An Imbalance of Two Functionally and Phenotypically Different Subsets of Plasmacytoid Dendritic Cells Characterizes the Dysfunctional Immune Regulation in Multiple Sclerosis

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Plasmacytoid dendritic cells (pDCs) are instrumental in peripheral T cell tolerance and innate immunity. How pDCs control peripheral immunotolerance and local parenchymal immune response and contribute to the altered immunoregulation in autoimmune disorders in humans is poorly understood. Based on their surface markers, cytokine production, and ability to prime naive allogenic T cells, we found that purified BDCA-2+BDCA-4+ pDCs consist of at least two separate populations, which differed in their response to oligodeoxynucleotides and IFNs (IFN-β), and differently induced IL-17– or IL-10–producing T cells. To evaluate the potential immunoregulatory role of these two types of pDCs in multiple sclerosis (MS) and other human autoimmune disorders (myasthenia gravis), we studied the phenotype and regulatory function of pDCs isolated from clinically stable, untreated patients with MS (n = 16). Patients with MS showed a reversed ratio of pDC1/pDC2 in peripheral blood (4.4:1 in healthy controls, 0.69:1 in MS), a phenomenon not observed in the other autoimmune disorders. As a consequence, MS pDCs had an overall propensity to prime IL-17–secreting cells over IL-10–secreting CD4+ T cells. Immunomodulatory therapy with IFN-β induced an increase of the pDC1 population in vivo (n = 5). Our data offer a plausible explanation for the disturbed immune tolerance in MS patients and provide evidence that immunomodulatory therapy acts at the level of reconstituting homeostasis of pDC, thus reconstituting the disturbed balance. The Journal of Immunology, 2010, 184: 5368–5374.

Plasmacytoid dendritic cells (pDCs) are considered to be safeguards of peripheral T cell tolerance and key players in innate immunity (1, 2). During immunoregulation, pDCs have both stimulatory (3, 4) and regulatory (5–7) effects on T cells. However, little is known regarding the contribution of pDCs to the balance of T cell activation during autoimmunity in the periphery or in the local control of immune reactions in inflamed tissue.

Multiple sclerosis (MS) is a chronic inflammatory disease of the CNS and is thought to be autoimmune in nature (8–10). The combination of genetic and environmental factors predisposes to disease susceptibility, severity, and course. Because of their tolerogenic and immunogenic functions, pDCs are assumed to play an important role in the immunoregulatory network in MS. A first hint to functional abnormalities of pDCs isolated from the peripheral blood of MS patients has been described previously (11).

pDCs are rarely detected in the CNS under nonpathologic conditions, but they are elevated under neuroinflammatory conditions (including MS) in the cerebrospinal fluid (12). Active recruitment of pDCs into the CNS and their accumulation in white matter lesions and leptomeninges of MS brains has also been demonstrated (13). In experimental autoimmune encephalomyelitis, an animal model of human MS, a critical tolerogenic effect of pDCs was demonstrated (14). Unlike myeloid DCs, pDCs had only a minor role in T cell activation and epitope spreading, but negatively regulated pathogenic CNS CD4+ T cell responses, suggesting a regulatory role during experimental neuroinflammation (14). However, it has to be noted critically that the exact mechanism of pDC accumulation and their role during CNS inflammation are not well understood.

In this study, we provide a detailed characterization of two phenotypically and functionally different subsets of pDCs in human peripheral blood using specific markers for pDCs (15). These subsets (pDC1 and pDC2) clearly differ in their properties to induce proinflammatory versus regulatory T cell responses. We noted that MS is characterized by a different distribution of those pDC subsets in the periphery, which results in a high propensity of MS-derived pDCs to generate IL-17 over IL-10–producing CD4+ T cells in vitro. Immunomodulatory therapy with IFN-β (an established standard treatment of MS) was capable to reverse the altered pDC distribution in vivo. Our data therefore suggest that the alterations in pDC subsets might be responsible for the failure of immunotolerance in MS patients.
**Materials and Methods**

