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Nur77 deficiency leads to systemic inflammation in elderly mice

Xiu-Ming Li, Xing-Xing Lu, Qian Xu, Jing-Ru Wang, Shen Zhang, Peng-Da Guo, Jian-Ming Li and Hua Wu*

Abstract

Background: Nur77, an orphan member of the nuclear receptor superfamily, has been implicated in the regulation of inflammation. However, the *in vivo* function of Nur77 remains largely unexplored. In the current study, we investigated the role of Nur77 in inflammation and immunity in mice.

Findings: We found that elderly 8-month-old Nur77-deficient mice (Nur77^{-/-}) developed systemic inflammation. Compared to wild-type (WT) mice (Nur77^{+/+}), Nur77^{-/-} mice showed splenomegaly, severe infiltration of inflammatory cells in several organs including liver, lung, spleen and kidney, increased hyperplasia of fibrous tissue in the lung and enlargement of kidney glomeruli. Additionally, Nur77^{-/-} mice had increased production of pro-inflammatory cytokines and immunoglobulin, and elicited pro-inflammatory M1-like polarization in macrophages as revealed by increased expression of CXCL11 and INDO, and decreased expression of MRC1.

Conclusions: These *in vivo* observations provide evidence for a pivotal role for Nur77 in the regulation of systemic inflammation and emphasize the pathogenic significance of Nur77 *in vivo*.

Keywords: Nur77, Inflammation, Immunity, Animal study

Introduction

Nur77 (also called TR3 or NR4A1) belongs to the subfamily 4, group A (NR4A) of nuclear receptor that also comprises Nurr-1 (NR4A2) and NOR-1 (NR4A3) [1]. Accumulating studies have revealed a critical role of Nur77 in the regulation of cancer development [1], metabolism [2], and inflammation [3, 4]. Published findings have indicated that Nur77 is frequently overexpressed in a variety of cancer types, such as colon cancer and pancreatic cancer, and drives cancer development and progression [5, 6]. Nur77 also controls glucose metabolism through regulation of LKB1-AMPK signaling axis [2]. Nur77 is also aberrantly expressed in atherosclerotic lesions [7] and multiple sclerosis [8], indicating that abnormal expression of Nur77 is implicated in the development of immune and inflammatory diseases. Nur77 can be rapidly induced by several inflammatory stimuli such as tumor necrosis factor-alpha (TNFα) and lipopolysaccharide (LPS) in macrophages and monocytes [7, 9]. Moreover, Nur77 can interact with interferon-

However, previous data has revealed that Nur77 plays dual, contradictory roles in inflammation. On the one hand, Nur77 may mediate pro-inflammatory signaling by increasing the expression of NF-κB-activating kinase, IKKi [12]. Conversely, Nur77 may mediate antiinflammatory signaling by inducing the expression of IκBα, an anti-inflammatory modulator, and subsequently attenuate endothelial cell activation [13]. Recent studies have also shown that Nur77 was protective against the development of atherosclerosis by inhibiting the inflammatory responses [14]. Combined, these data indicate that Nur77 is involved in the regulation of inflammation and its potential functions depend on different physiologic and pathological conditions. However, the in vivo functions of Nur77 in inflammation are yet to be substantiated.

In order to further clarify the *in vivo* function of Nur77 in inflammation, we analyzed the phenotype and

^{*} Correspondence: wuhua@suda.edu.cn Pathology Center and Department of Pathology, Soochow University, Suzhou 215123, China



stimulated gene 12 (ISG12), a cofactor that stimulates nuclear export of nuclear receptors [10] and a critical modulator of innate immune responses in murine models of sepsis [11], further suggesting the potential critical role of Nur77 in the regulation of inflammation and immunity.

Table 1 Primers for gPCR

| Mouse gene name | Forward/Reverse |
|-----------------|------------------------------------|
| Tnfa | F: 5'-CTCACACTCAGATCATCTTCTC-3' |
| | R: 5'-CTTTCTCCTGGTATGAGATAGC-3' |
| 116 | F: 5'-TTCCATCCAGTTGCCTTCTTG-3' |
| | R: 5'-AGGTCTGTTGGGAGTGGTATC-3' |
| Cxcl11 | F: 5'-AGGAAGGTCACAGCCATAGC-3' |
| | R: 5'-CGATCTCTGCCATTTTGACG-3' |
| Indo | F: 5'-CACTGAGCACGGACGGACTGAGA-3' |
| | R: 5'-TCCAATGCTTTCAGGTCTTGACGC-3' |
| Mrc1 | F: 5'-AGAGCCCACAACAACTCCTG-3' |
| | R: 5'-TCCACTGCTCGTAATCAGCC-3' |
| β-actin | F: 5'-TGGAATCCTGTGGCATCCATGAAAC-3' |
| | R: 5'-TAAAACGCAGCTCAGTAACAGTCCG-3' |

pathological features of Nur77^{-/-} mice. Our *in vivo* investigations showed that Nur77 deficiency in mice increased their susceptibility to systemic inflammation, indicating that Nur77 participates in the pathogenesis of inflammation.

