

Table 4: Functional classification of IFN β -upregulated genes in PBMC

Categories	Number of genes	Gene symbols (alternative symbols or names)
1 Conventional IFN-response markers	12	IFIT1 (IFI56), ISG15 (GIP2), IFIT4 (IFI60), MX1 (MXA), MX2 (MXB), IFI27, GIP3 (IFI6-16), ISG20, IFI16, IFITM1 (IFI17), IFITM3 (I-8U), ABCB2 (TAPI)
2 Components of IFN-signaling pathways	12	STAT1, IRF7, STAT2, JAK2, IRF2, ISGF3G (IRF9), MYD88, IRF8, STAT3, JAK3, IRF1, TLR3
3 Chemokines and receptors	11	SCYB11 (CXCL11, I-TAC), SCYB10 (CXCL10, IP-10), SCYA8 (CCL8, MCP2), SCYB9 (CXCL9, MIG), SCYA2 (CCL2, MCP1), CCR5, SCYA4 (CCL4, MIP1B), IL8RB (CXCR2), SCYA3 (CCL3, MIPIA), SCYA19 (CCL19, MIP3B), SCYA13 (CCL13, MCP4)
4 Cytokines, growth factors, and receptors	17	IL6, ILRN (IL-1 receptor antagonist), IL1R2, IL15RA, IL15, SPP1 (osteopontin), CSF1, IL12RB2, TNF (TNFA), IL2RB, IFNG, NTRK1 (TRKA), PDGFRL, TNFAIP6, KITLG (SCF), IL10, IL3RA
5 Apoptosis, DNA damage, and cell cycle regulators	29	TNFSF10 (TRAIL), CASP10, BAG1, TNFRSF6 (FAS), CASP4, TRADD, GZMA, CASP7, RIPK2, MAD, RIPK1, CFLAR (FLIP), RELA, STK3, CASP1, TNFSF6 (FASL), PARP4, TANK (I-TRAF), POLE2, LMNB1, E2F2, CCNA1 (cyclin A1), CDKN1A (p21), PPP1R15A (GADD34), CASP3, CDKN1C (p57), CDK5R2 (p39), TERF1, NBS1 (nibrin)
6 Heat shock proteins	9	HSPA6 (HSP70B), HSJ2 (HSPF4), HSPA1A (HSP70-1), HSPA1B (HSP70-2), HSPCA (HSP90A), HSPA5 (GRP78), HSPA1L (HSP70-HOM), HSPA8 (HSC70), HSPB1 (HSP27)
7 Costimulatory and adhesion molecules	7	CD80 (B7-1), SELL (selectin L), TNFRSF5 (CD40), CD163, CD86 (B7-2), HLA-DRA, FCER1G

The upregulated IRGs in PBMC listed in Additional files 3 and 5 were classified into seven functional categories.

Real-time RT-PCR analysis validated IFN β -regulated expression of IRGs identified by microarray analysis

Although the microarray we utilized contains total 64 spots of the G3PDH gene (see Additional file 1), G3PDH was neither identified as a significantly upregulated nor a downregulated gene in the microarray analysis, suggesting that G3PDH represents a reliable housekeeping gene in gene expression analysis of PBMC following treatment with IFN β . Therefore, quantitative real-time RT-PCR analysis was performed by evaluating the levels of expression of target genes standardized against those of G3PDH detected in the identical cDNA samples. It verified the key observations of microarray analysis, such as marked upregulation of ISG15, the prototype of IRGs (Figure 1a-c), and great elevation of SCYB10, SCYA8 and SCYA2 (Figures 2, 3, 4a-c) in PBMC at both 3 and 24 hours of IFN β treatment. Furthermore, the quantitative analysis confirmed substantial downregulation of FOS at both time points (Figure 5a-c), and RGS14 and SCYB2 predominantly at 3 hours (Figures 6, 7a-c). Exposure of PBMC to IFN γ greatly elevated the expression of SCYB10 and SCYA2, and to a lesser extent, ISG15 and SCYA8 at both time points (Figures 1, 2, 3, 4d), suggesting a functional overlap in induction of CXCR3 ligand and CCR2 ligand chemokines between type I and type II IFN signaling pathways. In contrast, TNF α and IL-1 β the prototype of proinflammatory cytokines, did not at all elevate the levels of expression of ISG15, SCYB10 or SCYA8 (Figures 1, 2, 3e, f), while IL-1 β significantly ($p = 0.041$ at 3 hours and $p = 0.004$ at 24 hours by two-sided paired t-test) but TNF α

only marginally ($p = 0.2102$ at 3 hours and $p = 0.0825$ at 24 hours by two-sided paired t-test) upregulated SCYA2 expression (Figure 4e, f). Treatment with IFN γ , TNF α or IL-1 β reduced the levels of FOS and RGS14 substantially at 24 hours (Figures 5, 6d-f). IFN γ reduced the expression of SCYB2, whereas TNF α and IL-1 β elevated its levels at both time points, suggesting differential regulation of SCYB2 gene expression in PBMC by exposure to distinct cytokines (Figure 7d-f). The IFN β -regulated gene expression pattern was similar among PBMC derived from three distinct healthy subjects #1, #2 and #3, supporting the reproducibility of these observations (Figures 1, 2, 3, 4, 5, 6, 7a-c).

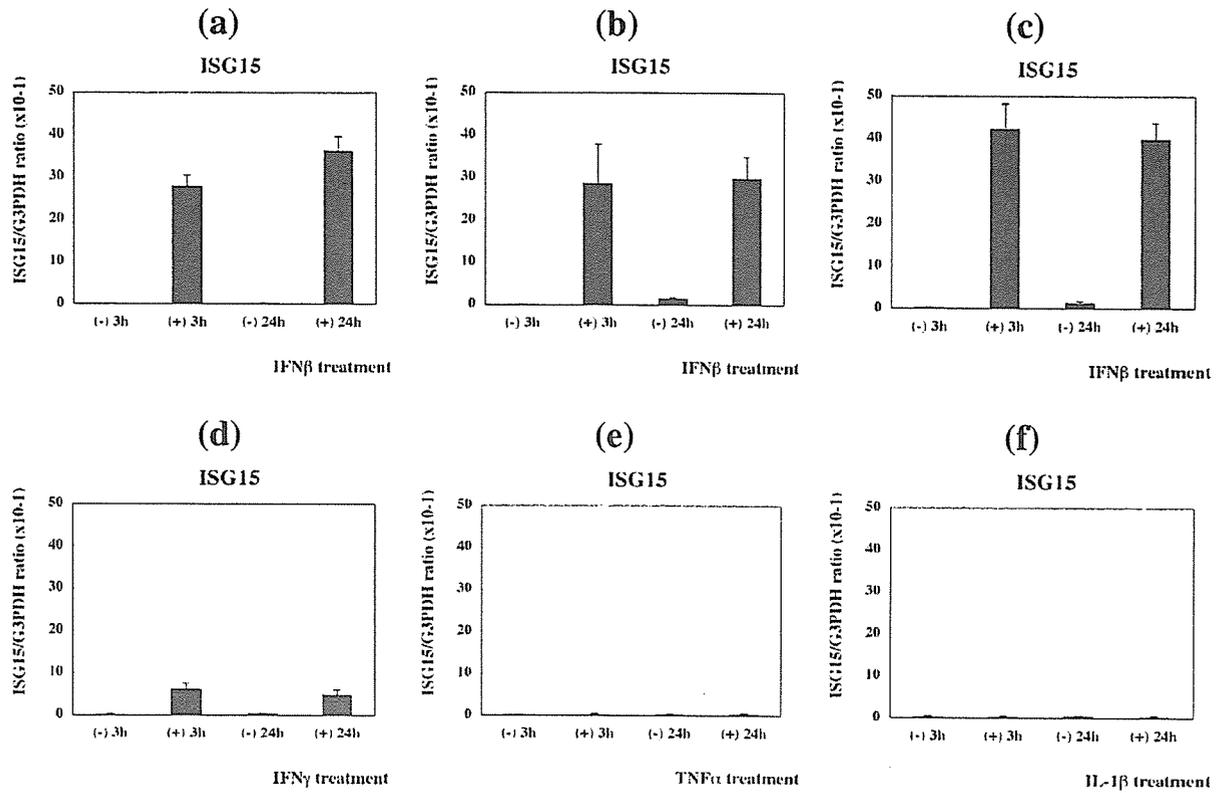


Figure 1
 Real-time RT-PCR analysis of ISG15 expression in PBMC. PBMC derived from three distinct healthy subjects numbered #1 (a 46 year-old man), #2 (a 28 year-old man), and #3 (a 42 year-old woman) were incubated for 3 hours or 24 hours in the culture medium with (+) or without (-) inclusion of recombinant human IFNβ, IFNγ, TNFα or IL-1β at a concentration of 50 ng/ml each. cDNA was processed for real-time PCR analysis using specific primers listed in Table 1. The levels of expression of ISG15 are standardized against those of the glyceraldehyde-3-phosphate dehydrogenase (G3PDH) gene detected in identical cDNA samples. The assays were performed in triplicate measurements of the same sample, and the results were expressed as the average with standard error. The panels represent the expression of ISG15 in (a) #1, IFNβ; (b) #2, IFNβ; (c) #3, IFNβ; (d) #1, IFNγ; (e) #1, TNFα; and (f) #1, IL-1β.