**Patients**

Fresh blood samples were obtained from 16 patients referred to the Department of Neurology (University of Wuerzburg). Diagnoses of MS were made according to the criteria of McDonald et al. (16). Patients included in the study were clinically stable and had not yet received immunomodulatory treatment except for corticosteroids, with the last dose at least 6 mo prior to enrollment. In addition, we included five patients who were diagnosed with AIDs and were followed for 12 mo. All patients gave informed consent in accordance with the Declaration of Helsinki and a protocol approved by the Ethics Committee of the University of Wuerzburg Medical School. Thirty to 50 ml of blood was collected by venous puncture and tourniquet. In parallel, 21 sex- and age-matched healthy donors (HDs), and 15 autoimmune disease controls (other disorders [OD]) were included in the study (15 patients with myasthenia gravis [MG]).

**Isolation and stimulation of pDCs**

pDCs were purified from freshly collected peripheral blood samples (<24 h processing time). PBMCs were isolated by density gradient centrifugation using lymphocyte separation medium (PAA Laboratories, Linz, Austria), followed by positive sorting using anti–BDCA-4–conjugated magnetic beads (Miltenyi Biotec, Bergisch-Gladbach, Germany). The purity of the recovered pDCs was determined by flow cytometry and was >90%. Where indicated, BDCA-4–isolated pDC were stained with anti–CD123/anti-CD58 and sorted by flow cytometry based on CD123highCD58low (named pDC1) expression and CD123lowCD58high (named pDC2) using a fluorescence-activated cell sorter (MoFlo; Cytomation, Freiburg, Germany).

Isolated and purified pDCs were cultured on 96-well culture plates (Nunc, Langenselbold, Germany) at a concentration of 2 × 10^5 per well in RPMI 1640 (PAA, Linz, Austria) supplemented with 2 mmol/l L-glutamine, 1% penicillin/streptomycin (Invitrogen, Karlsruhe, Germany), and 10% human serum (AB serum; PAA). The cells were stimulated with type A (CpG A) or type B (CpG B) unmethylated CG oligodeoxynucleotides (ODN) (2 μM, CpG 2216 and CpG 2016, respectively; TIB MOLBIOL, Berlin, Germany), unless specified otherwise in results. IFN-β concentration was 1000 U/ml.

**Flow cytometry**

Ex vivo isolated or cultured pDCs were washed with FACS-buffer (PBS supplemented with 1% BSA and 0.1% sodiumazide) and stained with fluorescence-labeled mAbs together with blocking mouse IgG (Sigma-Aldrich, Munich, Germany) at 4°C for 30 min. Cells then were analyzed with FACS-Calibur using Cell Quest (BD Biosciences, Heidelberg, Germany) and FlowJo (Tree Star, Ashland, OR) software. The following mAbs were used for counterstaining of BDCA-4–isolated pDCs: anti–HLA-DR (LS51, BD Biosciences), anti–CD123 (9F5, BD Pharmingen), anti–ILT2 (HP-F1), anti–ILT3 (ZM 3.8), anti–ILT4 (42D1, all Beckman Coulter, b. Aldrich, Munich, Germany) at 4°C for 30 min. Cells then were analyzed with FACS-Calibur using Cell Quest (BD Biosciences, Heidelberg, Germany) and FlowJo (Tree Star, Ashland, OR) software. The following mAbs were used for counterstaining of BDCA-4–isolated pDCs: anti–HLA-DR (LS51, BD Biosciences), anti–CD123 (9F5, BD Pharmingen), anti–ILT2 (HP-F1), anti–ILT3 (ZM 3.8), anti–ILT4 (42D1, all Beckman Coulter, Krefeld, Germany), and anti–CD86 (2361, BD Pharmingen), anti–CD85 (1C3, BD Pharmingen), anti–BDCA-1 (AD5-8E7, Miltenyi Biotec), anti–BDCA-2 (AC144; Miltenyi Biotec), anti–BDCA-3 (AD5-14H12; Miltenyi Biotec), and anti–BDCA-4 (AD5-17F6, Miltenyi Biotec). In flow cytometry, cells were fixed and permeabilized (BD Biosciences) according to the manufacturer’s protocol and then stained for 30 min at 4°C. The following mAbs were used for intracellular staining: anti–IFN-α (LT27; 295; Miltenyi Biotec), anti–TNF-α (c2A; Miltenyi Biotec), and anti–IL-6 (AS12; BD Biosciences), anti–IL-10 (B-T10, Miltenyi Biotec), anti–IL-17 (eBio4DEC17; eBiosciences, Frankfurt, Germany), anti–IFN-γ (45-15, Miltenyi), anti–TLR3 (TLR3.7, eBiosciences), anti–TLR7 (b5; IMMGENEX via Biomol, Hamburg, Germany), anti–TLR8 (g44C143, IMMGENEX), and anti–TLR9 (eB72-1665, eBiosciences). Before fixation, the cells were counterstained with anti–CD123 (9F5, BD Pharmingen).

