Research Paper

Dual Role of Ninjurin-1 in Myeloid Cell Adhesion and Inflammation in Relapse-

Remitting EAE

Coleen Thompson[1], Alex Annett[1], Anastasia Alkhimovitch[2], Kashish Singh Parihar[1], Igal

Ifergan[1,2,3]

[1]Department of Molecular and Cellular Biology, College of Medicine, University of

Cincinnati, Cincinnati, OH USA.

[2]Division of Immunobiology, Cincinnati Children's Hospital Medical Center, University of

Cincinnati College of Medicine, Cincinnati, OH USA

[3]Neuroscience Graduate Program, College of Medicine, University of Cincinnati,

Cincinnati, OH USA

<u>Corresponding author</u>:

Igal Ifergan, Ph.D.
Dept. of Molecular and Cellular Biology
College of Medicine
University of Cincinnati
MSB 2258
231 Albert Sabin Way
Cincinnati, OH 45267
E-mail: igal.ifergan@uc.edu
Phone: 513-558-7146
25

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ABSTRACT

Nerve Injury-Induced Protein 1 (Ninjurin-1) is an adhesion molecule implicated in

inflammation and tissue injury, yet its role in neuroinflammatory diseases such as multiple

sclerosis (MS) remains poorly defined. Here, we identify Ninjurin-1 as a key mediator of

immune activation and CNS infiltration in relapsing-remitting experimental autoimmune

encephalomyelitis (RR-EAE), a model of relapsing-remitting MS (RRMS). Using flow

cytometry, gene-expression profiling, and *in vivo* peptide blockade, we show that Ninjurin-

1 is markedly upregulated on CNS-infiltrating myeloid cells during disease progression.

Ninjurin-1$^+$ myeloid cells display a dual function, as both an adhesion molecule and a

marker of inflammatory activation, characterized by increased antigen presentation,

cytokine production, and transcriptional enrichment for genes regulating adhesion,

migration, and innate immune signaling. Importantly, therapeutic blockade of Ninjurin-1

significantly reduced clinical severity, CNS immune infiltration, and demyelination in RR-

EAE. These findings uncover a previously unrecognized role for Ninjurin-1 in myeloid-

driven neuroinflammation and highlight its potential as a therapeutic target for relapsing-

remitting MS.

1. Introduction

Multiple sclerosis (MS) is a chronic autoimmune disorder affecting over 2.8 million people worldwide, leading to progressive neurological disability and reduced quality of life [1, 2]. The disease is driven by the infiltration of peripheral immune cells into the central nervous system (CNS), where they attack the myelin sheath surrounding neurons, causing demyelination, inflammation, and neurodegeneration [3]. Although the precise etiology of MS remains unclear, a prevailing hypothesis proposes that antigen-presenting cells (APCs) present myelin-mimicking antigens to autoreactive T lymphocytes, thereby initiating immune-mediated demyelination and lesion formation within the CNS [4, 5].

Experimental autoimmune encephalomyelitis (EAE), a well-established preclinical animal model that recapitulates many clinical and pathological features of MS, including limb paralysis, CNS lesions, and immune cell infiltration [6, 7]. EAE studies have identified key roles for TH1 and TH17 CD4^{+} T cells in driving neuroinflammation and demyelination [8], providing a valuable model to investigate disease mechanisms and test potential therapies.

Immune cell migration into the CNS is orchestrated by a complex interplay of adhesion molecules, chemokines, and selectins expressed by blood–brain barrier endothelial cells (BBB-ECs) and CD45^{+} immune cells [9]. Among these, vascular cell adhesion molecule-1 (VCAM-1) and intercellular adhesion molecule-1 (ICAM-1) are well-established mediators of leukocyte trafficking in MS and EAE [10]. However, the molecular mechanisms governing immune cell infiltration into the CNS remain incompletely understood, suggesting that additional adhesion pathways contribute to neuroinflammatory progression.

One such candidate is Nerve Injury–Induced Protein-1 (Ninjurin-1), a 22-kDa homophilic adhesion molecule originally identified for its role in axonal regeneration following nerve injury [11]. Subsequent work, including a proteomic screen of human BBB-ECs by Ifergan et al. (2013), identified Ninjurin-1 as a molecule expressed at the neurovascular interface and upregulated under inflammatory conditions [12]. Importantly, Ninjurin-1 is also expressed by immune cells, positioning it as a bidirectional mediator of leukocyte-endothelial interactions.

More recently, Ninjurin-1 has emerged as a regulator of immune cell adhesion and inflammation across pathological contexts, including stroke [13], pulmonary fibrosis [14], liver ischemia-reperfusion injury [15], and MS [12]. Beyond its adhesive function, Ninjurin-1 promotes leukocyte adhesion, plasma membrane rupture (PMR), and the release of damage-associated molecular patterns (DAMPs) [16], highlighting its potential role in amplifying inflammatory cascades. These findings position Ninjurin-1 as a unique molecule bridging structural adhesion and innate immune activation.