Materials and methods

Mice

Nur77^{+/+} and Nur77^{-/-} mice were obtained from the Jackson Laboratory (Bar Harbor, Maine, USA). All mice were maintained in a pathogen-free environment with a 12-h/12-h light–dark cycle at the Laboratory Animal Center in Soochow University (China), and were provided with normal laboratory pellet diet and water. Animal chow was sterilized by irradiation with $60\text{Co-}\gamma$ rays. All procedures were performed in accordance with the guidelines of the Animal Care and Use Committee of Soochow University.

Isolation and culture of peritoneal macrophages

Peritoneal macrophages were isolated from Nur77^{+/+} and Nur77^{-/-} mice. Mice were intraperitoneally (i.p) injected with 2 ml of 4 % thioglycolate medium (BD Biosciences) for 3d, then, macrophages in the peritoneal exudates were collected by peritoneal lavage with 10 ml ice-cold DMEM. Collected cells were incubated in DMEM supplemented with 10 % fetal bovine serum (FBS) at 37 °C for 4 h and washed with PBS to

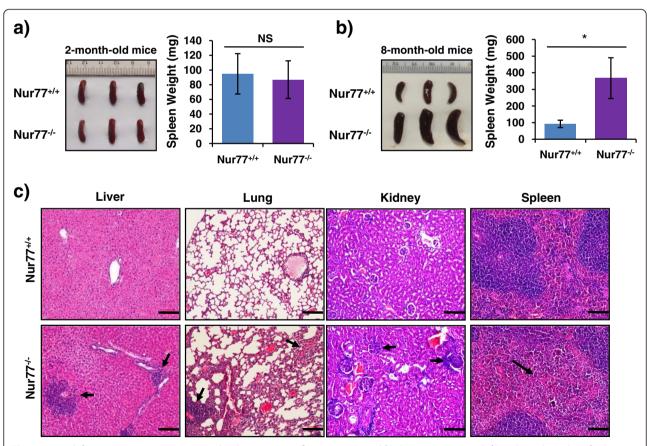


Fig. 1 Nur77-deficient mice are more prone to develop systemic inflammation. (**a** and **b**) Gross appearances (left) and weight (right) of spleens from 2-month-old (**a**) and 8-month-old (**b**) Nur77^{+/+} and Nur77^{-/-} mice (n = 6 per group). Representative images are shown. NS, not significant, *p < 0.05. (**c**) Hematoxylin and eosin (H&E) staining of indicated organ sections from 8-month-old Nur77^{+/+} and Nur77^{-/-} mice. Representative images are shown. Scale bars, 100 μM. Original magnification, ×100. Arrowheads indicate exacerbation of inflammatory pathology

eliminate non-adherent cells. The adherent cells were taken as peritoneal macrophages.

Tissue samples collection and evaluation

The organs including kidney, liver, lung and spleen from $Nur77^{+/+}$ and $Nur77^{-/-}$ mice were collected for pathological analysis. The spleen weight was measured and all tissues were fixed in 10 % neutral-buffered formalin and embedded in paraffin. After sectioning, the tissues were stained with hematoxylin and eosin (H&E) according to standard histological procedures.

qPCR Analysis

qPCR analysis was performed as previously described [5]. β -actin was used as internal control. The primers for PCR reactions are listed in Table 1.

ELISA assay

The concentrations of interleukin (IL)-6, immunoglobulin (Ig)G1, and IgE in serum were determined using commercially available kits (eBioscience) according to the manufacturer's instructions.

Statistical analysis

Data were expressed as mean \pm SD. Each assay was performed in three independent experiments. Statistics was analyzed using Student's t test. Values of p < 0.05 were considered statistically significant.

