect of lncRNA MEG3 on targeting microRNA-17 and ROR γ t affects the activity of Th17 cells. Thus, the abnormalities in the expression of lncRNAs as well as microRNAs in CD4 + T cells can help to diagnose asthma [11]. In this study, we found that the expression levels of MEG3 and ROR γ t mRNA/protein were evidently higher while the expression levels of miR-17, miR-125a, and FOXP3 mRNA/protein were markedly reduced by the ox-LDL treatment of NC siRNA-transfected THP-1 cells, and the transfection of MEG3 siRNA partly recovered the dysregulation in the expression of MEG3, relevant miRNAs and relevant mRNAs induced by ox-LDL. Also, the expression of miRNAs including miR-17 and miR-125a was evidently decreased upon the successful transfection of MEG3, which also promoted the ROR γ t mRNA/protein expression while inhibiting FOXP3 mRNA/protein expression.

ROR γ t has been considered as a crucial transcription factor in Th17 cells. Certainly, the ROR γ t expression in naïve CD4+ T cells induced by retroviral vectors promoted their differentiation to cells with IL-17A as well as IL-17F expression [19, 23]. Given that ROR γ t is crucial for the polarization of Th17 cells in mice, cytokines IL-6 as well as also TGF β can increase ROR γ t expression in Th17 cells [19]. Interestingly, mice fed with a diet enriched in trans fats revealed greater IL-17 as well as ROR γ t expression along with elevated Th17 responses in colitis and severe intestinal inflammation [24, 25].

Conclusion

Our results demonstrated that ox-LDL could promote the inflammatory responses of PNS by up-regulating the expression levels of IL-6 and IL-1 β . The MEG3/miR-125a/FOXP3 axis and MEG3/miR-17/ROR γ t axis were established by our study, indicating the up-regulated MEG3 expression induced by administration of ox-LDL could respectively down-regulate the expression of FOXP3 and up-regulate the expression of ROR γ t. Accordingly, the dysregulation of FOXP3 and ROR γ t respectively led to the decreased Treg/Th17 ratio, thus resulting in the up-regulation of IL-6 and IL-1 β in PNS.

Conflict of interest

300 None

301 **Acknowledgement**

302 This work was supported by the Basic Research Plan of Natural Science of Shaanxi Province
303 (2019JM-537).

304 **Author contributions**

305 LJ, XPW and XFX performed the majority of the laboratory work, statistics and data analysis and
306 participated in writing. PL and SFY were involved in writing. All authors conceived and designed
307 the experiments and drafted the manuscript.

308 **Data availability statement**

309 The data sets generated during and/or analyzed during the current study are available from the
310 corresponding author on reasonable request.

311 **References**

- 312 1 Plumb L, Boother EJ, Caskey FJ, Sinha MD, Ben-Shlomo Y: The incidence of and risk factors
313 for late presentation of childhood chronic kidney disease: A systematic review and meta-
314 analysis. PLoS One 2020;15(12):e0244709.
- 315 2 Sellier-Leclerc AL, Duval A, Riveron S, Macher MA, Deschenes G, Loirat C, Verpont MC,
316 Peuchmaur M, Ronco P, Monteiro RC, Haddad E: A humanized mouse model of idiopathic
317 nephrotic syndrome suggests a pathogenic role for immature cells. J Am Soc Nephrol
318 2007;18:2732-2739.
- 319 3 Shalhoub RJ: Pathogenesis of lipoid nephrosis: a disorder of T-cell function. Lancet
320 1974;2:556-560.
- 321 4 Wang L, Li Q, Wang L, Li C, Yang H, Wang X, Tao H: The role of Th17/IL-17 in the
322 pathogenesis of primary nephrotic syndrome in children. Kidney Blood Press Res
323 2013;37:332-345.

324 5 Kanai T, Shiraishi H, Yamagata T, Ito T, Odaka J, Saito T, Aoyagi J, Momoi MY: Th2 cells
 325 predominate in idiopathic steroid-sensitive nephrotic syndrome. Clin Exp Nephrol
 326 2010;14:578-583.

327 6 Zhu J, Yamane H, Paul WE: Differentiation of effector CD4 T cell populations (*). Annu Rev
 328 Immunol 2010;28:445-489.

329 7 Luo B, Feng L, Jintao D, Yafeng L, Shixi L, Nan Z, Bachert C: Immunopathology features of
 330 chronic rhinosinusitis in high-altitude dwelling Tibetans. Allergy Rhinol (Providence)
 331 2013;4:e69-76.

332 8 Narozna B, Langwinski W, Szczepankiewicz A: Non-Coding RNAs in Pediatric Airway
 333 Diseases. Genes (Basel) 2017;8:

334 9 Zhu YJ, Mao D, Gao W, Hu H: Peripheral whole blood lncRNA expression analysis in
 335 patients with eosinophilic asthma. Medicine (Baltimore) 2018;97:e9817.