In the context of MS and EAE, Ninjurin-1 is expressed in both acute and chronic MS lesions [17] and is upregulated on myeloid and endothelial cells during chronic EAE [12]. Our previous work demonstrated that Ninjurin-1 expression peaks at the height of disease in a chronic EAE model induced by MOG_{35-55}, and that its blockade alleviates clinical symptoms, reduces CNS inflammation, and limits immune cell infiltration [12]. Despite these insights, no studies have explored the role of Ninjurin-1 in relapse-remitting EAE (RR-EAE) or its relevance to relapse-remitting MS (RRMS). RRMS is the most prevalent MS subtype, representing approximately 85% of all cases. It is characterized

by episodic neuroinflammatory attacks followed by partial recovery, driven by waves of

peripheral immune cell infiltration into the CNS [18, 19].

In this study, we investigate the expression and function of Ninjurin-1 in RR-EAE.

We show that Ninjurin-1 is strongly upregulated in inflammatory environments, particularly

on myeloid cells and BBB-ECs, where it functions both as an adhesion molecule and as

a marker of inflammation. Furthermore, blockade of Ninjurin-1 homophilic binding

attenuates disease severity and reduces immune cell infiltration. Together, these findings

identify Ninjurin-1 as a dual-function mediator of immune activation and trafficking in RR-

EAE and suggest that targeting Ninjurin-1 may represent a promising therapeutic strategy

for RRMS.

2. Materials and Methods

2.1 Mice

Female SJL/J (cat# 000686) and C57BL/6 (cat# 000664) mice from 6-9 weeks old were purchased from The Jackson Laboratory (Bar Harbor, ME). 2D2 mice were bred in-house (originally from The Jackson Laboratory, cat# 006912) and used in experiments once they reached 12-16 weeks old. All CD4+ T cells from 2D2 mice possess a T cell receptor specific (TCR) for MOG_{35-55}. All mice were maintained under specific pathogen-free conditions in the University of Cincinnati's Laboratory Animal Medical Services (LAMS) facility and handled in accordance with AAALAC and IACUC-approved institutional guidelines.

2.2 Reagents

Peptides corresponding to the adhesion motif of Ninjurin-1 (amino acids 26-37; sequence PPRWGLRNRPIN) were synthesized and used as a blocking peptide (anti-$Ninj_{26-37}$). A scrambled control peptide (WRGNPGIRWAPH) was also generated for use as a control. Peptides were synthesized by Genemed Biotechnologies Inc. (Torrance, CA).

2.3 Active EAE

RR-EAE was induced in 8-10-week-old female SJL/J mice as previously described [20]. Mice received three subcutaneous flank injections (total 100 µL) of $PLP_{139-151}$ peptide (200 µg/mouse; Genemed Biotechnologies Inc.) emulsified in Complete Freund's Adjuvant (BD Biosciences) containing 200 µg of *Mycobacterium tuberculosis* H37Ra. At

peak of disease, mice were treated intraperitoneally three times per week with 200 µg of

either scrambled peptide or Ninj$_{26-37}$ blocking peptide (1 mg/mL) until the study endpoint

(n = 8/group). Clinical scores were recorded daily (0 = asymptomatic; 1 = limp tail; 2 =

hind limb weakness; 3 = partial paralysis; 4 = complete paralysis; 5 = moribund). Data

are presented as mean ± SEM daily score.

2.4 Isolation of splenocytes and CNS

Mice were incapacitated with CO_2 and then perfused with PBS prior to tissue

removal, following previously described methods [18]. Spleens were collected at pre-

onset, onset, peak, remission, and relapse phases of RR-EAE. Tissue was mechanically

dissociated through 100 µm cell strainers and red blood cells were lysed using 0.83%

ammonium chloride. Cells were then plated in 96-well plates (0.2-2 x 10^6 cells/well) in

RPMI-1640 supplemented with 10% FBS, 2 mM L-glutamine, and 100 U/mL penicillin-

streptomycin at 37 °C, 5% CO_2.

CNS tissues (brain and spinal cord) were collected at the same time as the spleen

and digested with 50 µg/mL DNase I and 500 µg/mL collagenase (Sigma). Mononuclear

cells were isolated by 40% Percoll gradient or 20% BSA centrifugation. White blood cells

were quantified using a Sysmex XP300 (Horst, IL).

2.5 Ex vivo cytokine stimulation

CD11b$^+$ cells were enriched from naïve SJL/J splenocytes using MACS Magnetic

separation columns (Miltenyi Biotec) and were plated at 0.5 x 10^6 cells/well in 24 well

plates. C57BL/6 brain microvascular endothelial cells (Cell Biologics, C57-6023) were

cultured to 90% confluency and then plated at 30,000 cells/well in a 24 well plate. Cells

were treated for 24 hours with the following cytokines: GM-CSF (200 ng/mL; R&D), IFN-

γ (200 ng/mL; R&D), IL-1β (200 ng/mL; R&D), IL-4 (200 ng/mL; Peprotech), IL-6 (50

ng/mL; R&D), IL-10 (200 ng/mL; R&D), IL-17 (200 ng/mL; R&D), TGF-β (200 ng/mL;

R&D), or TNF-α (50 ng/mL; R&D). Combination conditions included IFN-γ + TNF-α

(referred to as TH1-like) and IL-17 + GM-CSF (referred to as TH17-like). Cytokine

concentrations were based on manufacturer-reported ED_{50} values. After the 24-hour

incubation (37°C, 5% CO_2), Ninjurin-1 expression was analyzed by flow cytometry.

2.6 Flow cytometry staining and analysis

Fc receptors were blocked using anti-mouse CD16/32 (0.25 μg;

Thermofisher). Cells were then stained in PBS with fixable LIVE/DEAD reagents (Life

Technologies) for 20 minutes in PBS at room temperature in the dark to assess viability.

