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Elevation of Sema4A Implicates Th Cell Skewing and the Efficacy of IFN-β Therapy in Multiple Sclerosis

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Multiple sclerosis (MS) is a demyelinating autoimmune disease of the CNS and a leading cause of lasting neurologic disabilities in young adults. Although the precise mechanism remains incompletely understood, Ag presentation and subsequent myelin-reactive CD4+ T cell activation/differentiation are essential for the pathogenesis of MS. Although semaphorins were originally identified as axon guidance cues during neural development, several semaphorins are crucially involved in various phases of immune responses. Sema4A is one of the membrane-type class IV semaphorins, which we originally identified from the cDNA library of dendritic cell (DC). Sema4A plays critical roles in T cell activation and Th1 differentiation during the course of experimental autoimmune encephalomyelitis, an animal model of MS; however, its pathological involvement in human MS has not been determined. In this study, we report that Sema4A is increased in the sera of patients with MS. The expression of Sema4A is increased on DCs in MS patients and shed from these cells in a metalloproteinase-dependent manner. DC-derived Sema4A is not determined. In this study, we report that Sema4A is increased in the sera of patients with MS. The expression of Sema4A is increased on DCs in MS patients and shed from these cells in a metalloproteinase-dependent manner. DC-derived Sema4A is not only critical for Th1 but also for Th17 cell differentiation, and MS patients with high Sema4A levels exhibit Th17 skewing. Furthermore, patients with high Sema4A levels have more severe disabilities and are unresponsive to IFN-β treatment. Taken together, our results suggest that Sema4A is involved in the pathogenesis of MS by promoting Th17 skewing. The Journal of Immunology, 2012, 188: 000–000.

Although semaphorins were originally identified as axon guidance molecules during neural development, they are currently known to have diverse and important functions in other physiological processes (11), including heart morphogenesis (12), vascular growth (13), tumor progression (14, 15), and immune cell regulation (16, 17). Some semaphorins are crucially involved in immune responses, including Th differentiation (18, 19). Sema4A is a membrane-type class IV semaphorin that we originally identified using a dendritic cell (DC) cDNA library. We previously reported that Sema4A plays critical roles in T cell activation and Th1 differentiation (18, 19). Indeed, the development of myelin oligodendrocyte glycoprotein (MOG)-induced experimental autoimmune encephalomyelitis (EAE) in wild-type mice can be improved.
Supplemental Table I. The 59 MS patients were diagnosed according to diseases (OND). The OND patients had various diseases as shown in clinically isolated syndrome (CIS), and 126 patients with other neurologic Ficoll-Paque (GE Healthcare). Human CD14+ monocytes and CD4+ T cells were separated by density gradient centrifugation using GM-CSF (R&D Systems) as previously described (26). THP-1 monocytes and Jurkat cells were grown in RPMI 1640 medium supplemented with 10% FCS and 50 μM 2-mercaptoethanol (2-ME). Human PBMCs were separated from healthy mononuclear inflammatory cells into the spinal cord by intravenously injecting an anti-Sema4A mAb concurrently with MOG immunization (18). To isolate the PBMCs of healthy controls using a MACS sorting kit (Miltenyi Biotech) and then cultured in RPMI 1640 medium (Life Technologies) supplemented with 10% FCS (Life Technologies) and 50 μM 2-mercaptoethanol (2-ME). Mouse bone marrow-derived dendritic cells (BMDCs) were generated from bone marrow progenitors from wild-type or Sema4A-deficient mice, using GM-CSF (R&D Systems) as previously described (19). For the in vitro differentiation of monocyte helper T cells with BMDCs, CD62L high CD4+ naive T cells were prepared from OT-II TCR transgenic mice and purified by FACS sorting as previously described (19). CD62L high CD4+ naive T cells were cultured with wild-type or Sema4A-deficient BMDCs in the presence of IL-12 (1 ng/ml) and anti–IL-4 (10 ng/ml) (Th1-skewing conditions), in the presence of IL-4 (1 ng/ml) and anti–IFN-γ (10 ng/ml) (Th2-skewing conditions) or in the presence of IL-6 (20 ng/ml), TGF-β (5 ng/ml), anti–IL-4 (10 μg/ml), and anti–IFN-γ (10 μg/ml) (Th17-skewing conditions) with OT-II peptides (1 μM/ml; Sigma Genosys) for 5 d. The resulting CD4+ T cells were positively selected using a MACS sorting kit and restimulated with immobilized anti–CD3 Ab (2C11; 1 or 5 μg/ml) for 24 h in 96-well plates (1 × 10^5/ml). The IFN-γ, IL-4, and IL-17A levels were measured using mouse IFN-γ, IL-4, and IL-17A ELISA kits (R&D Systems), respectively.