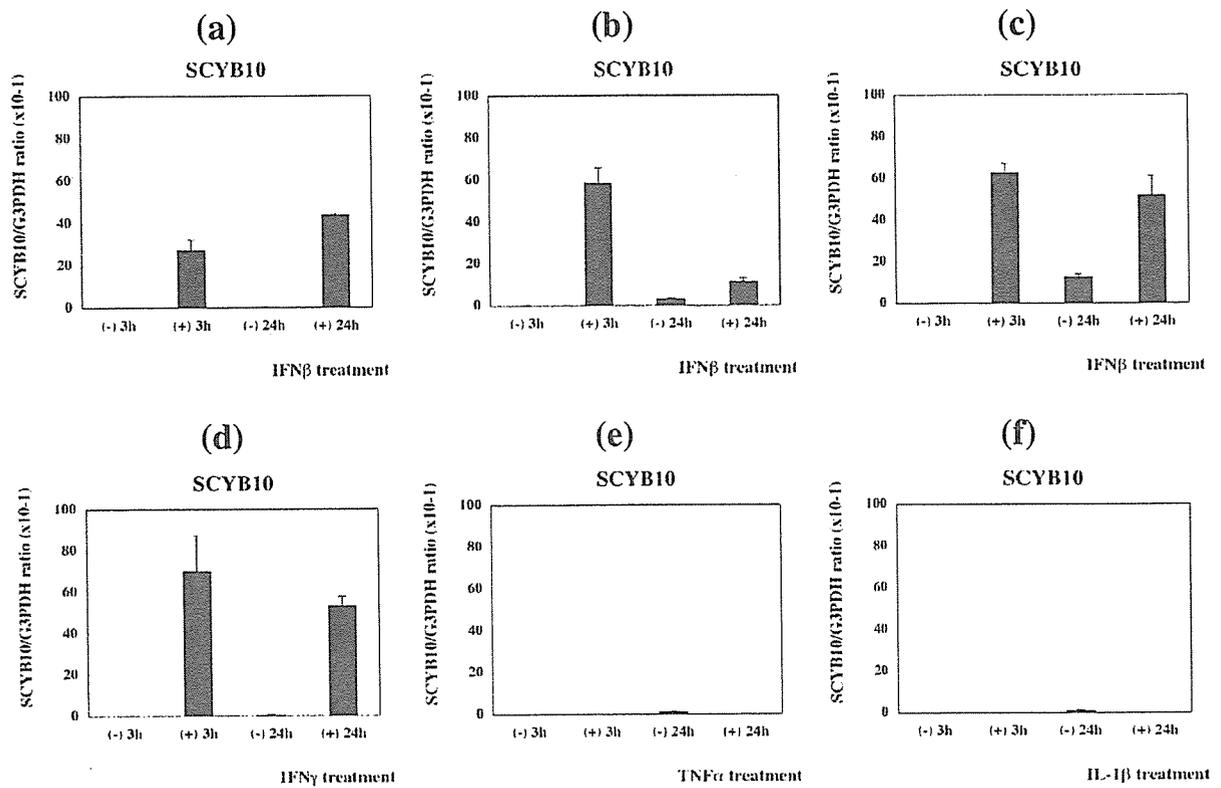


Figure 2
Real-time RT-PCR analysis of SCYB10 expression in PBMC. See the footnote of Figure 1. The panels represent the expression of SCYB10 in (a) #1, IFN β ; (b) #2, IFN β ; (c) #3, IFN β ; (d) #1, IFN γ ; (e) #1, TNF α ; and (f) #1, IL-1 β .

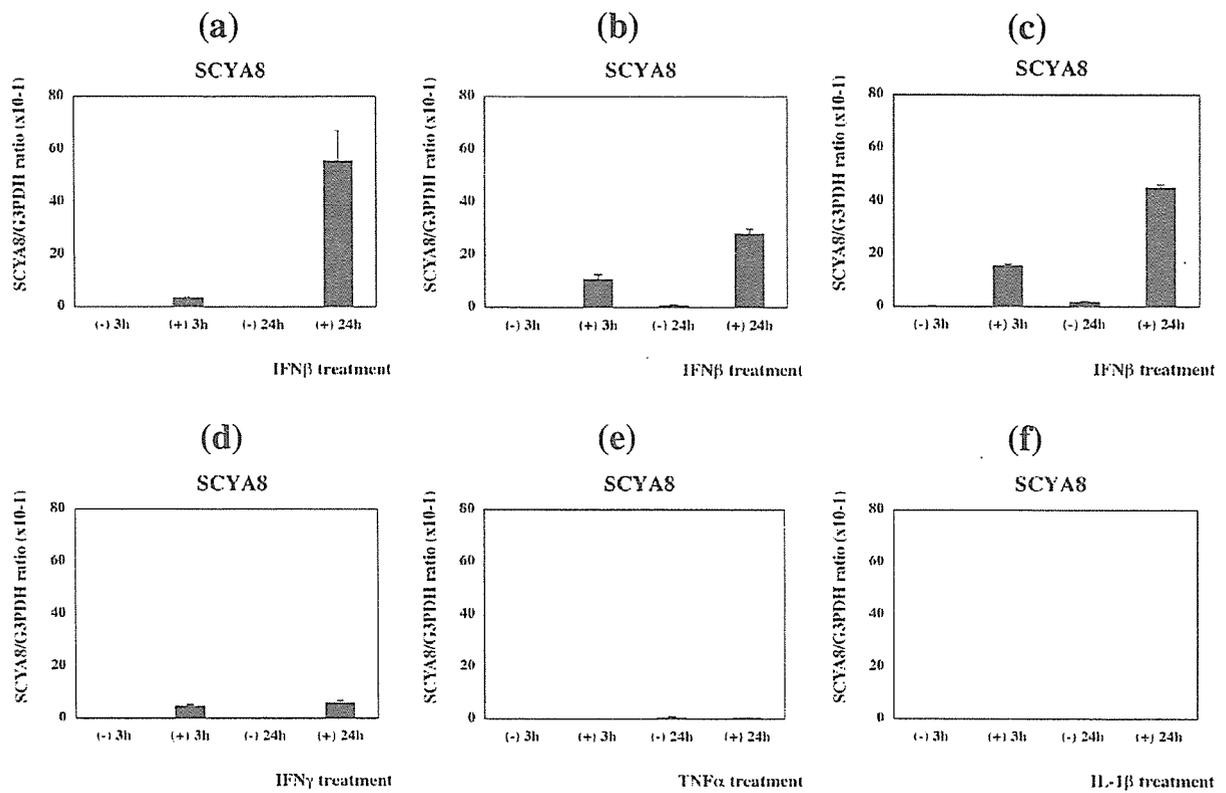


Figure 3
 Real-time RT-PCR analysis of SCYA8 expression in PBMC. See the footnote of Figure 1. The panels represent the expression of SCYA8 in (a) #1, IFNβ; (b) #2, IFNβ; (c) #3, IFNβ; (d) #1, IFNγ; (e) #1, TNFα; and (f) #1, IL-1β.

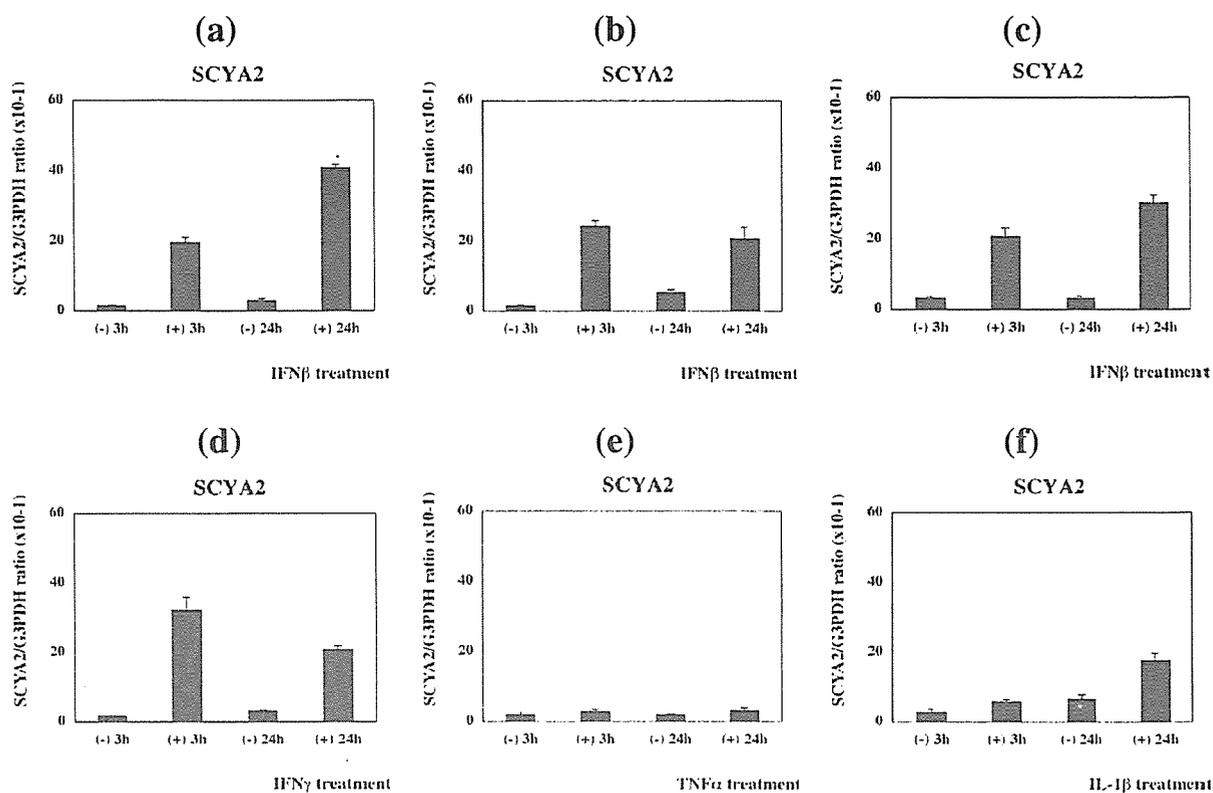


Figure 4
 Real-time RT-PCR analysis of SCYA2 expression in PBMC. See the footnote of Figure 1. The panels represent the expression of SCYA2 in (a) #1, IFNβ; (b) #2, IFNβ; (c) #3, IFNβ; (d) #1, IFNγ; (e) #1, TNFα; and (f) #1, IL-1β.