Then cells were stained for surface markers for 20 minutes at 4°C using the specified

antibodies (Ninjurin-1 from R&D Systems; all the others from BD Biosciences or

Biolegend). When needed, cells were fixed and permeabilized (ThermoFisher) to stain

for intracellular markers. To detect T cell cytokine expression, cells were activated for 4

hours with 1 mg/ml ionomycin (Iono) and 20 ng/ml phorbol 12-myristate 13-acetate 40

(PMA) in the presence of 2 mg/ml brefeldin A (BFA) (Sigma). To detect CD11b^{+} cytokine

expression, cells were activated for 18 hours with 100 ng/ml lipopolysaccharide (LPS)

from E. coli serotype 0111:B4 (Sigma) in the presence of 2 mg/ml BFA (Sigma) for the

last 2 hours of co-culture. Cells were stained for surface markers and a fixation and

permeabilization kit (ThermoFisher) was used. Cells were acquired using a BD

FACSCanto II and analyzed using Flowjo version 10.1 software.

2.7 Immunostaining of mouse CNS

173  CNS tissues from control and RR-EAE mice were fixed in 10% formaldehyde

174 overnight. Luxol Fast Blue (LFB) and hematoxylin and eosin (H&E) staining were

175 performed by the Immunohistochemistry (IHC) Core at the University of Cincinnati.

176 Images were acquired with an EVOS M5000 microscope (Invitrogen) at 10x

177 magnification.

178  For quantification of cellular infiltration in H&E-stained sections, hematoxylin-

positive nuclei were manually counted within standardized white matter regions using

ImageJ. Three non-overlapping regions of interest (ROIs; 300 × 300 μm each) were

analyzed per section, and counts were averaged to generate a single value per section.

Values from multiple sections were then averaged to yield one representative value per

mouse. Data are expressed as cells per mm².

2.8 Cell sorting

186  Splenocytes were removed from naïve C57BL/6 mice and enriched with CD11b

187 magnetic beads from Miltenyi Biotec. Cells were then stained with Ninjurin-1, CD45,

188 CD11b, CD3, B220, Ly6G, and Live Dead antibodies (**Fig. S4**) and sorted into two

189 populations, $CD45^+CD11b^+B220^-CD3^-Ly6G^-Ninjurin\text{-}1^+$ (Ninjurin-1$^+$) or

190 $CD45^+CD11b^+B220^-CD3^-Ly6G^-Ninjurin\text{-}1^-$ (Ninjurin-1$^-$) using a MA900 (Sony).

192 *2.9 Quantitative PCR*

193  After cell sorting, both populations obtained from cell sorting (Ninjurin-1$^+$ and

Ninjurin-1$^-$) were lysed using Trizol (Ambion). Purity of the isolated RNA was determined

by measuring the ratio of the optical density of the samples at 260/280nm using a

Nanodrop spectrophotometer (Thermo Scientific). The OD_{260}/OD_{280} ratio ranged from 1.7

to 2.1 for all samples. cDNAs were synthesized using the RT^2 First Strand kit (Qiagen)

according to the manufacturer's instructions. The RT^2 Profiler PCR Array Mouse Dendritic

and Antigen Presenting Cell (PAMM-406Z) plates were purchased from SABiosciences,

Qiagen. This array profiles the expression of 84 genes involved in antigen presentation

and includes 5 controls for housekeeping genes, one control for genomic DNA, and three

reverse transcription controls. PCRs were performed on a QuantStudio 3 (Thermofisher).

The data were analyzed using the web-based software RT^2 Profiler PCR Array data

analysis tool (Qiagen). The C_T cut off was 35 and the data was normalized using Beta-2

microglobulin (B2m), Heat shock protein 90 alpha (cytosolic), and class B member 1

(HSP90ab1) housekeeping genes. Fold-changes for each gene were calculated as the

difference in gene expression between the Ninjurin-1$^-$ cells and Ninjurin-1$^+$ cells. A

positive value indicates gene up-regulation, and a negative value indicated gene down-

regulation on the Ninjuirin-1$^+$ cells. Only fold changes of 1.5 or greater were considered

in our analysis.

2.8 2D2 Co-culture

Splenocytes were isolated from 2D2 mice, and CD4$^+$ cells were magnetically

separated via a negative CD4$^+$ selection kit (Stemcell) and then labeled with

carboxyfluorescein succinimidyl ester (CFSE) (Invitrogen). CFSE$^+$CD4$^+$ T cells

(100,000/well) were then co-cultured with either Ninjurin-1$^-$ or Ninjurin-1$^+$ sorted cells

(40,000/well) with 20 μg/ml MOG_{35-55} peptide (Genemed Biotechnologies Inc.) into a 96

well plate for 72 hours. After 72 hours, PMA/Iono/BFA was added for 4 hours to the culture

prior to cell staining. The expression of CFSE, CD25, GM-CSF, IL-17, IFNγ, and TNF-α

on T cells was analyzed via flow cytometry.

2.9 Statistical analysis

Statistical analyses were performed using GraphPad PRISM 10.0 (GraphPad

software). Data are presented as the mean $\pm$ the standard error of the mean (SEM). EAE

scores were analyzed by nonparametric Mann-Whitney test. All other analyses were

performed by a paired t- test or a two-way Anova. Only *p* values < 0.05 were considered

significant.