Results and discussion

Recent studies suggest that Nur77 deficiency in mice enhances atherosclerosis [3, 4] and LPS-induced sepsis [15], suggesting that Nur77 is implicated in inflammation. To further evaluate the potential role of Nur77 in inflammation *in vivo*, Nur77^{-/-} mice were observed in this

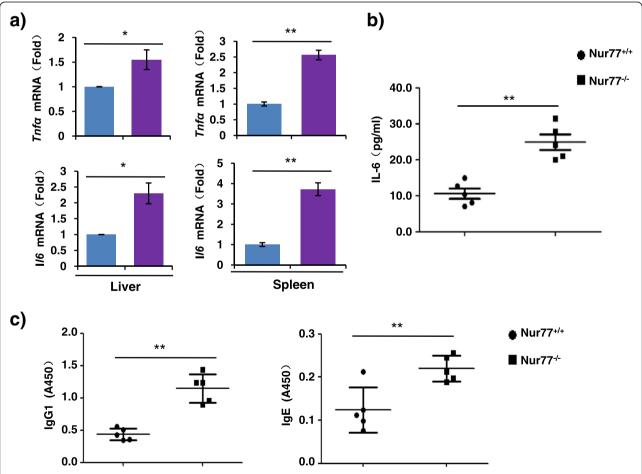


Fig. 2 Nur77 deficiency in mice enhances the production of pro-inflammatory cytokines and immunoglobulin. (a) qRT-PCR analysis of the expression of Tnfa and Il6 mRNA in liver and spleen samples from 8-monthold Nur77^{+/+} and Nur77^{-/-} mice (n = 6 per group). Error bars represent mean \pm s.d. from n = 3 biological triplicates. *p < 0.05 and **p < 0.01. (b) ELISA assay of IL-6 concentration in serum from 8-month-old Nur77^{+/+} and Nur77^{-/-} mice (n = 6 per group). Error bars represent mean \pm s.d. from n = 3 biological triplicates. **p < 0.01. (c) Titers of IgG1 and IgE in serum from 8-month-old Nur77^{-/-} mice (n = 6 per group). Error bars represent mean \pm s.d. from n = 3 biological triplicates. **p < 0.01

study. We compared splenic differences in 2-month-old Nur77^{-/-} mice and wild-type (WT) mice and found no significant differences in the size and weight of their spleens (Fig. 1a). Interestingly, we found that 8-month-old Nur77^{-/-} mice were more prone to develop splenomegaly (Fig. 1b, left) and increased spleen weight (Fig. 1b, right). Thus, these observations indicated that Nur77 deficiency was associated with an increased inflammatory pathology in elderly mice. Our results were consistent with a recent report that Nur77^{-/-} mice displayed hyperplasia in the jejunum and colon, and increased crypt depth and villus length of the jejunum and colon [16].

Our investigation further showed that Nur77 deficiency in elderly mice led to exacerbation of inflammatory pathology as characterized by increased inflammatory cell infiltration and inflammatory cytokines production. As shown in Fig. 1c, Nur77^{-/-} mice had more severe inflammatory cell infiltration in the liver, lung, spleen and kidney, and more hyperplasia of fibrous tissue in the lungs. The elderly Nur77-deficient mice also exhibited increased susceptibility to glomerulonephritis with enlargement of the kidney glomeruli, which can be linked to systemic disorders or certain infections [17, 18]. Additionally, the spleens of elderly Nur77^{-/-} mice showed expansion of red pulp and decreased white pulp than WT mice (Fig. 1c). Combined, these phenotypical findings suggest a progression of systemic inflammation in Nur77^{-/-} elderly mice.

Changes in inflammatory cytokines expression are known to readily occur in systemic inflammation [19]. Unsurprisingly, the mRNA expression of pro-inflammatory cytokines, including $Tnf\alpha$ and Il6, was higher in the liver and spleen tissues (Fig. 2a) from Nur77^{-/-} mice than those from Nur77^{+/+} mice. The concentration of IL-6 in serum of 8month-old Nur77^{-/-} mice was also elevated (Fig. 2b). There were no differences in the gene expression of $Tnf\alpha$ and Il6in 2-month-old mice in the two groups (Additional file 1: Figure S1a). A recent study found that mice lacking all Nr4a receptors including Nur77 had impaired regulatory T cell (Treg) development and resulted in systemic lethal autoimmunity [20], suggesting a potential role of Nr4a receptors in autoimmune disease. Nur77 has also been suggested to be implicated in Treg differentiation and self-reactive T cells selection [21, 22]. Herein, we also investigated whether Nur77 deficiency in mice was involved in the pathogenesis of autoimmune disease. Analysis of serum immunoglobulin showed increased IgG1 and IgE in elderly Nur77^{-/-} mice than in WT mice (Fig. 2c). However, we did not observe any differences in the Ig levels in younger 2-month-old mice in the two groups (Additional file 1: Figure S1b). Together, these data indicate that elderly Nur77^{-/-} mice developed systemic inflammation and autoimmunity, supporting a role of Nur77 in inflammation and immunity. Our results are consistent with previous reports that