336 10 Zhang XY, Tang XY, Li N, Zhao LM, Guo YL, Li XS, Tian CJ, Cheng DJ, Chen ZC, Zhang LX:
 337 GAS5 promotes airway smooth muscle cell proliferation in asthma via controlling miR-
 338 10a/BDNF signaling pathway. Life Sci 2018;212:93-101.

339 11 Qiu YY, Wu Y, Lin MJ, Bian T, Xiao YL, Qin C: LncRNA-MEG3 functions as a competing
 340 endogenous RNA to regulate Treg/Th17 balance in patients with asthma by targeting
 341 microRNA-17/ RORgammat. Biomed Pharmacother 2019;111:386-394.

342 12 Li JQ, Hu SY, Wang ZY, Lin J, Jian S, Dong YC, Wu XF, Dai L, Cao LJ: Long non-coding RNA
 343 MEG3 inhibits microRNA-125a-5p expression and induces immune imbalance of
 344 Treg/Th17 in immune thrombocytopenic purpura. Biomed Pharmacother 2016;83:905-
 345 911.

346 13 Shao XS, Yang XQ, Zhao XD, Li Q, Xie YY, Wang XG, Wang M, Zhang W: The prevalence of
 347 Th17 cells and FOXP3 regulate T cells (Treg) in children with primary nephrotic syndrome.
 348 Pediatr Nephrol 2009;24:1683-1690.

349 14 Li YY, Wei SG, Zhao X, Jia YZ, Zhang YF, Sun SZ: Th17/Treg cell expression in children with
 350 primary nephritic syndrome and the effects of ox-LDL on Th17/Treg cells. Genet Mol Res
 351 2016;15:

352 15 Li Q, Wang Y, Li H, Shen G, Hu S: Ox-LDL influences peripheral Th17/Treg balance by
353 modulating Treg apoptosis and Th17 proliferation in atherosclerotic cerebral infarction.
354 Cell Physiol Biochem 2014;33:1849-1862.

355 16 Livak KJ, Schmittgen TD: Analysis of relative gene expression data using real-time
356 quantitative PCR and the 2(-Delta Delta C(T)) Method. Methods 2001;25(4):402-8.

357 17 Yan L, Liu Z, Yin H, Guo Z, Luo Q: Silencing of MEG3 inhibited ox-LDL-induced inflammation
358 and apoptosis in macrophages via modulation of the MEG3/miR-204/CDKN2A regulatory
359 axis. Cell Biol Int 2019;43:409-420.

360 18 Liu MM, Wen L, Liu YJ, Cai Q, Li LT, Cai YM: Application of data mining methods to improve
361 screening for the risk of early gastric cancer. BMC Med Inform Decis Mak 2018;18:121.

362 19 Ivanov, II, McKenzie BS, Zhou L, Tadokoro CE, Lepelley A, Lafaille JJ, Cua DJ, Littman DR:
363 The orphan nuclear receptor RORgammat directs the differentiation program of
364 proinflammatory IL-17+ T helper cells. Cell 2006;126:1121-1133.

365 20 Sakaguchi S, Sakaguchi N, Asano M, Itoh M, Toda M: Immunologic self-tolerance
366 maintained by activated T cells expressing IL-2 receptor alpha-chains (CD25). Breakdown
367 of a single mechanism of self-tolerance causes various autoimmune diseases. J Immunol
368 1995;155:1151-1164.

369 21 Chen W, Jin W, Hardegen N, Lei KJ, Li L, Marinos N, McGrady G, Wahl SM: Conversion of
370 peripheral CD4+CD25- naive T cells to CD4+CD25+ regulatory T cells by TGF-beta induction
371 of transcription factor Foxp3. J Exp Med 2003;198:1875-1886.

372 22 Mucida D, Park Y, Kim G, Turovskaya O, Scott I, Kronenberg M, Cheroutre H: Reciprocal
373 TH17 and regulatory T cell differentiation mediated by retinoic acid. Science
374 2007;317:256-260.

375 23 Bettelli E, Carrier Y, Gao W, Korn T, Strom TB, Oukka M, Weiner HL, Kuchroo VK: Reciprocal
376 developmental pathways for the generation of pathogenic effector TH17 and regulatory
377 T cells. Nature 2006;441:235-238.

378 24 Okada Y, Tsuzuki Y, Sato H, Narimatsu K, Hokari R, Kurihara C, Watanabe C, Tomita K,
379 Komoto S, Kawaguchi A, Nagao S, Miura S: Trans fatty acids exacerbate dextran sodium
380 sulphate-induced colitis by promoting the up-regulation of macrophage-derived

proinflammatory cytokines involved in T helper 17 cell polarization. Clin Exp Immunol 2013;174:459-471.