3. Results

3.1 Myeloid cells upregulate Ninjurin-1 expression in the CNS during RR-EAE

We sought to determine whether Ninjurin-1 played a role in RR-EAE, a mouse model of RRMS, as this had not been previously investigated. To assess the dynamics of Ninjurin-1 expression over the course of RR-EAE, we analyzed immune cells isolated from the CNS (brain and spinal cord) and spleen using flow cytometry at defined disease stages: pre-onset (days 7-9), onset (days 11-13), peak (days 14-16), remission (days 21-23), and relapse (days 28-32) (**Fig. 1A**). RR-EAE was induced in female SJL/J mice with $PLP_{139-151}$. Our analysis focused on $CD11b^+$ myeloid cells and $CD3^+$ T cells, the principal immune cell populations infiltrating the CNS during RR-EAE [21-23]. The gating strategy can be found be found in (**Fig. S1**).

Across all disease phases, Ninjurin-1 expression was significantly higher on infiltrating CNS myeloid cells ($CD45^{hi}B220^-CD3^-CD11b^+$) compared to peripheral myeloid cells in the spleen (**Fig. 1B**). Specifically, $Ninjurin-1^+$ myeloid cells accounted for 29% versus 12% at pre-onset, 52% versus 6% at onset, 57% versus 9% at peak, 32% versus 5% at remission, and 36% versus 12% at relapse of the total myeloid cells recorded (CNS vs. spleen, respectively). This enrichment suggests that $Ninjurin-1^+$ cells may preferentially migrate to or upregulate Ninjurin-1 expression within the CNS microenvironment.

In contrast, $CD3^+$ T cells ($CD45^{hi}B220^-CD11b^-CD3^+$) exhibited consistently low Ninjurin-1 expression throughout RR-EAE, with no significant differences between CNS ($3.1 \pm 1.5\%$) and spleen ($1.7 \pm 1.0\%$) compartments (**Fig. 1C**).

Together, these results demonstrate that Ninjurin-1 is predominantly expressed by

CNS-infiltrating myeloid cells during RR-EAE, with maximal expression observed at

disease onset and peak of disease (**Fig. 1D**). These findings identify Ninjurin-1 as a

potential marker of inflammatory myeloid cell activation within the CNS during

neuroinflammatory progression.

3.2 CD4$^+$ TH17- and TH1-like conditions increase Ninjurin-1 expression in both BBB

endothelial and myeloid cells

Having observed elevated Ninjurin-1 expression on CNS infiltrating myeloid cells,

we next investigated the environmental cues that regulate its expression. We previously

demonstrated that Ninjurin-1 plays a role in mediating myeloid cell binding to BBB-ECs

through homophilic binding [12]. T helper cells, especially TH1 and TH17 subsets, are

known to promote inflammation and promote adhesion molecules through their cytokine

release in EAE/MS [21, 22, 24], we sought to determine whether cytokines associated

these T helper subsets could modulate Ninjurin-1 expression on either BBB-ECs and

myeloid cells.

Primary mouse BBB-ECs and splenic CD45$^+$CD11b$^+$ myeloid cells were incubated

for 24 hours under resting conditions or stimulated with individual cytokines: GM-CSF,

IFN-γ, IL-1β, IL-4, IL-6, IL-10, IL-17, TGF-β, or TNF-α, or under combined TH1-like (IFN-

γ + TNF-α) and TH17-like (IL-17 + GM-CSF) conditions. Ninjurin-1 expression was

quantified by flow cytometry relative to resting cells.

On BBB-ECs, only the TH1- and TH17-like conditions significantly increased

Ninjurin-1 expression, rising from 13.6% in resting cells to 24.8% and 21.7%, respectively

(n = 5; **Fig. 2A**). Similarly, CD11b$^+$ myeloid cells isolated from naïve spleens showed

marked upregulation of Ninjurin-1 under GM-CSF (14.3%; **p < 0.01), TNF-α (16.1%;

***p < 0.001), TH1-like (13.2%; **p < 0.01), and TH17-like (14.9%; ***p < 0.001)

conditions compared to resting cells (8.6%; n = 6; **Fig. 2B**). Other cytokines had no

significant effect on Ninjurin-1 expression in either BBB-ECs or myeloid cells.

These results align with our previous observations in human BBB-ECs [12], where

IFN-γ and TNF-α induced Ninjurin-1 upregulation. Because TH1 and TH17 cytokines are

key inflammatory mediators in EAE and MS [24], these findings suggest that cytokine-

rich environments characteristic of the inflamed CNS drive Ninjurin-1 upregulation on both

endothelial and myeloid cells, potentially facilitating immune cell adhesion and

recruitment across the BBB.

3.3 Ninjurin-1 $^+$ myeloid cells exhibit enhanced co-stimulatory and pro-inflammatory

profiles in vivo.

Given the elevated expression of Ninjurin-1 on CNS infiltrating myeloid cells and

their established role in EAE pathology, we next compared the phenotypic and functional

characteristics of Ninjurin-1$^+$ and Ninjurin-1$^-$ myeloid populations. Immune cells were

isolated from the CNS and spleen of EAE mice at disease onset (day 11-13) when

Ninjurin-1 expression was maximal in the CNS (**Fig. 1D**).