FACS analysis

For FACS analysis of Sema4A expression, the cells were stained with the following Abs: anti-Sema4A (5E3; MBL), anti-CD4, anti-CD8, anti-CD19, anti-CD14, anti-CD11c, and anti–HLA-DR conjugated with FITC, PE, or biotin (BD Pharmingen) in the presence of normal human serum (for human cells). Streptavidin–allophycocyanin (BD Pharmingen) was used as a second-step reagent for biotinylated Abs. The cells were washed and analyzed using a FACS Canto-2 and Diva software (Becton Dickinson).

Postacquisition analysis was performed using FlowJo software.

For intracellular cytokine analysis, an equal amount of RPMI 1640 supplemented with 10% FCS was added to whole blood samples and then incubated with 5 ng/ml PMA (Sigma), 0.5 μg/ml ionomycin (Sigma), and 10 μg/ml brefeldin A (Sigma) in a 24-well plate for 4 h at 37°C under 5% CO2. After washing with PBS containing 0.1% BSA (1% BSA–PBS), the cells were stained with a PerCP- or PE-conjugated anti-CD4 mAb (Becton Dickinson) and incubated on ice in the dark for 15 min. After lysing the red cells with FACS lysing solutions (Becton Dickinson), a FACS permeabilization solution (Becton Dickinson) was added, and the cells were then incubated for 10 min in the dark. After two washes with 1% BSA–PBS, the cells were stained with FITC-conjugated anti–IFN-γ mAb (Becton Dickinson), PE-conjugated anti–IL-4 (Becton Dickinson), and Alexa Fluor 647-conjugated anti–IL-17A (eBioscience) Abs for intracellular cytokine analyses. After a 30-min incubation on ice in the dark, the percentages of IFN-γ, IL-4, and IL-17-producing cells were immediately analyzed by flow cytometry using a Canto II (Becton Dickinson). The analysis gates were first set on lymphocytes based on the forward- and side-scatter properties and then on CD4+ lymphocytes. Postacquisition analysis was performed using FlowJo software.

Cell surface labeling

Cells were washed with PBS and labeled with 1 ml of PBS containing 50 μg of n-biotinyl-e-aminoacapric acid-N-hydroxysuccinimide ester (Roche) for 15 min. The reaction was stopped by adding 50 μl of 1 mol/l NHCl for 15 min, and then cells were washed with ice-cold PBS. For the shedding experiments, biotinylated cells (5 × 10^5) were resuspended at a cell density of 10^5/ml in G1T medium (Wako) and then incubated at 37°C for various time periods. When indicated, the reagents were added at the start of the incubation period. At the end of the incubation period, the cell suspensions were centrifuged, and the supernatants were collected. The cell pellets were washed with ice-cold PBS and solubilized in a 1% Nonidet P-40 detergent buffer containing 10 mmol/l Tris (pH 7.8), 150 mm NaCl, 10 mmol/l aprotinin, 1 mmol/l PMSF, and 5 μg/ml leupeptin for 1 h on ice. After centrifuging to remove the cellular debris, the lysates were subjected to immunoprecipitation analyses.

Immunoprecipitation and Western blot analyses

To measure Sema4A shedding, culture supernatants and lysates from 2 × 10^5 biotin-labeled cells were probed with protein G Sepharose (Protein G Sepharose 4 Fast Flow; GE Healthcare) and then immunoprecipitated with 2.5 μg of the Sema4A mAb 5E3 (MBL) and protein G Sepharose. Immune complexes were eluted by boiling the samples for 5 min in 0.1% sodium dodecyl sulfate (SDS) buffer.
Laemmli buffer [125 mM Tris-HCl (pH 6.8), 4% SDS, 20% glycerol, and 0.025% bromophenol blue] supplemented with or without 10% 2-ME. The solubilized proteins were separated by SDS-PAGE and electro-transferred onto polyvinylidene difluoride membranes. The blots were incubated with streptavidin–POD (Roche) for 1 h and then visualized by ECL reagents (GE Healthcare). In some experiments, the blots were incubated with an anti-Sema4A rabbit antiserum overnight at 4˚C, followed by the secondary Ab for 1 h, and then visualized with ECL.