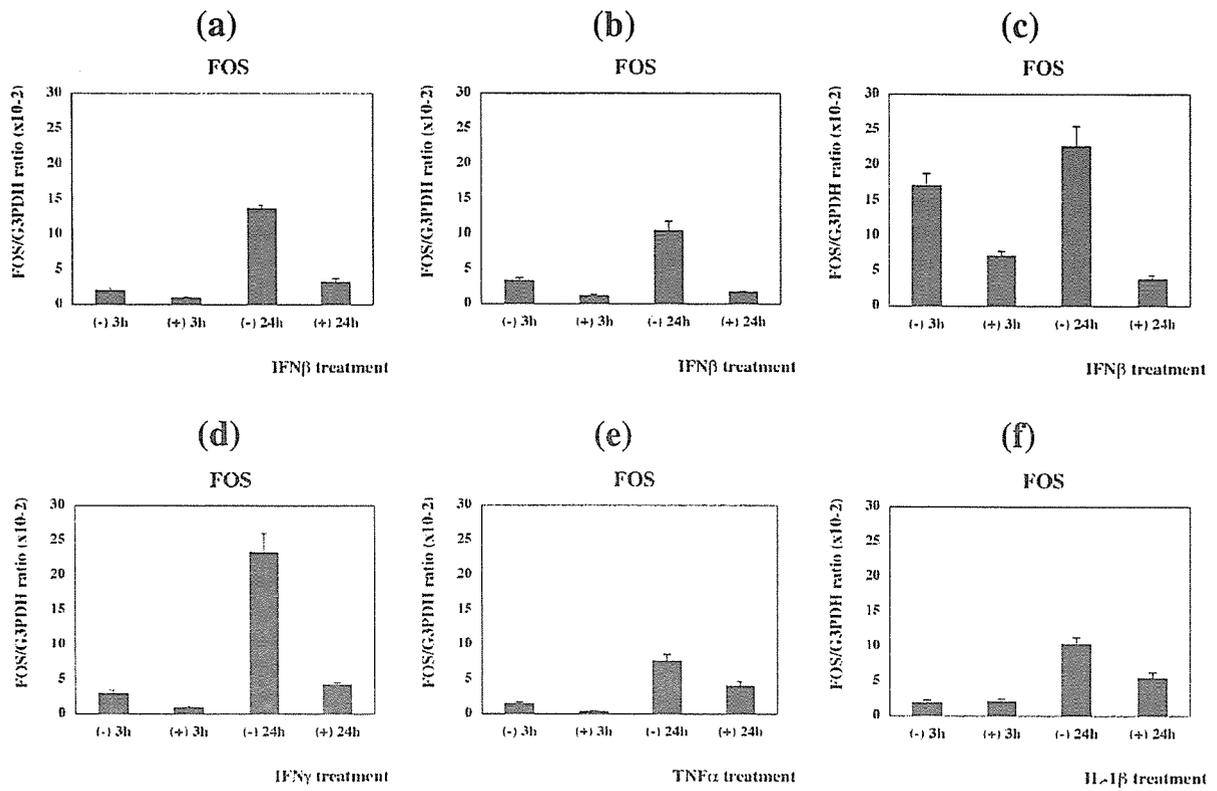


Figure 5
 Real-time RT-PCR analysis of FOS expression in PBMC. See the footnote of Figure 1. The panels represent the expression of FOS in (a) #1, IFNβ; (b) #2, IFNβ; (c) #3, IFNβ; (d) #1, IFNγ; (e) #1, TNFα; and (f) #1, IL-1β.

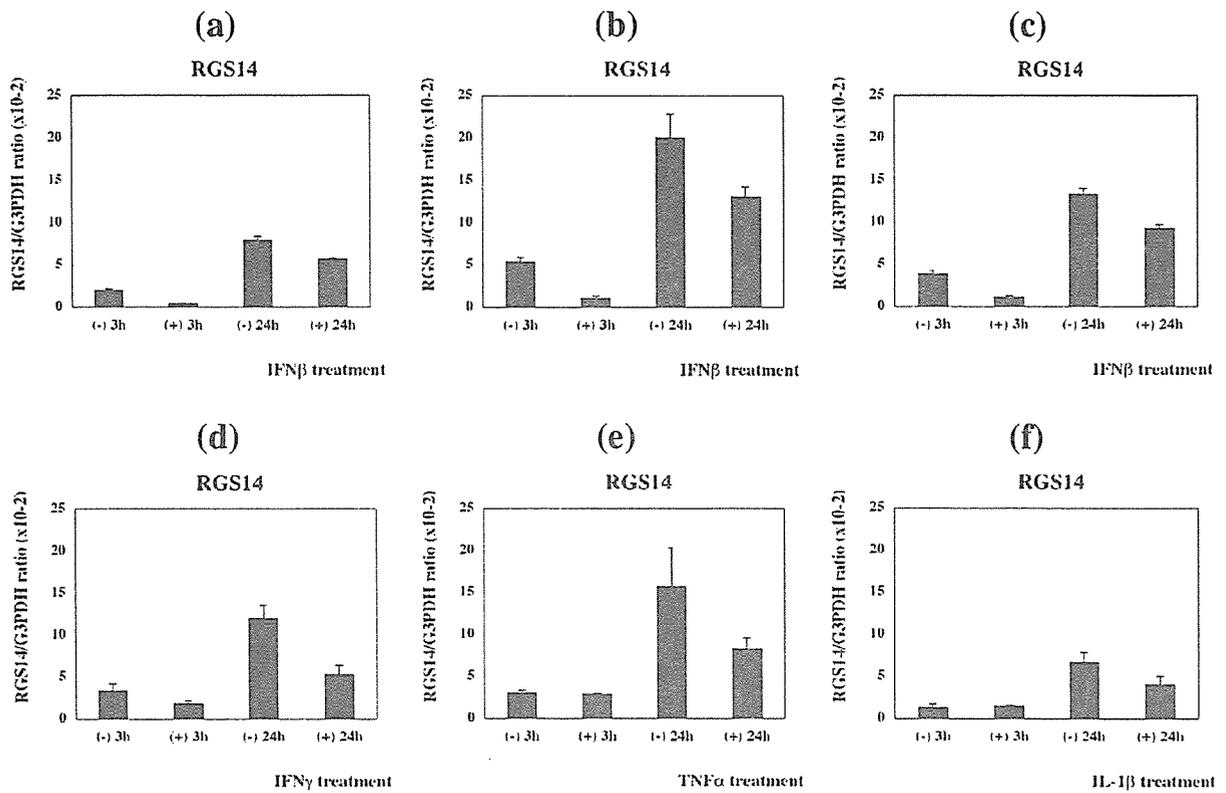


Figure 6
 Real-time RT-PCR analysis of *RGS14* expression in PBMC. See the footnote of Figure 1. The panels represent the expression of *RGS14* in (a) #1, IFN β ; (b) #2, IFN β ; (c) #3, IFN β ; (d) #1, IFN γ ; (e) #1, TNF α ; and (f) #1, IL-1 β .

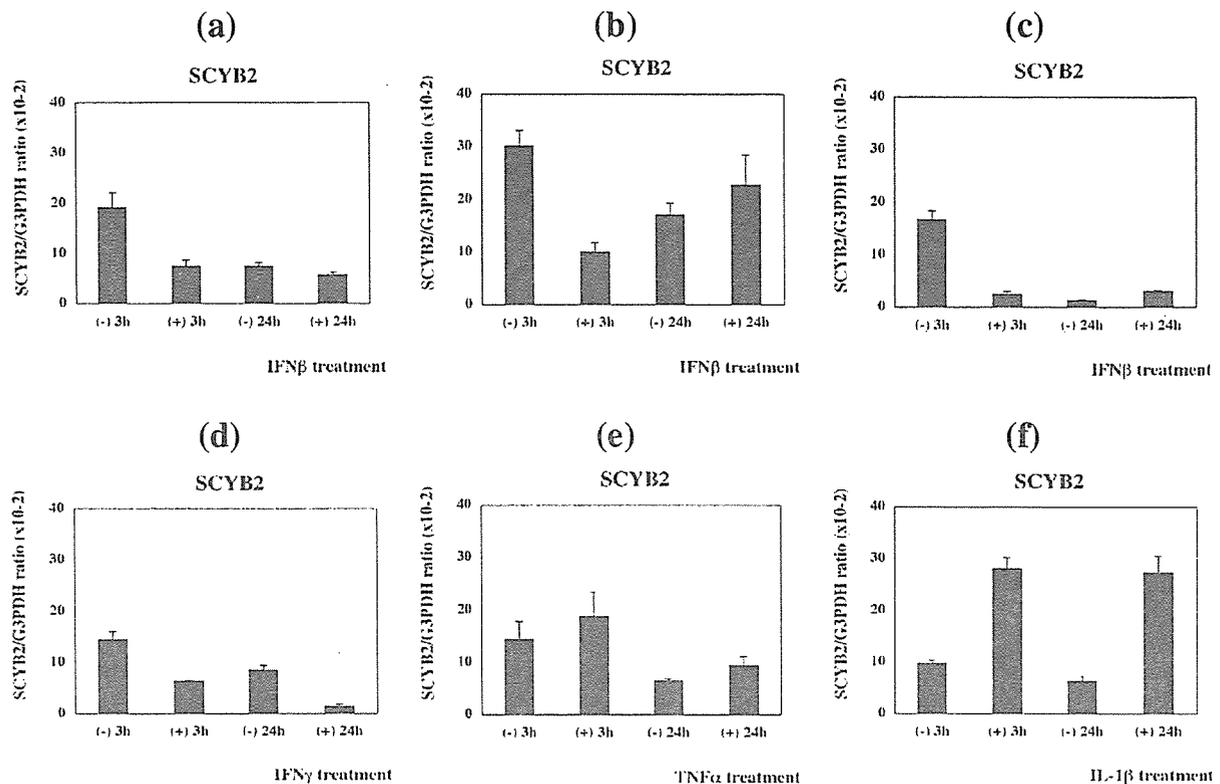


Figure 7

Real-time RT-PCR analysis of SCYB2 expression in PBMC. See the footnote of Figure 1. The panels represent the expression of SCYB2 in (a) #1, IFN β ; (b) #2, IFN β ; (c) #3, IFN β ; (d) #1, IFN γ ; (e) #1, TNF α ; and (f) #1, IL-1 β .