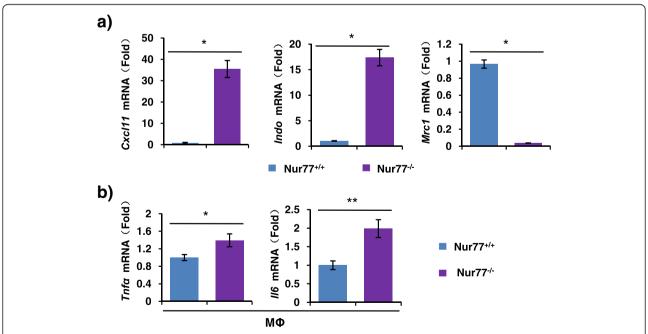


Fig. 3 Nur77 deletion polarizes macrophages toward a pro-inflammatory M1 phenotype. (a) The expression of Cxc111, Indo, and Mrc1 were determined by qRT-PCR in peritoneal macrophages (M Φ) of 8-month-old Nur77^{+/+} (n=6) and Nur77^{-/-} (n=6) mice. Error bars represent mean \pm s.d. from n=3 biological triplicates. *p<0.05. (b) The expression of Tnfa and Il6 mRNA were analyzed by qRT-PCR in peritoneal macrophages (M Φ) from 8-month-old Nur77^{+/+} (n=6) and Nur77^{-/-} (n=6) mice. Error bars represent mean \pm s.d. from n=3 biological triplicates. *p<0.05 and **p<0.01

Nur77^{-/-} mice showed increased susceptibility to atherosclerosis [4, 14] and restenosis [10], and demonstrate that Nur77 has functional roles in protecting mice from inflammatory and autoimmune diseases.

Accumulating studies have shown that polarization of macrophages occurs in response to inflammatory diseases [23]. Two opposite and competing macrophage phenotypes, M1 (pro-inflammatory) and M2 (anti-inflammatory), have been defined and identified in a range of physiologic and pathological processes [23]. Several genes, including CXCL11, INDO, and MRC1, have been shown to discriminate between M1 and M2 macrophages [24]. M1 phenotype is typically associated with an increased CXCL11 and INDO expression but associated with a decreased MRC1 expression [24]. In this study, we isolated peritoneal macrophages from elderly 8-month-old Nur77+/+ and Nur77-/- mice, and found that Nur77 deficiency in mice significantly enhanced Cxcl11 and Indo mRNA expression, but reduced Mrc1 expression (Fig. 3a), indicating that the absence of Nur77 in macrophages led to enhanced polarization of macrophages toward a pro-inflammatory M1 phenotype. M1-like macrophages are also generally considered to produce numerous pro-inflammatory mediators such as TNFα, IL-12, and IL-6 [25]. Similar phenomena were also observed in our current study. As shown in Fig. 3b, Nur77 deficiency in peritoneal macrophages markedly enhanced the expression of $Tnf\alpha$ and Il6, indicating that Nur77 plays an important role in regulation of macrophage phenotype and functions. These results are strongly supported by a recent report that Nur77 deletion polarizes macrophages toward an inflammatory phenotype and increases inflammatory cytokines production in atherosclerosis [14]. Together with our observations that increased inflammatory cells infiltration and inflammatory cytokines production in elderly Nur77^{-/-} mice (Figs. 1 and 2), thus, we speculate that Nur77deficiency skews the macrophage phenotype to M1 subset, and subsequently leads to the development of systemic inflammation in elderly mice.

In summary, we provide *in vivo* evidence that orphan nuclear receptor Nur77 is an essential negative regulator of systemic inflammation. This study associates the nuclear receptor Nur77 with systemic inflammation and implicates a new therapeutic target to preventing and treating inflammatory diseases.

Additional file

Additional file 1: Figure S1. Nur77 deficiency in 2-month-old mice does not affect pro-inflammatory cytokines expression and immunoglobulin production. (a) The expression of Tnfa and ll6 mRNA were analyzed by qRT-PCR in liver and spleen samples from 2-month-old Nur77^{+/+} and Nur77^{-/-} mice (n=6 per group). Error bars represent mean \pm s.d. from

n=3 biological triplicates. (b) Titers of IgG1 and IgE in serum from 2-month-old Nur77^{+/+} and Nur77^{-/-} mice (n=6 per group). Error bars represent mean \pm s.d. from n=3 biological triplicates.

Abbreviations

qPCR: Quantitative PCR; ELISA: Enzyme Linked Immunosorbent Assay; CXCL11: Chemokine (C-X-C motif) ligand 1; IDO1: Indoleamine 2,3-dioxygenase 1; MRC1: Mannose receptor, C type 1.

Competing interests

The authors declare that they have no competing interests.

Authors' contributions

HW designed the experiments, analyzed data and prepared the manuscript. XML, XXL, QX, JRW, SZ and PDG performed the experiments. JML contributed to the data analysis. All authors read and approved the final manuscript.

Authors' information

Xiu-Ming Li and Xing-Xing Lu are co-first author.

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