Gene expression profiling of human blood samples

Total cellular RNA from the peripheral blood of four healthy controls, three MS patients with high Sema4A levels, and three MS patients with low Sema4A levels was extracted with a QIAamp RNA blood Mini Kit (Qiagen) according to the manufacturer’s instructions. Approximately 10 μg of RNA was labeled and hybridized to GeneChip Human Genome U133 Plus 2.0 Arrays (Affymetrix) according to the manufacturer’s protocols. Expression values were determined using GeneChip Operating Software v1.1.1 and the MAS5 method. All data analysis was performed using GeneSpring software GX 11.0.1 (Agilent Technologies). Clustering analysis was performed using Cluster 3.0 (developed based on Eisen Lab’s Cluster and Tree View software). The normalized expression values for each gene were calculated and displayed in a heat map, with the gene expression colorimetrically represented from green to red, with green and red denoting low and high expression genes, respectively.

Induction of EAE

EAE was induced in 6- to 8-wk-old wild-type or Sema4A-deficient mice on a C57BL/6 background by s.c. injection of 100 μg mouse/rat MOG35-55 peptides (MEGWWYRRFPSPVHLVRNGK) emulsified in CFA, in addition to two i.v. injections of 100 ng pertussis toxin (List Laboratories) on days 0 and 2. The mice were treated with either Sema4A–Fc (15 μg, Sema4A-deficient n = 6) or control human IgG (15 μg, Sema4A-deficient n = 5, wild-type n = 5) on days 0, 1, 3, 5, 7, 9, and 11. All mice were monitored daily for clinical signs and were scored using a scale of 0–4 as follows: 0, no overt signs of disease; 1, limp tail; 2, complete hindlimb paralysis; 3, complete hindlimb paralysis plus forelimb paralysis, moribund state or death. The statistical significance was analyzed using an unpaired Student t test, and p values <0.05 were considered statistically significant.

For adoptive transfer, donor mice were immunized with MOG/CFA in the same fashion except for no pertussis toxin. Ten days later, spleens and draining lymph nodes were collected, single-cell suspensions were prepared, and RBCs were lysed. Cells (5 × 10⁶ cells/ml) were cultured with 40 μg/ml MOG35-55 peptide and 10 ng/ml of recombinant mouse IL-12 (R&D Systems). After 3 d of the culture, the cells were harvested, and CD4+ T cells were isolated by negative selection using Dynabeads (Invitrogen). Recipient mice irradiated sublethally (500 cGy) received the cells. The mice were treated with either Sema4A–Fc (15 μg, n = 5) or control human IgG (15 μg, n = 5) or anti-Sema4A blocking Ab (15 μg, n = 5) on days 0, 1, 3, and 5 after transfer.

For the recall assay, CD4+ T cells were purified from the draining lymph nodes by MACS, and 1 × 10⁵ cells were restimulated for 72 h with various concentrations of the MOG peptides in the presence of irradiated (3000 rad) splenocytes (5 × 10⁵). IFN-γ and IL-17A were detected using a mouse IFN-γ and IL-17A ELISA kit (R&D Systems).