Discussion

IFNs are a family of cytokines that mediates antiviral, anti-proliferative and immunoregulatory activities. Type I IFNs, IFN α and β , are produced principally by virus-infected host cells, whereas type II IFN, IFN γ , is produced by activated T cells and natural killer (NK) cells. Type I IFNs activate JAK protein tyrosine kinases associated with the cell surface receptors for IFNs, leading to formation of the complex of signal transducer and activator of transcription (STAT) molecules with the IFN regulatory factor (IRF) family of transcription factors. The STAT/IRF complex translocates into the nucleus, and binds to the DNA sequences termed the IFN-stimulated response element (ISRE) or the IRF-recognition element (IRE). This binding subsequently activates transcription of a wide variety of IFN-responsive genes (IRGs) as well as the genes of type I and type II IFNs, leading to the biological responses triggered by the IFNs [24]. Both type I and type II IFNs enhance the expression of class I and class II MHC molecules [25]. Among nine distinct IRFs, IRF7 and IRF3 play a central role in induction of type I IFN genes via the virus-

activated MYD88-independent pathway or Toll-like receptor (TLR)7, 8 or 9-activated MYD88-dependent pathway [26], while IRF1 plays more active roles in induction of IFN γ -target genes essential for Th1-type immune response [25].

The present study by analyzing DNA microarray characterized a comprehensive list of immediate early IRGs in PBMC *in vitro*. Following a 3 to 24 hour-exposure to IFN β , upregulated genes greatly outnumbered downregulated genes. All top 20 upregulated genes represent known IRGs previously identified in various cell types. The upregulated IRGs of PBMC were classified into several functional categories. The list included not only conventional IFN-response markers and components of IFN-signaling pathways, but also contained many proinflammatory chemokines and cytokines. This is surprising because IFN β acts principally as an anti-Th1, anti-inflammatory cytokine [6,7]. By analyzing global gene expression profile, the present study for the first time showed that IFN β induced a burst of gene expression of CXCR3 ligand chemokines

(SCYB11, SCYB10 and SCYB9) and CCR2 ligand chemokines (SCYA8 and SCYA2), which was verified by quantitative real-time RT-PCR analysis. The chemokine genes actually have ISRE or IRE in the promoter regions, indicating direct targets of IFN β [27,28].

CXCR3 is expressed predominantly on activated Th1 T cells, while CCR2 is expressed chiefly on monocytes [29]. The number of CXCR3⁺T cells is increased in the blood of RRMS, and they accumulate in perivascular infiltrates in active MS lesions [30,31], while SCYB10 (IP-10) and SCYB9 (MIG) are detected in the cerebrospinal fluid (CSF) of RRMS at acute relapse and expressed in reactive astrocytes in active MS lesions [31,32]. SCYA2 (MCP1) and SCYA8 (MCP2) immunoreactivities are also identified in reactive astrocytes in active demyelinating lesions of MS [33,34]. These observations suggest that CXCR3, CCR2, and their ligand chemokines positively regulate active inflammation in MS. Although the precise cell types expressing CXCR3 ligand and CCR2 ligand chemokines in PBMC in response to IFN β remain to be characterized, the chemokine burst plays a central role in rapid activation and systemic recruitment of Th1 T cells and monocytes immediately after initiation of IFN β treatment. A recent study showed that IFN β promotes trafficking of mouse leukocytes by regulating a specific set of chemokines [35]. However, concurrent upregulation of a set of CXCR3 and CCR2 ligand chemokines has not previously been reported in MS patients on a long-term IFN β treatment [16,17,20-22], suggesting that this phenomenon is an immediate early but transient event *in vivo*. IFN β immediately reduced the expression of RGS14 (the most significantly downregulated gene at 3 hours; see Table 3), a member of the regulator of G protein signaling (RGS) gene family that acts as a negative regulator of G protein-coupled receptor (GPCR) signaling. Since all chemokine receptors are GPCR, IFN β -induced downregulation of RGS14 might facilitate chemokine responsiveness in the cells expressing RGS14 [36,37]. Much less is known about the mechanism for regulation of IFN β -repressed genes [38]. We identified IL-8 as one of IFN β -repressed genes in PBMC (Table 3). IFN β inhibits the transcription of IL-8 gene, possibly by binding of NF- κ B repressing factor (NRF) to a negative regulatory element of the IL-8 promoter [39]. Serum IL-8 levels and IL-8 secretion from PBMC are elevated in untreated MS, and then reduced following IFN β therapy [40]. Downregulation of IL-8 expression in PBMC during IFN β treatment provides a predictive indicator for the responders in RRMS [20].

IFN β also promptly upregulated a variety of proinflammatory cytokines, such as IL-6, IL-15, osteopontin, TNF α , and IFN γ in PBMC (Table 4). IFN β promotes production of TNF α and IFN γ in unstimulated PBMC but decreases their levels in preactivated PBMC [41-43]. IFN β increases

the number of IFN γ -secreting cells *in vivo* at the early period of the treatment [44]. Most importantly, proinflammatory cytokines and chemokines induced by IFN β have relevance to treatment-related early adverse effects. There exists a close relationship between flu-like symptoms and increased levels of IL-6 [45]. A single injection of IFN β induces a transient burst of SCYB10 (IP-10) in the plasma of RRMS patients, which correlates with an incidence of flu-like symptoms [46]. IFN β enhances the expression of CD80, SCYB10 (IP-10) and SCYA2 (MCP1) *in situ* at sites of injection, leading to chemotaxis of lymphocytes and monocytes in the lesions of skin reaction [47-49]. We found that IFN β aberrantly regulated the levels of expression of several cytochrome P450 (CYP) enzymes (see Additional files 3,4,5,6). Type I IFN reduces the activity of CYP enzymes that metabolize various endogenous and exogenous substrates, probably leading to an increase in the potential for IFN-related hepatotoxicity [50].

Finally, the list of IRGs included various apoptosis regulators and HSP family members. ISRE-like sequences are identified in the regulatory element of CASP1, CASP4, CASP8, TNFRSF6 (FAS), TNFSF6 (FASL) and TNFSF10 (TRAIL), suggesting that IFN β acts as a proapoptotic cytokine [51,52]. A recent study showed that early and sustained induction of TRAIL provides a marker for IFN β treatment response in MS [53]. Furthermore, IFN β -inducible apoptosis regulators play an immunoregulatory role. TNFR1-associated via death domain (TRADD) inhibits IFN γ -induced STAT1 α activation [54]. Receptor-interacting serine-threonine kinase 1 (RIPK1) regulates TLR3-independent viral double-stranded RNA-induced type I IFN production [55]. Because HSPs in general act as an anti-apoptotic defender, the induction of HSP gene expression might occur as a counterbalance against upregulation of proapoptotic regulators. Alternatively, IRGs could directly enhance HSP expression. IFN β -induced STAT1, by interacting with heat shock factor-1 (HSF1), activates the HSP70 and HSP90 β gene promoters [56].

Conclusion

Microarray analysis showed that IFN β immediately induces a burst of gene expression of proinflammatory chemokines and cytokines *in vitro* that have potential relevance to IFN β -related early adverse effects in MS patients *in vivo*.

Abbreviations

MS = multiple sclerosis; IFN β = interferon-beta; IRGs = IFN β -responsive genes; PBMC = peripheral blood mononuclear cells; CNS = central nervous system; IFN γ = interferon-gamma; Th1 = T helper type 1; MHC = major histocompatibility complex; RRMS = relapsing-remitting multiple sclerosis; ISG = IFN stimulated gene; TLR = Toll-

like receptor; STAT = signal transducer and activator of transcription; IRF = interferon regulatory factor; ISRE = interferon-stimulated response element; IRE = interferon regulatory factor-recognition element; HSPs = heat shock proteins; CSF = cerebrospinal fluid; GPCR = G protein-coupled receptor; RGS = regulator of G protein signaling.

Competing interests

The author(s) declare that they have no competing interests.

Authors' contributions

JS, YN and HT carried out DNA microarray and real-time RT-PCR analysis, and JS drafted the manuscript. TY participated in the design of the study and helped to draft the manuscript. All authors read and approved the final manuscript.

Additional material

Additional File 1

The gene list of cDNA microarray utilized in the present study. The complete gene list of cDNA microarray utilized in the present study is shown. It includes 1,258 well-annotated genes, selected from cytokines, growth factors and their receptors, apoptosis regulators, oncogenes, transcription factors, cell cycle regulators and housekeeping genes.

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Additional File 2

Scatter plots of three distinct microarray experiments. The figure represents a scatter plot exhibiting the comparison between the fluorescence intensity (FI) of C γ 5 signals in the longitudinal axis and FI of C γ 3 signals in the horizontal axis. (a) the subject #1 (a 46 year-old healthy man), (b) the subject #2 (a 28 year-old healthy man), and (c) the subject #4 (a 27 year-old woman with RRMS who was a dropout of IFN β treatment due to induction of frequent severe relapses).

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Additional File 3

The complete list of upregulated genes in PBMC following exposure to IFN β for 3 hours. Upregulated genes in PBMC of the subject #1 (a 46 year-old healthy man) by a 3 hour-exposure to 50 ng/ml recombinant human IFN β are listed with C γ 5/C γ 3 signal intensity ratio, gene symbol, GenBank accession number, and gene name. *In vivo* IRG in T cells and non-T cells of RRMS patients reported previously (Ref. 16) are underlined.

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Additional File 4

The complete list of downregulated genes in PBMC following exposure to IFN β for 3 hours. Downregulated genes in PBMC of the subject #1 (a 46 year-old healthy man) by a 3 hour-exposure to 50 ng/ml recombinant human IFN β are listed with C γ 5/C γ 3 signal intensity ratio, gene symbol, GenBank accession number, and gene name.

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Additional File 5

The complete list of upregulated genes in PBMC following exposure to IFN β for 24 hours. Upregulated genes in PBMC of the subject #1 (a 46 year-old healthy man) by a 24 hour-exposure to 50 ng/ml recombinant human IFN β are listed with C γ 5/C γ 3 signal intensity ratio, gene symbol, GenBank accession number, and gene name. *In vivo* IRG in T cells and non-T cells of RRMS patients reported previously (Ref. 16) are underlined.

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Additional File 6

The complete list of downregulated genes in PBMC following exposure to IFN β for 24 hours. Downregulated genes in PBMC of the subject #1 (a 46 year-old healthy man) by a 24 hour-exposure to 50 ng/ml recombinant human IFN β are listed with C γ 5/C γ 3 signal intensity ratio, gene symbol, GenBank accession number, and gene name.