Flow cytometric analysis revealed that CD45^{hi}CD11b$^+$Ninjurin-1$^+$ myeloid cells

from the CNS expressed significantly higher levels of the co-stimulatory molecules CD80

and CD86, as well as MHC II, compared with their Ninjurin-1$^-$ counterparts (**Fig. 3A**; n =

5). A similar upregulation of these activation markers was also observed in splenic

CD11b⁺Ninjurin-1⁺ cells (**Fig. S2A**). PD-L1 expression did not differ significantly between

Ninjurin-1⁺ and Ninjurin-1⁻ populations in either compartment.

We next assessed the expression of inflammatory cytokines associated with TH1

and TH17 polarization, including TNF-α, IL-1β, IL-12p40, and IL-23p19. In the CNS,

Ninjurin-1⁺ myeloid cells expressed significantly higher levels of TNF-α, IL-1β, and IL-

12p40 than Ninjurin-1⁻ cells (**Fig. 3B**). In the spleen, Ninjurin-1⁺ myeloid cells also

exhibited increased expression of IL-1β, IL-6, IL-12p40, IL-23p19, TGF-β, and TNF-α

(**Fig. S2B**).

Together, these findings indicate that Ninjurin-1⁺ myeloid cells display a

heightened activation state characterized by elevated co-stimulatory molecule expression

and robust production of pro-inflammatory cytokines. This phenotype suggests an

enhanced capacity of Ninjurin-1⁺ cells to promote T-cell activation and sustain CNS

inflammation during RR-EAE.

3.4 Ninjurin-1⁺CD11b⁺Ly6G⁻ splenocytes exhibit differential expression of antigen-

presentation and inflammatory genes

Given the marked differences in co-stimulatory molecule and cytokine expression

between Ninjurin-1⁺ and Ninjurin-1⁻ myeloid cells, we next investigated whether these

populations possess distinct transcriptional profiles independent of disease context. To

this   end,   CD45⁺CD11b⁺B220⁻CD3⁻Ly6G⁻Ninjurin-1⁺   and

CD45⁺CD11b⁺B220⁻CD3⁻Ly6G⁻Ninjurin-1⁻ splenocytes were flow-sorted from naïve

mice (gating shown in **Fig. S3**). RNA was extracted, converted to cDNA, and subjected

to targeted qPCR profiling of genes involved in antigen presentation and innate immune

activation.

Overall, the transcriptional data support the hypothesis that Ninjurin-1$^+$ myeloid

cells are intrinsically more pro-inflammatory than their Ninjurin-1$^−$ counterparts. Genes

associated with antigen presentation and immune activation, including Tnf, Cd40, H2-

DMa, and Relb, were significantly upregulated in Ninjurin-1$^+$ cells (**Table 1**). Enhanced

expression of Tlr1 and Tlr7 further indicates increased responsiveness to innate immune

stimuli. In parallel, elevated expression of adhesion and migration molecules such as

Icam1 and Cd44 suggests that Ninjurin-1$^+$ cells are well equipped to traffic to and interact

with inflamed tissues, reinforcing their potential role in amplifying CNS inflammation.

Interestingly, several chemokines involved in leukocyte recruitment, including

Ccl3, Ccl4, and Ccl5 (RANTES), were downregulated, whereas Cxcl10 (IP-10) was

upregulated, indicating a shift toward a more selective chemokine profile that may favor

specific immune-cell interactions within inflammatory microenvironments.

Collectively, these transcriptional data indicate that Ninjurin-1 expression defines

a subset of myeloid cells with heightened antigen-presenting capacity, migratory

potential, and pro-inflammatory gene expression, positioning Ninjurin-1 as both a

functional adhesion molecule and a marker of inflammatory myeloid activation.

3.5 Ninjurin-1$^+$ myeloid cells enhance activation and proliferation of MOG$_{35-55}$-specific

CD4$^+$ T cells

Building on our previous findings, we hypothesized that Ninjurin-1$^+$ myeloid cells

act as more potent antigen-presenting cells (APCs), leading to stronger CD4$^+$ T cell

activation. To test this, we co-cultured FACS-sorted Ninjurin-1$^+$ or Ninjurin-1$^-$ myeloid

cells with MOG$_{35-55}$ peptide (20 μg/ml) and CFSE-labeled CD4$^+$ T cell isolated from 2D2

transgenic mice, which express a T cell receptor specific for MOG$_{35-55}$. 2D2 T cells were

also cultured with MOG$_{35-55}$ with no myeloid cells and co-cultured with myeloid cells

without MOG$_{35-55}$ as controls. After 72 hours of co-culture, T cell proliferation and

phenotype was assessed by CFSE dilution and expression of CD25, IL-17, GM-CSF,

IFN-γ, and TNF-α.

CD4$^+$ T cells co-cultured with Ninjurin-1$^+$ APCs displayed markedly greater

proliferation compared to those cultured with Ninjurin-1$^-$ cells (**Fig. 4A**). This enhanced

proliferation was accompanied by increased CD25 expression, consistent with elevated

T cell activation (**Fig. 4B**). Furthermore, cytokine profiling revealed that CD4$^+$ T cells

stimulated by Ninjurin-1$^+$ APCs produced higher levels of TNF-α (**Fig. 4B**), suggesting a

stronger pro-inflammatory response.

Together, these results demonstrate that Ninjurin-1$^+$ myeloid cells exhibit superior

antigen-presenting capacity and promote a more robust and inflammatory CD4$^+$ T cell

response, further supporting their role as key drivers of neuroinflammation during EAE.