Statistical analysis

Continuous variables are expressed as the mean ± SD. Because we were interested in differences and/or trends in the mean values of Sema4A, t tests were consistently used to compare two independent groups. Welch’s t test was selected if the SDs of the two groups were highly different. Otherwise, Student t test was used for statistical analyses. To control for the effects of different baseline covariates (age and gender) among patients, we used the matching method and the analysis of covariance (ANCOVA) method. Both methods were used to compare the MS and OND groups. However, the matching method was not used to compare the CIS and OND groups because the sample size was inadequate when comparing the CIS group (22 patients) with the age- and gender-matched OND patients due to the significantly smaller sample size in the CIS group than that in the MS group. To compare the CIS and OND groups, we adopted the ANCOVA model with age and gender as adjusted factors, which simultaneously controls for the effects of between-group age and gender in the linear model and then provides adjusted mean differences. In addition, the ANCOVA method was used to produce the residual (expanded disability status scale; EDSS). The residual (EDSS) represents the EDSS score that was adjusted by estimating the mean effects of gender, age, duration from the last relapses, and the illness duration in the MS and OND groups because the sample size was inadequate when comparing the CIS group (22 patients) with the age- and gender-matched OND patients. *p < 0.05, **p < 0.01. (B) Sema4A levels before and after the induction of IFN-β therapy were assayed in eight MS patients. IFN-β therapy did not affect the Sema4A levels (means 5128 ± 7581 U/ml versus 4616 ± 6009 U/ml, p = 0.675, Welch’s t test). The black squares show the means. The top and bottom of the box in the box–whisker plot indicate the 25th and 75th percentiles, respectively, and the end of the whisker represents 1.5 times the interquartile range from the top of the box or the maximum point of all the data.
MS patients. There was no significant differences between the remitting phase (5199 ± 1509 U/ml) and the relapsing phase (4239 ± 1325 U/ml) (p = 0.249, Supplemental Fig. 1A). Collectively, these data suggest that serum Sema4A is involved in MS pathogenesis even at an early stage but do not reflect the disease activity.

*Sema4A is shed from DCs*

Sema4A was originally cloned from a cDNA library of mouse DCs (18). To identify the source of increased Sema4A in MS patients, we analyzed Sema4A expression in PBMCs from healthy controls and MS patients by FACS. Although CD4+ T cells, CD8+ T cells, and CD19+ B cells from healthy controls and MS patients expressed very low levels of Sema4A, Sema4A was moderately expressed on CD11c+ HLADR+ cells in healthy controls and was further increased in MS patients (Fig. 2A). These results suggest that monocytes or DCs are likely the main source of soluble Sema4A in MS. Because Sema4A is a transmembrane-type semaphorin, we examined if it could be cleaved from the cell surface, resulting in a soluble form. To evaluate the soluble form of Sema4A that is potentially released from CD14+ monocytes and CD14+ monocyte-derived DCs, the cell surface proteins were biotinylated and incubated for 48 h. The cell lysates and supernatants were collected, immunoprecipitated with an anti-Sema4A Ab, and then analyzed by Western blotting with peroxidase-conjugated streptavidin. Although neither CD4+ T cells nor CD4-CD14- cells produced detectable levels of soluble Sema4A, soluble Sema4A was detected in the culture supernatants of CD14+ monocytes, and these levels further increased after the cells were differentiated into DCs (Fig. 2B, 2C). Soluble Sema4A was detected in the culture supernatants of wild-type mouse DCs and human monocyte-derived cell line (Fig. 3A, Supplementary Fig. 2). A number of transmembrane proteins such as TNF-α and Sema4D undergo proteolysis and are released from the plasma membrane through a process called ectodomain shedding (16, 27), in which proteasomes, including ADAMs and MMPs, have been shown to be involved. To determine whether soluble Sema4A is also secreted through ectodomain shedding, we examined the effects of a set of inhibitors for various protease subclasses. Light metal chelators, EDTA and EGTA, and metalloproteinase inhibitors, GM6001 and phosphoramidon, inhibited Sema4A shedding from monocytes and DCs (Fig. 3A, 3B). Of note, a microarray analysis showed that metalloproteinases such as ADAM10 and MMP-1, -3, -9, -12, and -25, which are reportedly involved in the pathogenesis of MS (28–34), were increased in PBMCs from MS patients with high Sema4A levels compared with those in PBMCs from patients with low Sema4A levels and from healthy controls (Fig. 3C) [the data have been deposited in the Gene Expression Omnibus database and are accessible through GEO Series accession number GSE26484 (http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE26484)]. Taken together, these findings suggest that Sema4A is abundantly expressed on monocytes and DCs in MS patients and proteolytically cleaved from the cell surface of DCs, contributing to the high serum Sema4A levels in a portion of MS patients.