**Statistical analysis**

Statistical significance of differences was determined by ANOVAs without assuming Gaussian distribution (Kruskal-Wallis test) and subsequent Dunn’s multiple comparison test. Differences were considered statistically significant with *p* values < 0.05 and highly significant with *p* = 0.01 and **p** < 0.001. Software for statistical assessment was Prism 5 (GraphPad).

**Results**

**Purified pDCs contain at least two phenotypically different subsets**

pDCs represent a population of DCs with relatively low frequency (~0.4%) in human peripheral blood (1). Recently, two additional markers (BDCA-2 and BDCA-4) were identified with a restriction to human pDCs in peripheral blood and bone marrow (15). Since then, these markers have been used widely to identify and purify pDCs from human blood. We found that pDCs purified by BDCA-4*+* contain at least two distinct subpopulations in the peripheral blood of HDs that can be identified based on the cell size and granularity (Fig. 1A, left panel). Using mAb to CD123 (IL-3Rα) we could distinguish between CD123high (pDC1 subset) and CD123low cells (pDC2 subset). A subpopulation that was negative for CD123 expression could also be identified (Fig. 1A, left panel). Because CD123 negative cells were also negative for other important cell surface proteins (e.g., CD80, CD86, MHCII, TLRs, ICOS-L), this population was not studied in detail here.

Further phenotypic analysis revealed a lower expression of MHC class II and other markers associated with DC maturation (e.g., CD86, TLR2, and CD58) by pDC1 in comparison with pDC2 (Fig. 1A, right panel). In addition to MHCII, CD123, and CD86, pDC1 and pDC2 differed in the expression of CD58, ILT2, ILT3, ILT4, CD1c, CD303, and TLR2 (Fig. 1A, left panel). No differences between pDC1 and pDC2 could be observed in the expression of TLR1, TLR3, TLR4, TLR5, TLR7, TLR8, and TLR9 (data not shown). To rule out the autofluorescence-non-specific Ab binding common for matured DCs, isotype stains were performed differentially on pDC1 and pDC2 (Supplemental Fig. 1). The stains revealed a weak increase in the fluorochromes FITC, PE, and APC and some increase on pDC2 in the PE-Cy5-channel.

**Functional differences in pDC1 and pDC2 subsets in response to stimulation**

We also observed profound differences in the cytokine secretion by both pDC subsets (Fig. 1B). pDCs were analyzed either directly (no stimulus) or after stimulation using CpG A (ODN 2216), which was shown to induce high amounts of IFN-α/β in pDCs, or CpG B (ODN 2006), which strongly promotes pDC maturation and activation but induces only small amounts of IFN-α/β (17–19). Unlike CpG A, pDC stimulation with CpG B altered the pDC1/pDC2 ratio observed under noninflammatory conditions. CpG B treatment stimulated a profound shift of total pDCs into pDC2, as indicated by lower expression of CD123 (Fig. 1B) and high expression of various maturation markers (not shown). In our assays, pDC1 was the main source of IFN-α under both steady state and proinflammatory stimulus delivered by CpGs, whereas pDC2 was a poor cytokine producer at a steady state and produced TNF-α upon CpG treatment (Fig. 1C, left and middle rows). TNF-α could be differentially induced in pDC1 in response to CpG A and in pDC2 by CpG B (Fig. 1C, middle and lower rows). pDC2 also produced more IL-6 than did pDC1 (data not shown). This behavior further corroborates our finding that pDCs in human blood contain at least two phenotypically different subsets.