3.6 Anti-Ninjurin-1 treatment at peak disease ameliorates RR-EAE

Given that Ninjurin-1 remains highly expressed in the CNS throughout all phases

of RR-EAE, we next tested whether blocking its function could modify disease

progression. To this end, SJL/J mice were treated intraperitoneally with 1 mg/mL of the

anti-Ninjurin-1$_{26-37}$ blocking peptide or a scramble control three times per week, beginning

at the peak of disease (~day 15). Mice were monitored and disease severity was scored

daily until day 30, at which point the CNS was harvested for histological and flow

cytometric analyses.

Mice treated with anti-Ninjurin-1 displayed significantly lower clinical scores and

were largely protected from relapse, indicating a marked improvement in disease

outcome (**Fig. 5A**). Consistent with the known role of Ninjurin-1 as an adhesion molecule,

its blockade resulted in a substantial reduction in immune cell infiltration into the CNS,

including total $CD45^+$ leukocytes, $CD3^+$ and $CD4^+$ T cells, $B220^+$ B cells, and $CD11b^+$

myeloid cells (**Fig. 5B**).

Histological assessment at the end of treatment confirmed these findings, as spinal

cord sections from anti-Ninjurin-1-treated mice exhibited fewer immune cell infiltrates

compared to controls (**Fig. 5C**). Quantification of cellular infiltration in H&E-stained spinal

cord sections revealed a significant reduction in anti-Ninjurin-1-treated EAE mice

compared with controls, as assessed by nuclear density within standardized white matter

regions (**Fig. 5D**; cells/mm²; n = 3 mice per group). These results are consistent with

previous studies reporting reduced APC infiltration in chronic EAE following Ninjurin-1

blockade, supporting a role for Ninjurin-1 in mediating immune cell adhesion and

trafficking into the CNS.

Together, these findings demonstrate that therapeutic blockade of Ninjurin-1

ameliorates RR-EAE when administered at peak disease, at least in part by limiting CNS

immune infiltration and inflammation, thereby supporting Ninjurin-1 as a promising

immunomodulatory target for relapsing-remitting MS.

4. Discussion

This study identifies Ninjurin-1 as a critical regulator of neuroinflammation in RR-EAE, revealing its dual roles as both an adhesion molecule and a marker of inflammatory activation in myeloid cells. We show that Ninjurin-1 expression is markedly upregulated in the CNS during active disease and that its blockade mitigates immune infiltration and clinical severity. These findings establish Ninjurin-1 as a previously unrecognized mediator linking peripheral immune activation to central neuroinflammation.

Our data demonstrates that Ninjurin-1 expression defines a population of myeloid cells with enhanced pro-inflammatory and antigen-presenting functions. Ninjurin-1^{+} myeloid cells exhibited higher expression of MHC II and co-stimulatory molecules, increased production of cytokines such as TNF-α and IL-1β, and a distinct transcriptional profile enriched for genes associated with antigen presentation, Toll-like receptor signaling, and cell adhesion. The upregulation of Tlr1 and Tlr7 in these cells is particularly relevant, as both receptors have been implicated in MS and EAE [25, 26]. Activation of TLR1 enhances microglial and macrophage responsiveness to bacterial lipoproteins and misfolded proteins, and promotes pro-inflammatory cytokine release [27, 28], while TLR7 stimulation induces type I interferons and TNF-α, contributing to CNS inflammation and demyelination [29, 30]. Thus, Ninjurin-1^{+} cells may represent a population highly responsive to TLR-driven inflammatory cues within the CNS, further amplifying innate and adaptive immune activation. Together, these transcriptional changes outline a multifaceted activation program in Ninjurin-1^{+} myeloid cells that integrates innate sensing, adhesion, and cytokine signaling.

The concurrent upregulation of Icam1 and Cd44 suggests that these cells are primed for tissue infiltration and sustain interaction with other immune cells within the inflamed CNS. Interestingly, Cxcl10 (IP-10), a chemokine known to recruit CXCR3^{+} Th1 cells across the BBB [31], was also increased in Ninjurin-1^{+} myeloid cells. Elevated CXCL10 levels have been observed in active MS lesions and in EAE, where they promote the accumulation of pathogenic T cells and perpetuate the inflammatory milieu [32, 33]. These features parallel pathogenic myeloid subsets identified in MS lesions, which have been shown to drive demyelination and neurodegeneration [34-37], and support a model in which Ninjurin-1^{+} myeloid cells drive lesion formation and disease progression through both antigen presentation and chemokine-mediated immune recruitment.

Importantly, we found that TH1- and TH17-associated cytokines, including IFN-γ, TNF-α, GM-CSF, and IL-17 induce Ninjurin-1 expression on both BBB-ECs and myeloid cells. This places Ninjurin-1 downstream of key inflammatory pathways known to dominate during MS relapses. Such cytokine-driven upregulation provides a mechanistic link between systemic immune activation and localized BBB disruption, where Ninjurin-1 may facilitate leukocyte adhesion and transmigration. The observed upregulation of Ninjurin-1 on both endothelial and infiltrating myeloid cells supports the concept of homophilic interactions across the BBB, potentially stabilizing immune cell adhesion and promoting CNS entry.