*Link between Sema4A levels and Th17 skewing in patients with MS*

Sema4A has been shown to be crucial for T cell activation and Th differentiation in mouse experimental systems. To investigate whether high Sema4A levels are relevant to the Th cell-mediated autoimmune pathogenesis in MS, we measured the serum cytokine levels in MS patients. Consistent with our previous report on the role of Sema4A in T cell activation (18), MS patients with high levels of serum IL-2 had significantly higher Sema4A levels (MS patients with more than 1.4 ng/ml IL-2: 5576 ± 8838 U/ml; MS patients with less than 1.4 ng/ml: 1370 ± 1552 U/ml, p = 0.0048, Supplemental Fig. 1B). In addition, we observed that low serum IL-10 levels in MS patients were associated with high Sema4A levels (MS patients with less than 1.7 ng/ml IL-10: 5224 ± 7433 U/ml; MS patients with more than 1.7 ng/ml: 258 ± 4884 U/ml, p = 0.0078, Supplemental Fig. 1C), which is consistent with our previous finding that Sema4A suppresses IL-10 production (35). Next, we analyzed intracellular cytokine expression in CD4+ T cells. Blood samples were collected from MS patients with high Sema4A levels (>2500 U/ml, n = 7), MS patients with low Sema4A levels (<2500 U/ml, n = 11), and healthy controls (n = 11). Notably, MS patients with high Sema4A levels had a signifi-

FIGURE 2. Soluble Sema4A is secreted from DCs. (A) Increased Sema4A expression in DCs. Sema4A expression was higher in CD11c+ HLADR+ cells in MS patients (red lines) than in the normal controls (filled histograms). (B) Sema4A expression increased when monocytes were differentiated into DCs. Flow cytometric analysis of Sema4A expression in CD14+ monocytes (filled histograms) and monocyte-derived DCs (red line). (C) Sema4A is cleaved from CD14+ monocytes and monocyte-derived DCs. The cell lysates and supernatants of biotinylated cells were immunoprecipitated with an anti-Sema4A Ab and then blotted with streptavidin–peroxidase. Data shown in (A)–(C) are representative of five or three independent experiments.
The IFN-γ among CD4+ T cells were determined by intracellular cytokine staining. The ratios of IL-17–producing cells in patients with high Sema4A levels (6.74 ± 3.74) than that of patients with low Sema4A levels (2.05 ± 1.08, \( p = 0.0011 \)) or healthy controls (2.30 ± 1.07, \( p = 0.0017 \), Fig. 4C). However, there is no direct correlation between the serum Sema4A levels and the percentage of IL-17+ cells (rank-correlation coefficient = 0.107, \( p = 0.8397 \)), suggesting that Sema4A may determine the threshold of Th17 differentiation. Less than 0.5% of CD4+ T cells were positive for both IL-17 and IFN-γ. The ratios of IL-4– and IFN-γ–producing cells in patients with high Sema4A levels (1.39 ± 0.58 and 5.18 ± 1.51) were not statistically different from those of patients with low Sema4A levels (1.88 ± 0.98, \( p = 0.2555 \) and 5.87 ± 3.97, \( p = 0.6667 \), respectively) or healthy controls (2.46 ± 1.56, \( p = 0.1023 \) and 8.26 ± 3.97, \( p = 0.0692 \), respectively) (Fig. 4A, 4B). These findings suggest that elevated serum Sema4A levels in MS patients reflect the underlying Th17-mediated pathogenesis of MS.

**Correlation between DC-derived Sema4A and Th differentiation**

Next, we investigated whether Sema4A expressed on DCs affects the differentiation of naïve CD4+ T cells into Th17 cells. Naive CD4+ T cells were derived from OT-II OVA-TCR transgenic mice and then cocultured with wild-type or Sema4A-deficient DCs under Th1-, Th2-, or Th17-skewing conditions in the presence of OT-II peptides. IL-17 production was considerably impaired when the naïve CD4+ T cells were cocultured with Sema4A-deficient DCs under Th17-skewing conditions, whereas neither IFN-γ production under Th1-skewing conditions nor IL-4 production under Th2-skewing conditions was affected (Fig. 5A). Even under neutral conditions without cytokines, IL-17 and IFN-γ production was significantly impaired when naïve CD4+ T cells were cocultured with Sema4A-deficient DCs. In contrast, IL-4 production was not affected (Fig. 5B, Supplemental Fig. 2D, 2E). Collectively, these findings suggest that DC-derived Sema4A is critically involved in Ag-specific Th17 and Th1 differentiation.