25 Burkett PR, Meyer zu Horste G, Kuchroo VK: Pouring fuel on the fire: Th17 cells, the environment, and autoimmunity. J Clin Invest 2015;125:2211-2219.

Figure legends

Table 1

Demographic and clinical characteristics of PNS patients and HC individuals.

Fig.1

The Treg/Th17 ratio was evidently decreased in PNS patients (* P value < 0.05 vs. HC group)

A: The percentage of Th17 cells in the PNS group was significantly increased compared with that in the HC group;

B: The percentage of Treg cells in the PNS group was markedly reduced compared with that in the HC group.

Fig.2

Differential expression of MEG3, relevant miRNAs and relevant mRNAs in PBMC samples collected from PNS and HC groups (* P value < 0.05 vs. HC group)

A: PBMC MEG3 expression was increased in the PNS group compared with that in the HC group;

B: PBMC miR-17 expression was inhibited in the PNS group compared with that in the HC group;

C: PBMC RORyt mRNA expression was promoted in the PNS group compared with that in the HC group;

D: The expression of PBMC miR-125a was inhibited in the PNS group compared with that in the HC group;

E: The expression of PBMC FOXP3 mRNA was inhibited in the PNS group compared with that in the HC group.

Fig.3

Differential expression of MEG3, miR-17 and miR-125a in plasma samples collected from PNS and HC groups (* P value < 0.05 vs. HC group)

A: Plasma MEG3 expression was increased in the PNS group compared with that in the HC group;

B: Plasma miR-17 expression was inhibited in the PNS group compared with that in the HC group;

C: Plasma miR-125a expression was inhibited in the PNS group compared with that in the HC group.

Fig.4

Pro-inflammatory cytokines were up-regulated in the PNS group (* P value < 0.05 vs. HC group)

A: The level of IL-6 was highly increased in the PNS patients compared with that in the HC group;

B: The level of IL-1 β was highly increased in the PNS patients compared with that in the HC group.

Fig.5

Ox-LDL regulated the expression of MEG3, relevant miRNAs and relevant mRNA in THP-1 cells (* P value < 0.05 vs. PBS group; ** P value < 0.05 vs. ox-LDL+NC siRNA group)

A: The expression of MEG3 in the PBS group, ox-LDL+NC siRNA group and ox-LDL+MEG3 siRNA group;

B: The expression of miR-17 in the PBS group, ox-LDL+NC siRNA group and ox-LDL+MEG3 siRNA group;

C: The expression of ROR γ t mRNA in the PBS group, ox-LDL+NC siRNA group and ox-LDL+MEG3 siRNA group;

D: The expression of miR-125a in the PBS group, ox-LDL+NC siRNA group and ox-LDL+MEG3 siRNA group;

E: The expression of FOXP3 mRNA in the PBS group, ox-LDL+NC siRNA group and ox-LDL+MEG3 siRNA group;

429 F: The expression of RORyt protein in the PBS group, ox-LDL+NC siRNA group and ox-LDL+MEG3
430 siRNA group;

431 G: The expression of FOXP3 protein in the PBS group, ox-LDL+NC siRNA group and ox-LDL+MEG3
432 siRNA group.

433 **Fig.6**

434 MEG3 regulated the expression of relevant miRNAs and mRNAs in THP-1 cells (* P value < 0.05
435 vs. NC group)

436 A: The expression of MEG3 in THP-1 cells transfected with MEG3 compared with that in the
437 negative controls;

438 B: The expression of miR-17 in THP-1 cells transfected with MEG3 compared with that in the
439 negative controls;

440 C: The expression of RORyt mRNA in THP-1 cells transfected with MEG3 compared with that in
441 the negative controls;

442 D: The expression of miR-125a in THP-1 cells transfected with MEG3 compared with that in the
443 negative controls;

444 E: The expression of FOXP3 mRNA in THP-1 cells transfected with MEG3 compared with that in
445 the negative controls;

446 F: The expression of RORyt protein in THP-1 cells transfected with MEG3 compared with that in
447 the negative controls;

448 G: The expression of FOXP3 protein in THP-1 cells transfected with MEG3 compared with that in
449 the negative controls.

450 **Fig.7**

451 MEG3 could sponge miR-17 and miR-125a expression, while RORyt mRNA expression was
452 targeted by miR-17 (* P value < 0.05 vs. blank group).

453 A: Bioinformatic tools and luciferase assay validated that MEG3 could sponge miR-17 expression;

454 B: Bioinformatic tools and luciferase assay validated that RORyt mRNA was targeted by miR-17;
455 C: Bioinformatic tools and luciferase assay validated that MEG3 could sponge miR-125a
456 expression.