Therapeutic blockade of Ninjurin-1 at the peak of disease attenuated clinical scores, reduced immune cell infiltration, and decreased CNS inflammation. This effect resembles the efficacy of adhesion-molecule inhibitors such as Natalizumab, which targets α4-integrin/VCAM-1 interactions [38]. However, Ninjurin-1's unique dual role

distinguishes it from canonical adhesion molecules. Unlike ICAM-1 and VCAM-1, which

primarily mediate leukocyte-endothelial interactions, Ninjurin-1 exerts a dual influence by

functioning both on vascular and immune compartments. Its homophilic binding supports

leukocyte adhesion at the BBB, while its intracellular signaling capacity enhances myeloid

activation and antigen presentation within the CNS. This combination positions Ninjurin-

1 as both a structural and signaling mediator of neuroinflammation, extending its role

beyond passive adhesion to active immune modulation.

Beyond its adhesive role, Ninjurin-1 may also influence inflammatory cell survival

and signaling. Previous reports have implicated Ninjurin-1 in plasma membrane rupture

and the subsequent release of damage-associated molecular patterns [16, 39, 40],

processes that can propagate sterile inflammation. Together with our findings, this raises

the possibility that Ninjurin-1 contributes to a feed-forward loop wherein inflammatory

cytokines induce its expression, promoting adhesion, activation, and additional cytokine

release that sustain neuroinflammation.

Our findings extend the understanding of adhesion molecules in MS by

emphasizing immune cell-intrinsic regulation rather than endothelial expression alone. By

integrating cytokine signaling, adhesion, and immune activation, Ninjurin-1 bridges

molecular pathways that have traditionally been studied in isolation. Given that Ninjurin-

1 is upregulated in multiple inflammatory conditions, including stroke and fibrosis, its role

may not be limited to demyelinating disease but may represent a broader mechanism of

leukocyte-mediated tissue injury.

In conclusion, we identify Ninjurin-1 as a novel adhesion and activation molecule

driving myeloid-mediated inflammation in RR-EAE. Through its induction by TH1/TH17

cytokines and expression on both BBB-endothelial and immune cells, Ninjurin-1

orchestrates key steps in immune cell recruitment and activation within the CNS. Its

blockade alleviates disease even at advanced stages, underscoring its therapeutic

potential. Future studies should assess Ninjurin-1 expression in human MS lesions and

determine whether its signaling partners and downstream pathways can be targeted to

modulate disease progression. Elucidating the intracellular signaling cascades engaged

by Ninjurin-1 will be essential to understand how this molecule bridges adhesion and

immune activation, and may uncover new opportunities for therapeutic intervention.

Author Contributions

C.T. conducted most the experiments. A.Annett assisted with EAE studies. C.T., A.

Alkhimovitch, and K.S.P had intellectual input and revised the manuscript. I.I. supervised

the project and revised the manuscript. All authors contributed to manuscript preparation.

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   FIGURES LEGENDS

Figure 1. Ninjurin-1 is highly expressed on myeloid cells in the CNS throughout

RR-EAE. RR-EAE was induced in female SJL/J mice using $PLP_{139-151}$ emulsified in

complete Freund's adjuvant. Spleen and CNS tissues were collected at defined disease

stages and analyzed for Ninjurin-1 expression by flow cytometry. (**A**) RR-EAE clinical

disease course (n = 8). (**B**) $CD45^{hi}$ $B220^-$ $CD3^-$ $CD11b^+$ infiltrating myeloid cells in the

CNS displayed a marked increase in Ninjurin-1 expression compared with splenic myeloid

cells at all disease stages (pre-onset, onset, peak, remission, and relapse). (**C**) $CD45^{hi}$

$CD3^+$ $CD11b^-$ T cells in the CNS displayed consistently low Ninjurin-1 expression, with no

significant differences compared to splenic $CD3^+$ T cells at any disease stage. (**D**)

Ninjurin-1 expression in CNS-infiltrating myeloid cells peaked at disease onset and

remained elevated at the peak phase. All time points include n = 4 mice, except relapse

(n = 3). Data are representative of two independent EAE experiments. Results are shown

as mean ± SEM and were analyzed using two-way ANOVA (*p < 0.05, **p < 0.01, ***p <

0.001).

Figure 2. Inflammatory conditions increase Ninjurin-1 expression on BBB

endothelial and myeloid cells. Primary brain microvascular endothelial cells (BBB-ECs)

and splenic myeloid cells were cultured for 24 hours under resting conditions or in the

presence of inflammatory cytokines to assess Ninjurin-1 expression by flow cytometry.

(**A**) BBB-ECs upregulated Ninjurin-1 expression following stimulation with TH1-like (IFN-

γ + TNF-α) or TH17-like (GM-CSF + IL-17) cytokine combinations (n = 5 independent

experiments). (**B**) CD45$^+$ CD11b$^+$ Ly6G$^-$ myeloid cells isolated from spleens of naïve

C57BL/6 mice exhibited increased Ninjurin-1 expression when stimulated with GM-CSF,

TNF-α, or TH1-/TH17-like cytokine conditions (n = 6 independent experiments). Data are

presented as mean ± SEM and analyzed using two-way ANOVA (*p < 0.05, **p < 0.01,

***p < 0.001).

Figure 3. Ninjurin-1$^+$ myeloid cells exhibit enhanced activation and inflammatory

cytokine expression in the CNS. CD45^{hi} B220$^-$ CD11b$^+$ infiltrating myeloid cells were

isolated from the CNS of SJL/J mice at disease onset during RR-EAE and analyzed by

flow cytometry. (**A**) Ninjurin-1$^+$ myeloid cells (open squares) displayed significantly higher

expression of the co-stimulatory molecules CD80 and CD86, as well as MHC class II,

compared with Ninjurin-1$^-$ counterparts (closed circles). (**B**) Ninjurin-1$^+$ myeloid cells also

exhibited increased expression of the inflammatory cytokines TNF-α, IL-1β, and IL-12p40.