**Pathogenic implications of Sema4A in EAE**

To explore the pathogenic implications of Sema4A, recombinant Sema4A proteins were injected into actively immunized wild-type or Sema4A-deficient mice during the course of EAE. Although Sema4A-deficient mice exhibited less severe EAE, administration of recombinant Sema4A exacerbated EAE to a similar degree as that observed in wild-type mice with EAE (Fig. 5C). Furthermore, in the case of IL-17 and IFN-γ production by CD4+ T cells, Sema4A-deficient mice exhibited impaired production of both cytokines, but recombinant Sema4A significantly increased CD4+ T cell activation to produce IL-17 as well as IFN-γ in Sema4A-deficient mice (Fig. 5D, Supplemental Fig. 2F, 2G). However, administration of recombinant Sema4A or anti-Sema4A-blocking Abs did not have an influence on the effector phase of the disease course, in which MOG-specific CD4+ T cells were transferred (Fig. 5E). These findings support that Sema4A plays an important role in the development of EAE by promoting Th17 and Th1 differentiation in the priming phase rather than the effector phase.

**MS patients with high Sema4A levels exhibit more severe clinical course**

Finally, we examined whether high serum Sema4A levels, which implicate underlying Th17 pathology, are linked to the clinical course of MS. A heat map of the normalized expression data of genes encoding various proteinases in PBMCs from MS patients with high Sema4A levels (\( n = 2500 \), \( n = 3 \)), MS patients with low Sema4A levels (\( n = 2500 \), \( n = 3 \)), and healthy controls (\( n = 4 \)). The expression levels of MMP-1, -3, -9, -12, and -25 and ADAM10 were higher in MS patients with high Sema4A levels than in MS patients with low Sema4A levels or healthy controls. Data shown in (A) and (B) are representative of three independent experiments.
severity and/or responsiveness to IFN-β treatment. The 59 MS patients were divided into two groups based on a Sema4A threshold of 2500 U/ml. Patients with higher Sema4A levels had a significantly more severe EDSS score (36) (p = 0.042), and their relapse rate tended to increase, although this difference was not significant (Fig. 6A, Table I). Furthermore, when the MS patients under IFN-β treatment were classified into two groups based on serum Sema4A levels, the difference in the EDSS score became more apparent (p = 0.00064, Fig. 6B), suggesting that IFN-β exacerbates the neurologic disabilities of MS patients with high Sema4A levels. Thus, MS patients with high Sema4A levels tended to have more severe disability, and IFN-β treatment was not beneficial to these patients.

Discussion
In the current study, we highlighted the clinical implications of Sema4A in MS. Serum Sema4A is significantly elevated in patients with MS, and about one-third of these patients exhibit remarkably high serum Sema4A levels. Those patients with high Sema4A levels have underlying Th17 pathogenesis. Furthermore, we...
showed that high Sema4A levels were associated with severe disabilities and unresponsiveness to IFN-β therapy. Sema4A, which is a transmembrane-type semaphorin, was originally identified as a molecule expressed in mouse DCs. We extended the findings in human studies and showed not only that Sema4A is expressed in human DCs but also that Sema4A is upregulated on the surface of DCs in MS patients. These findings suggest that DCs are potentially a major source of increased serum Sema4A. Of note, high levels of soluble Sema4A were accompanied by increased MMP levels, which suggests that Sema4A is proteolytically cleaved from the cell surface by MMPs to produce soluble Sema4A in the sera of MS patients. It is also possible that Sema4A contributes to these increased MMP levels. Further studies will be required to determine the pathological relationship between soluble Sema4A and MMPs.