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Additional File 7

Top 20 upregulated genes in PBMC following exposure to IFN β for 3 hours: two additional subjects. Upregulated genes in PBMC of the subject #2 (a 28 year-old healthy man) and #4 (a 27 year-old woman with RRMS who was a dropout of IFN β treatment due to induction of frequent severe relapses) following a 3 hour-exposure to 50 ng/ml recombinant human IFN β are listed with C γ 5/C γ 3 signal intensity ratio, gene symbol, and gene name. Both CXCR3 ligand (yellow) and CCR2 ligand (blue) chemokines are highlighted.

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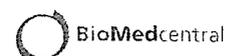
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Selective COX-2 inhibitor celecoxib prevents experimental autoimmune encephalomyelitis through COX-2-independent pathway

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Cyclooxygenase (COX) is a key enzyme of arachidonic acid metabolism and exists as two distinct isoforms. COX-1 is constitutively expressed in most tissues, whereas COX-2 is inducibly expressed at the site of inflammation. Selective inhibitors of COX-2 have been developed and have been used as anti-inflammatory agents. Here, we show that a new-generation COX-2 inhibitor, celecoxib, inhibited experimental autoimmune encephalomyelitis (EAE). Celecoxib, but not other COX-2 inhibitors such as nimesulid, prevented myelin oligodendrocyte glycoprotein (MOG) induced EAE when administrated orally on the day of disease induction. Moreover, celecoxib inhibited EAE in COX-2-deficient mice, indicating that celecoxib inhibited EAE in a COX-2-independent manner. In celecoxib-treated mice, interferon- γ (IFN- γ) production from MOG-specific T cells was reduced and MOG-specific IgG1 was elevated compared with vehicle-treated mice. Infiltration of inflammatory cells into the central nervous system and the expression of adhesion molecules, P-selectin and intercellular adhesion molecule-1 (ICAM-1), and a chemokine, monocyte chemoattractant peptide-1 (MCP-1), were inhibited when mice were treated with celecoxib. These results suggest that celecoxib may be useful as a new additional therapeutic agent for multiple sclerosis.

Keywords: COX-2 inhibitor; celecoxib; experimental autoimmune encephalomyelitis; multiple sclerosis

Abbreviations: CMC = carboxymethylcellulose; COX = cyclooxygenase; EAN = experimental autoimmune neuritis; EAE = experimental autoimmune encephalomyelitis; ELISA = enzyme-linked immunosorbent assay; ICAM-1 = intercellular adhesion molecule-1; IFN = interferon; IL = interleukin; LN = lymph node; MCP-1 = monocyte chemoattractant peptide-1; MOG = myelin oligodendrocyte glycoprotein; PBS = phosphate-buffered saline

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Introduction

Cyclooxygenase (COX) catalyses the conversion of arachidonic acid to prostaglandins and has two isoforms, COX-1 and COX-2 (Vane *et al.*, 1994; Warner and Mitchell, 2004). COX-1 is constitutively expressed in most tissues and produces prostaglandins involved in maintenance of the gastric mucosa, regulation of renal blood flow and platelet aggregation. On the other hand, COX-2 is inducibly expressed in cells involved in inflammation and in neoplastic tissues by proinflammatory and mitogenic stimuli, and is primarily responsible for the synthesis of prostanoids involved in acute and chronic inflammation (Xie *et al.*, 1997). COX-2

therefore appears to be a suitable target for the anti-inflammatory effects of non-steroidal anti-inflammatory drugs. These findings have provided the rationale for the development of selective inhibitors of COX-2.

Celecoxib is a new generation of highly specific COX-2 inhibitors that have been approved for the treatment of rheumatoid arthritis and other inflammatory diseases. The selectivity of COX-2 inhibition is much higher than traditional COX-2 inhibitors (Penning *et al.*, 1997). Furthermore, celecoxib has been shown to exert a potent anti-tumour effect. Interestingly, the anti-tumour effect by celecoxib

has been reported via both COX-2-dependent and COX-2-independent mechanisms (Grosch *et al.*, 2001). For example, cell cycle arrest and apoptosis of various kinds of cells induced by celecoxib appeared to be COX-2-independent effects (Hsu *et al.*, 2000; Arico *et al.*, 2002; Liu *et al.*, 2004).

Experimental autoimmune encephalomyelitis (EAE) is a widely used animal model for multiple sclerosis that can be induced by immunization with myelin antigens such as myelin oligodendrocyte glycoprotein (MOG). EAE is mediated primarily by CD4⁺ Th1 T cells producing interferon- γ (IFN- γ) and tumour necrosis factor- α (TNF- α) (Nicholson and Kuchroo, 1996; Kumar *et al.*, 1997; Zhang *et al.*, 1997). COX-2 is expressed in neurons and endothelial cells in healthy brain. In rats with EAE, the expression of COX-2 was reported to be upregulated in endothelial cells in inflammatory lesions. In addition, non-selective COX-2 inhibitors have been reported to moderately ameliorate EAE (Prosiegel *et al.*, 1989; Weber *et al.*, 1991; Simmons *et al.*, 1992), suggesting that COX-2 may have an important role in the pathogenesis of EAE (Deininger and Schluesener, 1999). Furthermore, we recently demonstrated that COX-2 inhibitors suppress experimental autoimmune neuritis (EAN), a model of Guillain-Barré syndrome, which is also characterized as a CD4⁺-Th1 T-cell-mediated autoimmune neurological disease model similar to EAE (Miyamoto *et al.*, 1998, 1999, 2002). These findings led us to investigate the effect of COX-2 inhibitors on EAE.

In the present study, we found that celecoxib greatly suppressed EAE in comparison with traditional COX-2 inhibitors. Furthermore, we have demonstrated that celecoxib inhibited EAE by inhibiting Th1 response of autoreactive T cells and that this inhibition was COX-2-independent. Finally, we demonstrated that celecoxib prevented cell entry into the CNS in association with the inhibition of the expression of P-selectin, intercellular adhesion molecule-1 (ICAM-1) and monocyte chemoattractant peptide-1 (MCP-1). These results highlighted the COX-2-independent therapeutic potential of celecoxib for multiple sclerosis.

Material and methods

Mouse

Wild-type C57BL/6 (B6) mice were purchased from Clea Japan (Tokyo, Japan). COX-2-deficient mice (COX-2^{-/-}) have been backcrossed to B6 background for more than five generations and were purchased from Tacom (Germantown, NY, USA). These mice were maintained under specific pathogen-free conditions.

Induction of EAE

For induction of EAE, mice were immunized (5–10 mice per group) subcutaneously in flanks with 100 μ g of MOG_{35–55} peptide (MEVGWYRSPFSRVVHLYRNGK) in 0.1 ml phosphate-buffered saline (PBS) and 0.1 ml complete Freund's adjuvant (CFA) containing 1 mg *Mycobacterium tuberculosis* H37Ra (Difco Laboratories, Detroit, MI, USA) and were injected intravenously with 200 ng

of pertussis toxin (List Biological Laboratories, Campbell, CA, USA) on the day of immunization and 2 days later.

Clinical assessment of EAE

EAE was scored on the following scale: 0 = no clinical signs; 1 = partial loss of tail tonicity; 2 = completely limp tail and abnormal gait; 3 = partial hindlimb paralysis; 4 = complete hindlimb paralysis; and 5 = fore- and hindlimb paralysis or moribund state.

Treatment with COX-2 inhibitors

Mice were orally administered 5 μ g/g of COX-2 inhibitor, celecoxib (Searle, St Louis, MO, USA) (Penning *et al.*, 1997), nimesulid (Nakarai Tesque, Kyoto, Japan) (Nakatsuji *et al.*, 1996), or indomethacin (Nakarai Tesque) in 0.5% carboxymethylcellulose (CMC) via a feeding cannula every 2 days. Control mice were orally administered vehicle (0.5% CMC) alone.

Measurement of MOG_{35–55}-specific IgG1 and IgG2a titres

Enzyme-linked immunosorbent assay (ELISA) plates (Sumitomo, Tokyo, Japan) were coated with 10 μ g/ml MOG_{35–55} in PBS overnight at 4 °C. After blocking with 2% bovine serum albumin (BSA) in PBS, different dilutions of the serum from animals at Day 30 after immunization, or normal mice or PBS were added to the plate. MOG_{35–55}-specific antibodies were detected using biotin-labelled anti-IgG1 and anti-IgG2a antibodies (Vector Laboratories, Burlingame, CA, USA). After adding streptavidin-peroxidase (BD Biosciences, San Jose, CA, USA) and a substrate, plates were read at OD₄₅₀ values.

MOG_{35–55}-specific T-cell proliferation assay

On Day 11 after immunization with MOG_{35–55}, draining lymph nodes (LN) were harvested and single cell suspensions were prepared. Cells were cultured in RPMI1640 medium (Gibco, Grand Island, NY, USA) supplemented with 5 \times 10⁻⁵ M 2-mercaptoethanol, 2 mM L-glutamine, 100 U/ml penicillin and streptomycin and 1% autologous mouse serum, and seeded onto 96-well flat-bottom plates (1 \times 10⁶ cells/well). The cells were stimulated with peptide for 72 h at 37 °C in a humidified air condition with 5% CO₂. To measure cellular proliferation, [³H]-thymidine was added (1 μ Ci/well) and uptake of the radioisotope during the final 18 h of culture was counted with a beta-1205 counter (Pharmacia, Uppsala, Sweden). To evaluate proliferative responses of LN cells to peptide, we determined the Δ c.p.m. value for cells in each well by subtracting the background c.p.m.

Detection of cytokines and chemokine

LN cells from the MOG_{35–55}-immunized mice were cultured in the standard medium in 96-well flat-bottom plates at 1 \times 10⁶/well for 48 h in the presence of the different concentrations of MOG_{35–55}. The concentrations of IFN- γ , interleukin-4 (IL-4) and IL-10 in the supernatants were measured by using a sandwich ELISA following the protocol provided by BD Biosciences. A chemokine, MCP-1, in the serum from mice on Day 7, 10 and 14 after induction of EAE was also measured by using a sandwich ELISA following the protocol provided by BD Biosciences. All reagents, including recombinant mouse cytokines, chemokine and antibodies were purchased from BD Biosciences.