Data represent n = 5 mice and are presented as mean ± SEM. Statistical significance was

determined using paired t-test (*p < 0.05, **p < 0.01).

Table 1. List of genes differentially expressed between Ninjurin-1$^+$ and Ninjurin-1$^-$

myeloid cells. Shown are genes with their corresponding fold-regulation values and *p*-

values comparing Ninjurin-1$^+$ versus Ninjurin-1$^-$ CD45$^+$CD11b$^+$B220$^-$CD3$^-$Ly6G$^-$ myeloid

cells, as determined by RT² Profiler PCR Array analysis.

† Only genes showing ≥1.5-fold difference between groups are represented. Positive

values indicate upregulation in Ninjurin-1$^+$ cells relative to Ninjurin-1$^-$ cells.

†† *p*-values were calculated using a Student's *t*-test on replicate $2^{(-\Delta CT)}$ values for each

gene in the Ninjurin-1$^+$ and Ninjurin-1$^-$ groups (*n* = 3 independent experiments).

Figure 4. Ninjurin-1$^+$ myeloid cells enhance CD4$^+$ T cell activation and cytokine

production. CD45$^+$ B220$^-$ CD3$^-$ CD11b$^+$ Ly6G$^-$ Ninjurin-1$^+$ or Ninjurin-1$^-$ myeloid cells

were flow-sorted and co-cultured with CFSE-labeled CD4$^+$ T cells isolated from 2D2 mice.

Cells were stimulated with MOG$_{35-55}$ peptide in 96-well plates for 72 hours. (**A**) T cell

proliferation, measured by CFSE dilution, was greater when CD4$^+$ T cells were co-

cultured with Ninjurin-1$^+$ myeloid cells compared to Ninjurin-1$^-$ cells. Controls included

CD4$^+$ T cells cultured without antigen-presenting cells (APCs) or without MOG$_{35-55}$

peptide. (**B**) CD4$^+$ T cells co-cultured with Ninjurin-1$^+$ myeloid cells showed increased

expression of CD25 and TNF-α, indicating higher levels of activation and inflammatory

cytokine production. Data represent n = 4 independent experiments and are shown as

mean ± SEM. Statistical analysis was performed using two-way ANOVA (*p < 0.05, **p ≤

0.01, ***p < 0.001).

Figure 5. Anti-Ninj$_{26-37}$ treatment at peak RR-EAE protects against relapse and

reduces CNS immune cell infiltration. RR-EAE was induced in SJL/J mice by

subcutaneous injection of PLP$_{139-151}$ emulsified in CFA. Mice were treated

intraperitoneally three times per week with anti-Ninj$_{26-37}$ peptide (1 mg/mL; n = 11) or

scramble control (n = 11), starting at the peak of disease (day 15) and continuing until

day 30 post-induction. (**A**) Anti-Ninj$_{26-37}$–treated mice (open circles) displayed

significantly reduced clinical scores and were protected from relapse compared with

scramble-treated controls (closed squares; ***$p < 0.001$ by Mann–Whitney test). (**B**) Flow

cytometry of CNS mononuclear cells showed a marked reduction in total CD45^{hi}

leukocytes, including CD3$^+$ T cells, CD4$^+$ T cells, B220$^+$ B cells, and CD11b$^+$ myeloid

cells, in anti-Ninj$_{26-37}$–treated mice (n = 5; *$p < 0.05$ by multiple unpaired t-tests).

(**C**) Representative H&E-stained spinal cord sections collected at day 30 show reduced

inflammatory infiltrates in anti-Ninj$_{26-37}$–treated mice compared to controls. Data are

representative of at least three sections per mouse from four mice per group. Scale bar

= 200 μm. (**D**) Cellular infiltration was quantified by counting hematoxylin-positive nuclei

within standardized 300 × 300 μm white matter regions (three ROIs per section, averaged

per mouse) and expressed as cells per mm². Each dot represents one mouse; bars

indicate mean ± SEM.

Figure 1

Figure 2

A

B

Figure 3

Table 1: List of genes differentially expressed between Ninjurin-1$^+$ and Ninjurin-1$^-$ myeloid cells

Gene Symbol	Fold Regulation†	p-value††
Lrp1	6.04	0.006112
Fcgrt	4.59	0.016751
Tlr1	4.49	0.025853
Relb	3.85	0.037913
Cd40	3.59	0.025442
Csf1r	3.12	0.035088
Icam1	3.01	0.035127
Cxcl10	2.87	0.023356
Tlr7	2.57	0.009076
Lyn	2.49	0.023053
Cd44	2.47	0.000941
H2-DMa	2.14	0.024490
Thbs1	2.04	0.045327
Tnf	2.03	0.024954
Itgam	1.55	0.003831
Ccl3	-6.20	0.048783
Ccl4	-10.16	0.008899
Ccl5	-29.53	0.003971

Figure 4

A

B

Figure 5