Preprint

Table 1. Demographic and clinical characteristics of PNS patients and HC individuals.

Characteristics	HC (N=42)	PNS (N=40)	<i>P</i> value
Age (years)	6.5 ± 1.8	6.1 ± 2.2	0.710
Sex			0.710
Male	30	26	
Female	12	14	
Histological classification			0.538
Minor change	1	0	
Focal glomerulone	2	1	
MCNS	7	8	
MsPGN	18	16	
FSGS	6	6	
MN	8	9

The Treg/Th17 ratio was evidently decreased in PNS patients (* P value < 0.05 vs. HC group)

A: The percentage of Th17 cells in the PNS group was significantly increased compared with that in the HC group;

B: The percentage of Treg cells in the PNS group was markedly reduced compared with that in the HC group.

Differential expression of MEG3, relevant miRNAs and relevant mRNAs in PBMC samples collected from PNS and HC groups (* P value < 0.05 vs. HC group)

A: PBMC MEG3 expression was increased in the PNS group compared with that in the HC group;

B: PBMC miR-17 expression was inhibited in the PNS group compared with that in the HC group;

C: PBMC RORγt mRNA expression was promoted in the PNS group compared with that in the HC group;

D: The expression of PBMC miR-125a was inhibited in the PNS group compared with that in the HC group;

E: The expression of PBMC FOXP3 mRNA was inhibited in the PNS group compared with that in the HC group.

Differential expression of MEG3, miR-17 and miR-125a in plasma samples collected from PNS and HC groups (* P value < 0.05 vs. HC group)

A: Plasma MEG3 expression was increased in the PNS group compared with that in the HC group;

B: Plasma miR-17 expression was inhibited in the PNS group compared with that in the HC group;

C: Plasma miR-125a expression was inhibited in the PNS group compared with that in the HC group.

Pro-inflammatory cytokines were up-regulated in the PNS group (* P value < 0.05 vs. HC group)

A: The level of IL-6 was highly increased in the PNS patients compared with that in the HC group;

B: The level of IL-1 β was highly increased in the PNS patients compared with that in the HC group.

Fig.5

Ox-LDL regulated the expression of MEG3, relevant miRNAs and relevant mRNA in THP-1 cells (* P value < 0.05 vs. PBS group; ** P value < 0.05 vs. ox-LDL+NC siRNA group)

A: The expression of MEG3 in the PBS group, ox-LDL+NC siRNA group and ox-LDL+MEG3 siRNA group;

B: The expression of miR-17 in the PBS group, ox-LDL+NC siRNA group and ox-LDL+MEG3 siRNA group;

C: The expression of RORγt mRNA in the PBS group, ox-LDL+NC siRNA group and ox-LDL+MEG3 siRNA group;

D: The expression of miR-125a in the PBS group, ox-LDL+NC siRNA group and ox-LDL+MEG3 siRNA group;

E: The expression of FOXP3 mRNA in the PBS group, ox-LDL+NC siRNA group and ox-LDL+MEG3 siRNA group;

F: The expression of RORγt protein in the PBS group, ox-LDL+NC siRNA group and ox-LDL+MEG3 siRNA group;

G: The expression of FOXP3 protein in the PBS group, ox-LDL+NC siRNA group and ox-LDL+MEG3 siRNA group.

Fig.6

MEG3 regulated the expression of relevant miRNAs and mRNAs in THP-1 cells (* P value < 0.05 vs. NC group)

A: The expression of MEG3 in THP-1 cells transfected with MEG3 compared with that in the negative controls;

B: The expression of miR-17 in THP-1 cells transfected with MEG3 compared with that in the negative controls;

C: The expression of RORyt mRNA in THP-1 cells transfected with MEG3 compared with that in the negative controls;

D: The expression of miR-125a in THP-1 cells transfected with MEG3 compared with that in the negative controls;

E: The expression of FOXP3 mRNA in THP-1 cells transfected with MEG3 compared with that in the negative controls;

F: The expression of RORyt protein in THP-1 cells transfected with MEG3 compared with that in the negative controls;

G: The expression of FOXP3 protein in THP-1 cells transfected with MEG3 compared with that in the negative controls.

MEG3 could sponge miR-17 and miR-125a expression, while RORyt mRNA expression was targeted by miR-17 (* P value < 0.05 vs. blank group).

A: Bioinformatic tools and luciferase assay validated that MEG3 could sponge miR-17 expression;

B: Bioinformatic tools and luciferase assay validated that RORyt mRNA was targeted by miR-17;

C: Bioinformatic tools and luciferase assay validated that MEG3 could sponge miR-125a expression.