Analysis of infiltrating cells isolated from CNS

Mice were anaesthetized with diethyl ether on Day 14 after induction of EAE. After perfusion with PBS, brain and spinal cord were removed and homogenized. After washing with PBS, mononuclear cells were isolated using Ficoll gradient (Amersham Biosciences, Piscataway, NJ, USA) (Krakowski *et al.*, 1997). The cells were stained with APC-labelled anti-CD3 antibody, fluorescein isothiocyanate (FITC) labelled anti-CD4 or CD8 or CD19 antibody (BD Biosciences) and were analysed by flow cytometer (BD FACS Calibur). Apoptosis of lymphocytes was analysed by using Annexin-5 apoptosis kit (BD Biosciences).

Pathological analysis

The brain and spinal cord were removed on Day 7, 10 and 14 after induction of EAE. Ten-micrometre frozen sections were fixed with acetone and stained with haematoxylin and eosin (HE), Luxol fast blue or antibodies of adhesion molecule ICAM-1 (CD54), vascular cell adhesion molecule-1 (VCAM-1: CD106), E-selectin (CD62E) and P-selectin (CD62P) (BD Biosciences), following the protocol provided by BD Biosciences.

Statistics

For statistic analysis, non-parametric Mann–Whitney *U*-test was used to calculate significant levels for all measurements. Values of $P < 0.05$ were considered statistically significant.

Results

Celecoxib inhibits EAE

To examine the effect of celecoxib on the development of EAE, we first administered celecoxib at the time of immunization with MOG_{35–55}. Oral administration of celecoxib reduced the incidence of disease and suppressed maximum EAE score and cumulative score compared with the control group (Fig. 1A, Table 1). Histological comparison between the thoracic region of the spinal cord demonstrated reduced monocyte infiltration and demyelination in celecoxib-treated mice compared with vehicle-treated mice (Fig. 2A–D). Celecoxib was also effective in reducing the severity of disease when administered at Day 8

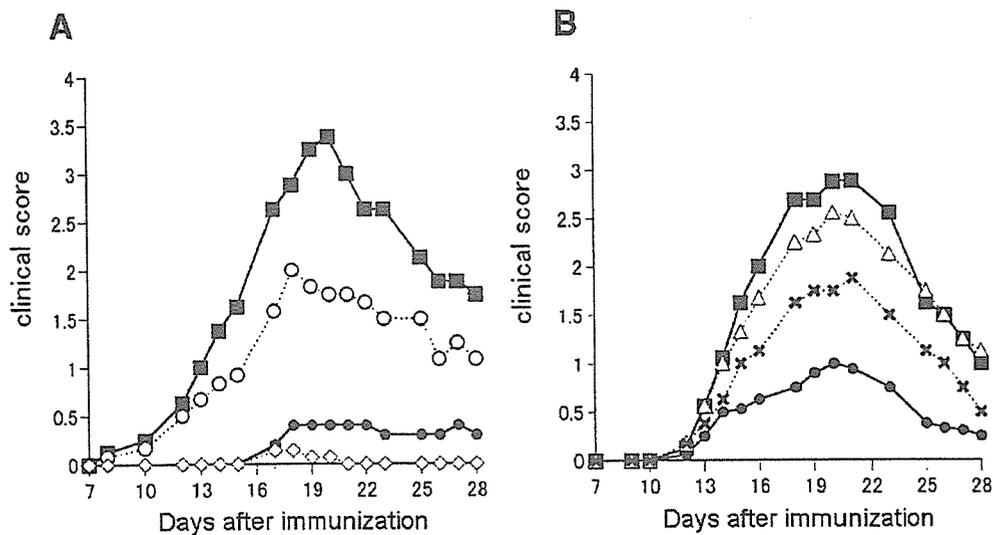


Fig. 1 Effect of celecoxib on actively induced EAE. EAE was induced in female B6 mice by immunization with MOG_{35–55} in CFA as described in Material and methods. (A) Mice were orally administered 5 µg/g (closed circles) or 10 µg/g (open diamond) of celecoxib starting from the day of the immunization, or with 5 µg/g of celecoxib starting from 8 days after the immunization (open circles). Control mice were administered vehicle alone (closed squares). Statistical analysis is shown in Table 1. (B) Mice were orally administered 5 µg/g of celecoxib (closed circles) or nimesulid (open triangle) or indomethacin (crosses) every 2 days from the day of EAE induction. Control mice were administered vehicle alone (closed squares). Statistical analysis is shown in Table 2. One representative experiment of two independent experiments is expressed as mean \pm SEM.

Table 1 Clinical scores of EAE treated with celecoxib

	Max. score	Day of onset	Incidence (%)	Cumulative score
Control (CMC)	3.50 \pm 0.20	12.50 \pm 1.56	100 (10/10)	33.00 \pm 5.05
Celecoxib 10 µg/g	0.14 \pm 0.05*	17.50 \pm 0.50	20.0 (2/10)	0.42 \pm 0.04*
Celecoxib 5 µg/g	0.40 \pm 0.40*	17.00 \pm 0.00	20.0 (2/10)	3.80 \pm 3.80*
Celecoxib 5 µg/g (from Day 8)	2.42 \pm 0.57	14.20 \pm 1.83	83.3 (10/12)	20.17 \pm 5.22

Four groups of mice were immunized with MOG_{35–55} peptide for induction of EAE. The control CMC solution, 5 or 10 µg/g of celecoxib diluted in CMC, was orally injected via a cannula every 2 days starting from Day 0 or 8 after induction of EAE. Mean \pm SEM of the following parameters are shown: maximum score of EAE (Max. score), the days of EAE onset, incidence of paralysed mice among sensitized mice (Incidence) and summation of the clinical scores from Day 0 to 30 (Cumulative score). * $P < 0.05$ versus control.

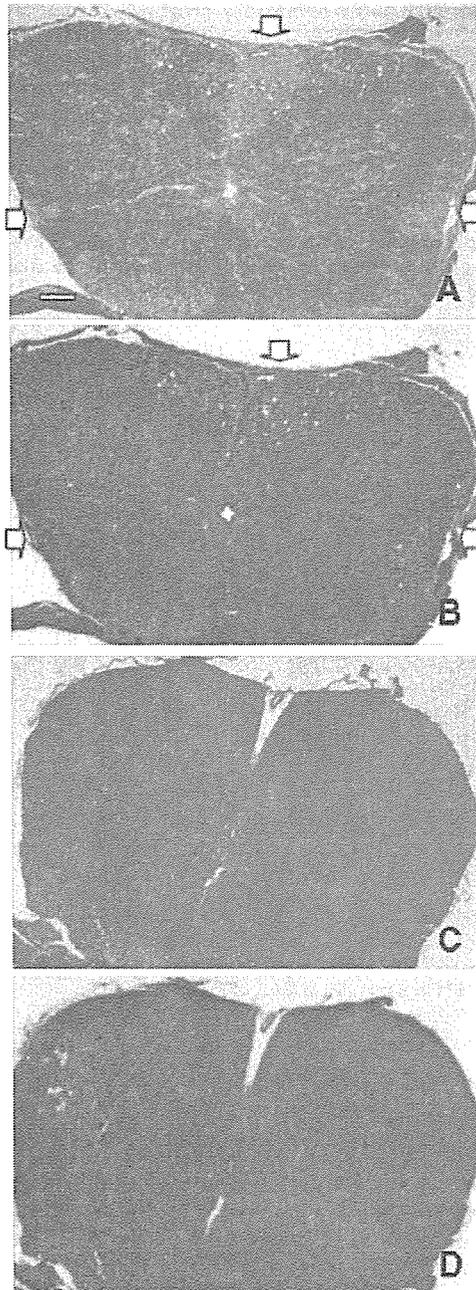


Fig. 2 Histopathological assessment of the CNS region in EAE-induced mice. Brains and spinal cords from EAE mice were removed on Day 14 after immunization as described in Material and methods. Thinly sliced (10 μ m) frozen sections of the brains obtained from vehicle-treated mice (**A** and **B**) or celecoxib-treated mice (**C** and **D**) were stained with haematoxylin and eosin (**B** and **D**), or Luxol fast blue (**A** and **C**).

post-EAE-induction. Although indomethacin suppressed EAE to some extent, all mice died around Day 30 after immunization owing to intestinal ulcer. In contrast, oral administration of nimesulid, another COX-2 inhibitor, did

not suppress either the incidence or the severity of EAE (Fig. 1B). Composite data from experiments is shown in Tables 1 and 2.

Celecoxib inhibits MOG-specific Th1 response

To determine the mechanisms by which celecoxib inhibits EAE, we examined the level of MOG-specific IgG1 and IgG2a in the serum samples collected from individual EAE-induced mice on Day 30. It is generally accepted that elevation of antigen-specific IgG2a antibody results from augmentation of a Th1 immune response to the antigen, whereas a higher level of IgG1 antibody would reflect a stronger Th2 response to the antigen. There was a significant elevation of the level of MOG_{35–55}-specific IgG1 and a slight reduction in the level of MOG-specific IgG2a in celecoxib-treated group compared with vehicle-treated group (Fig. 3A). In contrast, there was no significant difference in the level of either IgG1 or IgG2a in nimesulid-treated mice compared with vehicle-treated group (Fig. 3B).

To further investigate the response of T cells to MOG_{35–55} in celecoxib-treated mice, we examined the proliferative response and cytokine production of draining LN cells *in vitro*. Mice were immunized with MOG_{35–55} and were administered celecoxib or vehicle on the day of immunization. Ten days after immunization, draining LN cells were collected and cultured with MOG_{35–55} peptide. As shown in Fig. 4A, there was no significant difference in a proliferative response of MOG-reactive T cells between celecoxib-treated and vehicle-treated groups. We next examined the levels of cytokines in the culture supernatant by ELISA. The level of IFN- γ was reduced in the culture supernatants of LN cells obtained from mice treated with celecoxib compared with that from control mice (Fig. 4B). IL-4 and IL-10 were not detected in either culture supernatant. These results indicate that celecoxib reduces Th1 cytokine production from MOG-reactive T cells.