MS is thought to occur in genetically predisposed individuals after they are exposed to an environmental trigger that stimulates myelin-specific T cells (6, 37). In addition, the aberrant differentiation of Th cells and their subsequent transmigration across the blood–brain barrier (BBB) have been implicated in the pathogenesis of MS (37). We previously reported that Sema4A plays critical roles in Th cell activation and Th1 differentiation during the course of EAE (18, 19). In this study, we show that patients with high serum Sema4A levels had Th17 skewing. We further confirmed that Sema4A is involved in Th17- as well as Th1-mediated pathogenesis in our experimental models. The involvement of Sema4A in Th1 or Th17 differentiation may depend on aspects of each situation, including Ag doses and DC numbers. In addition, there may be differences between human and mice regarding the Th1/Th17 preference. Recent reports suggest that Th17 cells play vital roles in the pathogenesis of MS (7–9, 37), in which Th17 cells have been shown to contribute to the disruption of BBB and to infiltrate the CNS (38). The increased number of Th17 cells in MS patients with high Sema4A levels suggests that Sema4A contributes to MS pathogenesis by promoting BBB permeability. In addition, Th17 cells have been shown to enhance CNS inflammation by inducing the expression of inflammatory chemokines and IL-6 in astrocytes (39–41). In fact, patients with NMO, who generally have higher IL-17 and IL-6 levels in the cerebrospinal fluid than those of MS patients, tend to exhibit severe pathological changes (42–45). The clinical severities in MS patients with high Sema4A levels may be partially explained by the increased permeability of the BBB and subsequent infiltration of Th17 cells into the CNS. In addition, we showed that PBMCs from MS patients with high levels of Sema4A had increased MMP-9 mRNA levels. Because MMP-9 is increased in the sera of MS patients and involved in BBB disruption (30, 31), Sema4A may also contribute to the increased permeability of the BBB via increasing MMP-9 expression.

Notably, the difference in the EDSS scores between patients with high Sema4A levels and those with low Sema4A levels became more apparent when the patients were further subclassified into patients who had received IFN-β therapy. Our findings suggest that IFN-β therapy does not ameliorate but rather exacerbates MS in patients with high Sema4A levels. Therefore, these findings suggest that IFN-β therapy is not clinically beneficial for MS patients with high Sema4A levels. Consistent with our findings, IFN-β administration was reported to exacerbate EAE that was induced by adoptively transferring Th17 cells (24). In addition, NMO patients, who are thought to have greater Th17 pathology than MS patients, have been shown to deteriorate after receiving IFN-β therapy (46, 47). More notably, consistent with an inhibitory role of Sema4A in IL-10 production (35), we found that patients with high serum Sema4A levels had low serum IL-10 levels. Because IL-10 has been linked to the beneficial effects of IFN-β treatment (24, 48), it is plausible that high Sema4A levels result in decreased IL-10 levels, leading to the unresponsiveness to IFN-β therapy.

Further studies would be important to elucidate the mechanism for the increase in Sema4A expression on DCs in MS patients and to develop Sema4A-targeted immunotherapy.

Table I. The characteristics of patients with higher and lower Sema4A levels based on a Sema4A threshold of 2500 U/ml

<table>
<thead>
<tr>
<th>Sema4A, U/ml</th>
<th>Number of Patients (F/M)</th>
<th>Age, y</th>
<th>Duration of Illness, mo</th>
<th>Relapse Number/2 y</th>
<th>Mean EDSS Score</th>
</tr>
</thead>
<tbody>
<tr>
<td>&lt;2500</td>
<td>40 (35/5)</td>
<td>38.7 ± 11.3</td>
<td>91.8 ± 104.1</td>
<td>1.84 ± 1.29</td>
<td>2.27 ± 1.94</td>
</tr>
<tr>
<td>≥2500</td>
<td>19 (16/3)</td>
<td>35.8 ± 11.5</td>
<td>72.6 ± 40.2</td>
<td>2.44 ± 2.3</td>
<td>3.34 ± 1.7*</td>
</tr>
<tr>
<td>&lt;2500</td>
<td>16 (14/2)</td>
<td>36.7 ± 11.9</td>
<td>81.1 ± 108.4</td>
<td>2.27 ± 1.4</td>
<td>2.34 ± 2.4</td>
</tr>
<tr>
<td>≥2500</td>
<td>14 (13/1)</td>
<td>33.3 ± 7.9</td>
<td>67.2 ± 31.6</td>
<td>2.62 ± 2.5</td>
<td>3.74 ± 1.6**</td>
</tr>
</tbody>
</table>

*p < 0.05.  
**p < 0.01.
Acknowledgments

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Disclosures

The authors have no financial conflicts of interest.

References


8. Sema4A AND MULTIPLE SCLEROSIS