Celecoxib prevents EAE even in COX-2-deficient mice

Since another COX-2 inhibitor, nimesulid, did not have the inhibitory effect on EAE, we examined whether celecoxib could inhibit EAE in COX-2-deficient mice. As shown in Fig. 5A, the maximum EAE score, the day of onset and the severity of EAE were not significantly different between COX-2^{-/-} and wild-type mice. Administration of celecoxib prevented the development of EAE in COX-2^{-/-} mice as well as in wild-type mice. Consistent with the severity of EAE, the levels of MOG-specific IgG1 and IgG2a in COX-2^{-/-} mice were not different compared with wild-type B6 mice (Fig. 5B). Moreover, celecoxib treatment increased the level of MOG-specific IgG1 even in COX-2^{-/-} mice, resulting in the elevation of IgG1 : IgG2a ratio similar to that in wild-type mice (CMC = 0.29, celecoxib = 3.00) and COX-2^{-/-} mice (CMC = 0.42, celecoxib = 2.52). These results indicate that the effect on the inhibition of EAE

Table 2 Clinical scores of EAE treated with celecoxib or other non-steroidal anti-inflammatory drugs

	Max. score	Day of onset	Incidence (%)	Cumulative score	Death (%)
Control (CMC)	3.05 ± 0.20	13.10 ± 1.16	100 (10/10)	26.47 ± 5.13	10 (1/10)
Celecoxib	1.02 ± 0.53*	14.30 ± 1.77	90 (9/10)	7.58 ± 6.72*	0 (0/10)
Nimesulid	2.54 ± 0.68	13.50 ± 1.56	100 (10/10)	22.15 ± 4.75	0 (0/10)
Indomethacin	1.70 ± 0.83	13.90 ± 1.93	100 (10/10)	15.21 ± 3.89	100 (10/10)*

Each mouse was immunized with MOG_{35–55} peptide for induction of EAE. The control CMC solution, or 5 µg/g of drugs diluted in CMC, was orally administered via a cannula every other day. Mean ± SEM of the following parameters are shown: maximum score of EAE (Max. score), the days of EAE onset, incidence of paralysed mice among sensitized rats (Incidence), summation of the clinical scores from Day 0 to 30 (Cumulative score) and the incidence of death during EAE (Death). **P* < 0.05 versus control.

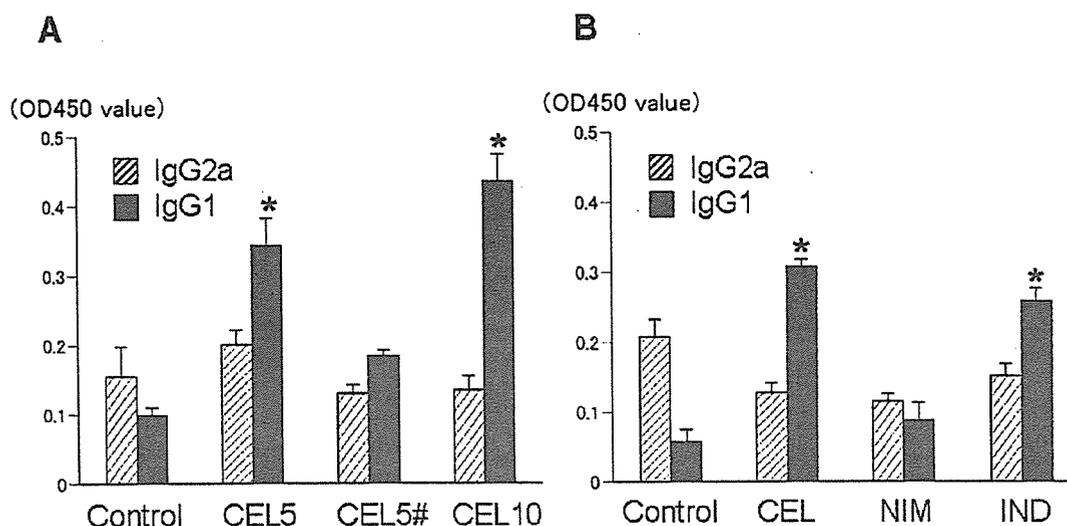


Fig. 3 Analysis of MOG_{35–55} IgG1 and IgG2a in EAE-induced mice. The relative titers of anti-MOG IgG1 and IgG2a in serum samples from individual mice (*n* = 10) on Day 30 after immunization were analysed as indicated in Methods. Data represent mean ± SEM. **P* < 0.05 versus control. (a) Control = vehicle alone, CEL5 = 5 µg/g of celecoxib, CEL5# = 5 µg/g of celecoxib from Day 8 after the immunization, CEL10 = 10 µg/g of celecoxib. (b) Control = vehicle alone, CEL = celecoxib, NIM = nimesulid, IND = indomethacin.

and Th1 response by celecoxib is mediated by a COX-2-independent pathway (Table 3)

Celecoxib inhibits an infiltration of immune cells into CNS

To characterize the infiltrated cells into CNS, we isolated mononuclear cells from CNS obtained from celecoxib-treated or vehicle-treated mice. Mononuclear cells isolated from the CNS of vehicle-treated mice include CD3⁺ T cells that comprised >80% of CD4⁺ cells. In mice treated with celecoxib, the number of infiltrated cells was less than one-seventh compared with vehicle-treated mice (Table 4). In addition, we analysed apoptotic cells from CNS, spleen and draining LNs using annexin-5 staining. There was no difference in the frequency of apoptotic cells in all organs examined from celecoxib-treated and vehicle-treated mice (data not shown). These results suggest that celecoxib inhibits an infiltration of inflammatory cells into the CNS rather than induction of apoptosis of autoreactive T cells.

Celecoxib suppresses the expression of adhesion molecules and a chemokine related to cell infiltration into CNS

For the recruitment of autoreactive T cells into the brain through the blood–brain barrier (BBB), some adhesion molecules such as ICAM-1, VCAM-1 and P-selectin, and chemokines such as MCP-1 are required (Engelhardt *et al.*, 1997; Hofmann *et al.*, 2002). We performed an immunohistostaining of sliced brain sections from mice with EAE using antibodies against adhesion molecules. ICAM-1, VCAM-1 and P-selectin (Fig. 6A, C and E) were expressed on choroid plexus in the brain obtained from EAE-induced mice. In contrast, in brains obtained from celecoxib-treated mice, the expression level of P-selectin and ICAM-1 was lower compared with the control (Fig. 6B, D and F). In addition, we examined the level of MCP-1, which is an important chemokine involved in recruiting autoreactive T cells into the brain. As shown in Table 5, the level of MCP-1 in the serum obtained from

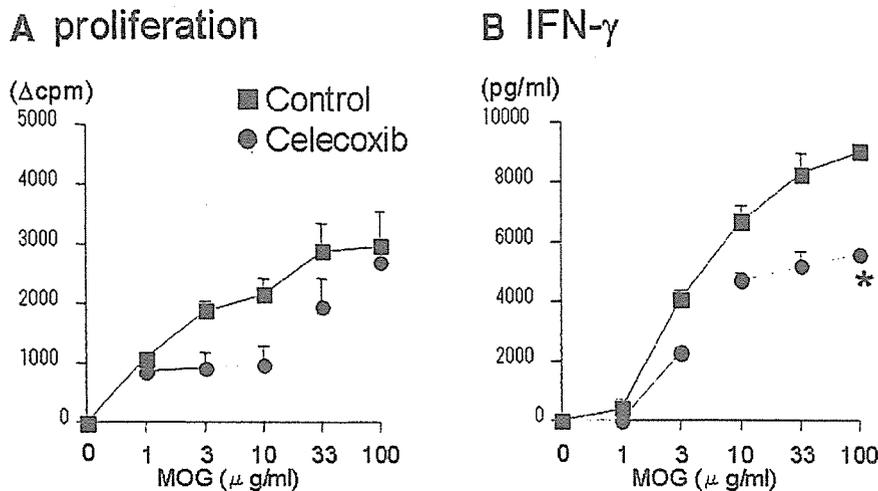


Fig. 4 Comparison of MOG_{35–55}-specific T-cell response after treatment with celecoxib. Popliteal and inguinal LN cells from treated and control animals were incubated in the presence of MOG_{35–55} for 48 h. Proliferative response was determined by the uptake of [³H] thymidine (A), and IFN- γ was detected by ELISA (B). Representative data of two independent experiments are shown ($n = 5$ for each group). Error bars represent SEM. * $P < 0.05$ versus control.

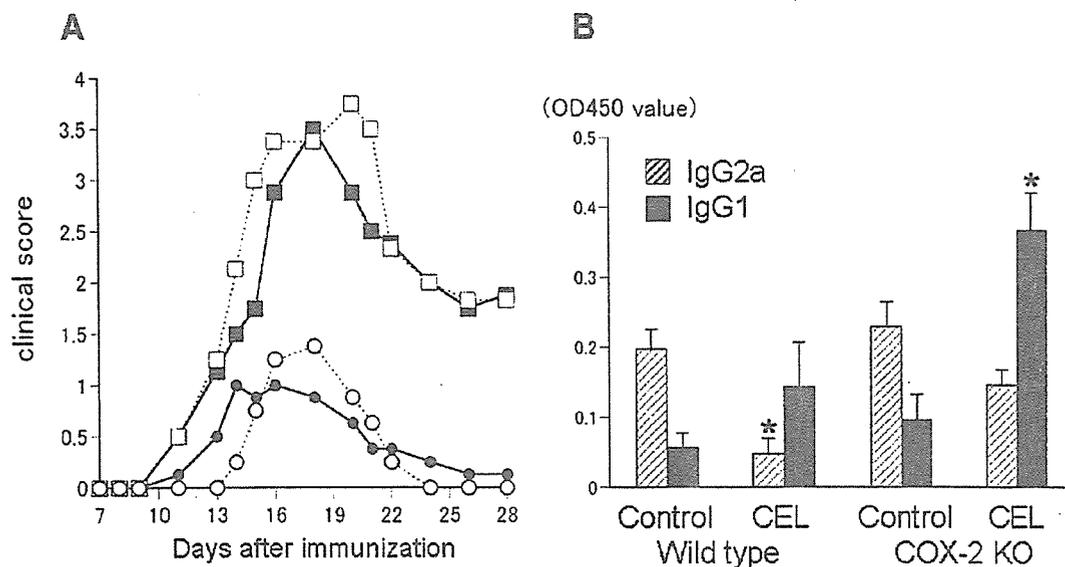


Fig. 5 Effect of celecoxib on actively induced EAE in COX-2-deficient mice. B6 mice and COX-2-deficient mice were immunized with MOG_{35–55} in CFA as described in Material and methods. (A) Mice were orally administered celecoxib (5 μ g/g) every 2 days starting from the day of the immunization. Statistical analysis is shown in Table 3. Closed squares = vehicle alone for wild-type mice; closed circles = 5 μ g/g of celecoxib for wild-type mice; open squares = vehicle alone for COX-2-deficient mice; open circles = 5 μ g/g of celecoxib for COX-2-deficient mice. (B) The relative titres of anti-MOG IgG1 and IgG2a in serum samples from individual mice on Day 30 after immunization were analysed as indicated in Material and methods. Data represent mean \pm SEM. * $P < 0.05$ versus control. Control = vehicle alone, CEL = celecoxib. One representative experiment of two independent experiments is expressed as mean \pm SEM.

celecoxib-treated mice was significantly lower compared with that obtained from vehicle-treated mice. These findings suggested that celecoxib inhibits an infiltration of immune-mediated cells into CNS through the BBB by suppression of P-selectin, ICAM-1 and MCP-1.

Discussion

In the present study, we have demonstrated that a new-generation selective COX-2 inhibitor, celecoxib, strongly inhibited the development of EAE as compared with vehicle treatment or a traditional COX-2 inhibitor, nimesulid. The

Table 3 Clinical scores of EAE in COX-2-deficient mice

Mouse	Treatment	Max. score	Day of onset	Incidence (%)	Cumulative score
Wild-type	CMC	3.54 ± 0.28	12.60 ± 1.15	100 (10/10)	24.85 ± 6.37
	Celecoxib	1.13 ± 0.39*	13.20 ± 1.80	80 (8/10)	6.29 ± 4.02*
COX-2 ^{-/-}	CMC	3.75 ± 0.44	12.78 ± 1.57	100 (8/8)	29.88 ± 5.62
	Celecoxib	1.46 ± 0.51*	14.13 ± 1.96	87.5 (7/8)	5.39 ± 3.36*

Wild-type and COX-2^{-/-} mice were immunized with MOG_{35–55} peptide to induce EAE. The control CMC solution, or 5 µg/g of celecoxib diluted in CMC, was administered every other day. Mean ± SEM of the following parameters are shown: maximum score of EAE (Max. score), the days of EAE onset, incidence of paralysed mice among sensitized mice (Incidence) and summation of the clinical scores from Day 0 to 30 (Cumulative score). **P* < 0.05 versus control.

Table 4 Cell infiltration into the CNS of EAE-induced mice

	Mononuclear cell	CD3 ⁺ cell	CD4 ⁺ cell	CD19 ⁺ cell
EAE mice				
Control (CMC)	667 ± 176	203 ± 69	158 ± 50	6 ± 1
Celecoxib	90 ± 57*	12 ± 8*	9 ± 5*	0 ± 0
Naive mice	20 ± 6	5 ± 2	3 ± 2	1 ± 0

CNS tissues from each group mouse were homogenized on Day 18 after immunization with MOG_{35–55} peptide. Mononuclear cells were isolated by Percoll solution. The cells were stained with cell markers and analysed by flow cytometer. Mean ± SEM of cell number (10³ cells/mouse) is shown. Representative data of two independent experiments are shown (*n* = 5 for each group). **P* < 0.05 versus control.

inhibitory effect on EAE by celecoxib was also evident in COX-2-deficient mice, indicating that celecoxib suppressed EAE in a COX-2-independent mechanism. In celecoxib-treated mice, MOG-specific Th1 responses were reduced and infiltration of immune cells was significantly inhibited compared with vehicle-treated mice, which were associated with lower expression of ICAM-1 and P-selectin on the choroid plexus in the brain.

Since EAE is an autoimmune inflammatory disease, administering COX-2 inhibitor was expected to inhibit disease as well as other COX inhibitors. Recently, Muthian *et al.* (2006) showed that some COX-2 inhibitors such as NS398 and LM01 suppressed EAE, when administered intraperitoneally every other day. In our study, we could not observe the inhibitory effect of nimesulid on EAE when orally administered every 2 days using the same conditions in which celecoxib exhibited a strong inhibitory effect. The route and timing of administration might be critical to modulate diseases. The inhibitory effect mediated by celecoxib was stronger compared with other COX inhibitors, suggesting that different mechanisms may be occurring in addition to the suppression of production of prostanoids that occurred at sites of disease and inflammation. In fact, COX-2 was not required for the celecoxib-mediated inhibitory effect on EAE. Recent studies have suggested that COX-2-independent pathways may contribute to celecoxib-mediated anti-tumour or anti-arthritis effect through enhanced apoptosis of tumour cells or synovial cells (Kusunoki *et al.*, 2002;

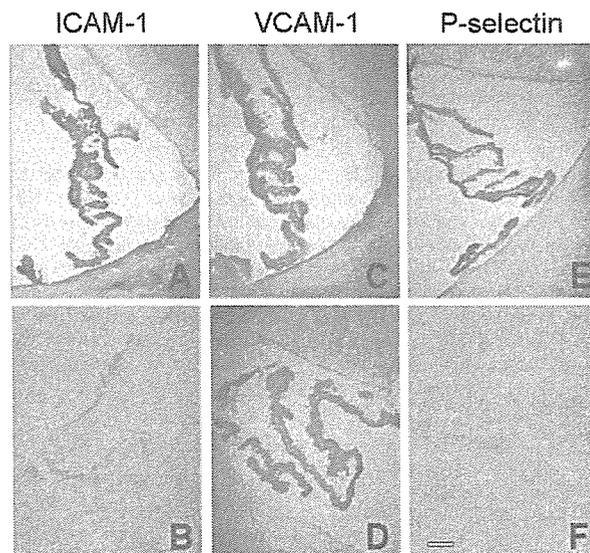


Fig. 6 Immunohistochemical staining with ICAM-1, VCAM-1 and P-selectin of the brain in EAE-induced mice. Brains from EAE mice were removed on Day 14 after immunization as described in Material and methods. Thinly sliced (10 µm) frozen sections of the brain were immunostained with anti-ICAM-1 antibody (A and B), anti-VCAM-1 antibody (C and D) and anti-P-selectin antibody (E and F). Figure shows choroid plexus region. Bar = 100 µm.

Shishodia *et al.*, 2004). In our study, enhancing apoptosis of immune cells was not detected, indicating that different COX-2-independent mechanisms might be important for celecoxib-mediated inhibition of EAE. We observed that celecoxib treatment inhibited Th1 responses of MOG-reactive T cells. In the regulation of Th1/Th2 responses, prostaglandin E2 synthesized by COX has been reported to suppress IL-2 and IFN-γ production by a Th1 clone (Snijdwint *et al.*, 1993). In addition, Meyer *et al.* (2003) reported that administration of COX-2 inhibitor, NS398, increased *Helicobacter*-stimulated IL-12 and IFN-γ production, suggesting that COX-2 inhibition resulted in enhanced Th1 responses. In contrast, celecoxib inhibited Th1 responses of autoreactive T cells. Therefore, this COX-2-independent effect on immune system may be a mechanism to explain why celecoxib suppresses EAE to a greater degree compared with that of other COX-2 inhibitors. Allonza *et al.* (2006) reported that

Table 5 Serum level of MCP-1 in EAE mice after treatment with celecoxib

	Day 0	Day 7	Day 10	Day 14
EAE mice				
Control (CMC) (n = 18)	ND	60.0 ± 21.0	42.6 ± 17.0	ND
Celecoxib (n = 16)	ND	8.5 ± 5.0*	12.9 ± 8.5	ND
Naive mice (n = 10)	ND	ND	ND	ND

B6 mice were immunized with MOG_{35–55} peptide as described in Material and methods. Serum samples from individual mice were collected on Day 0, 7, 10 and 14 after immunization. Serum concentration of MCP-1 was measured by ELISA. Data represent mean ± SEM (pg/ml). ND = not detectable. *P < 0.05 versus control.

celecoxib inhibits IL-12 $\alpha\beta$ and $\beta 2$ folding and secretion in association with the increased interaction of IL-12 with calreticulin, an endoplasmic reticulum-resident chaperone in retention of misfolded cargo proteins, while blocking interaction with Erp44. They also demonstrated that an analogue of celecoxib lacking the COX-2 inhibitor activity showed identical effects to that of celecoxib on folding and secretion of IL-12, indicating that the effect is COX-2-independent. Since IL-12 is a key cytokine to provoke Th1 immune response, reduction in MOG-specific Th1 response is consistent with these previous findings.

The infiltration of immune cells in the CNS was significantly inhibited in celecoxib-treated mice. Celecoxib has been reported to reduce expression of P-selectin and ICAM-1 in experimental inflammatory models such as experimental colitis (Cuzzocrea *et al.*, 2001, 2002). In our study, we observed that celecoxib suppressed expression of P-selectin and ICAM-1 in the brain of EAE mice. Since P-selectin and ICAM-1 are the adhesion molecules involved in the recruitment of inflammatory cells into CNS (Engelhardt *et al.*, 1997; Dietrich, 2002; Scott *et al.*, 2004), inhibition of cellular infiltration by celecoxib might be mediated by the downregulation of the expression of adhesion molecules.

Chemokines are also required for recruitment of immune cells into the CNS. MCP-1 is reported to be an essential chemokine in EAE (Hofmann *et al.*, 2002). In the mouse model of atherosclerosis, Wang *et al.* (2005) reported that celecoxib decreased the inflammatory response and hyperplasia following vascular injury through inhibition of MCP-1 induction. We detected a decreased level of MCP-1 in the serum in celecoxib-treated mice on EAE. The suppression of MCP-1 by celecoxib might also contribute to the reduction of infiltrating cells into the CNS.

In conclusion, celecoxib has a potent therapeutic potential for EAE by inducing a Th2 bias and suppressing infiltration of inflammatory cells into the CNS through a COX-2-independent mechanism. Further analysis of celecoxib-mediated suppression of EAE will help drug development for multiple sclerosis. Celecoxib is hoped to be a new choice of the treatment of multiple sclerosis.

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