We next studied whether the two identified pDC populations would change phenotype and/or function in response to CpGs. As already indicated in Fig. 1, pDC1 displayed a more immature...
phenotype with low expression of MHCII, CD86, and CD58 molecules. As a result, this cell population was more prone to mature upon CpG stimulation. CpG A and CpG B treatments both resulted in an increase of CD86 and MHCII expression by pDC1 with a percentage of double-positive cells increasing from 36% (unstimulated) to 58% (upon CpG A) and 83% (upon CpG B) (data not shown). pDC2 consistently revealed CD86 and MHCII expression before or after CpGs treatment (data not shown). Therefore, we suggest that CpG A activated total pDCs, but did not induce their maturation, whereas CpG B appeared to result in maturation of pDC1 into cells with pDC2 phenotype. Thus, blood-derived pDCs could be converted by CpG B into pDC2, whereas the immunomodulatory agent IFN-β, had an opposite effect on pDCs, inducing a pDC1 phenotype (Fig. 2A). To experimentally evaluate the behavior of pDC subpopulations in response to different stimuli, we used (in addition to CD123) CD58 as a marker because of its high expression on pDC2 (Fig. 1A). In a representative experiment, we could show in a HD that a percentage of 11% pDC2 (CD58 high) under CpG A treatment could be converted to 57% pDC2 by CpG B and could be reduced to 3% pDC2 under IFN-β treatment (Fig. 2A).

After demonstrating the behaviors of pDC1 (CD123highCD58low) and pDC2 (CD123lowCD58high) in response to different stimuli, and their relative changes, we were interested in the effects these cells could have under conditions of allogeneic T cell priming. Thus, we sorted pDC1 (CD123highCD58low) and pDC2 (CD123lowCD58high) by flow cytometry from human blood-derived pDCs and directly cocultured them with allogeneic naive T cells. Interestingly, pDC1 induced 3.8-fold more IL-10–producing T cells (Tr1) (Fig. 2B) than did pDC2, whereas pDC2 induced 4.8-fold more IL-17–secreting IL-17–producing T cells (T H17) than did pDC1 (Fig. 2B). Because matured DCs are generally prone to reduced viability, we included 7-AAD staining to control the ability of pDC subsets to survive over time and under different experimental conditions. Although both pDC1 and pDC2 were stable and viable in culture under all conditions, CpG A treatment resulted in reduced viability of mainly pDC2 (Supplemental Fig. 2 and data not shown).

FIGURE 1. Human pDCs consist of at least two phenotypically and functionally different subsets. A, BDC4–MACS-purified human pDCs show cell populations that differ in size (forward scatter) and granularity (side scatter). Based on CD123 expression, pDC1 (in blue) and pDC2 (in red) could be identified (left panel). The histograms presented are representative analyses of the expression of MHCII, CD86, CD58, ILT2, ILT3, ILT4, CD1c (BDCA-1), CD303 (BDCA-2), and TLR2 proteins for pDC1 (blue) and pDC2 (red). B, The dot plots represent the distribution of blood-derived human pDC1 and pDC2 populations before (unstimulated, upper row) and after CpG A (middle row) and CpG B (lower row) stimulations. Numbers in quadrants indicate percent of CD123 high (pDC1) to CD123low (pDC2) populations. C, The secretion of TNF-α and IFN-α before and after CpG stimulation is shown for pDC1 (left column), pDC2 (middle column), and merged pDC1/pDC2 (right column) subsets. Numbers in quadrants indicate the percentage of cells in each gating. Representative histograms are shown.
numbers demonstrate the percentage of IL-10 secreting cells. Data acquired with allogeneic naive CD4+ T cells. The secretion of IL-17 and IL-10 by treated with CpG A or CpG B for 48 h prior to coculture with allo-corroborate our previous observations. Total pDCs were isolated and (containing pDC1 and pDC2 subsets) on T cell priming in vitro to CpGB (gray line), and IFN-

\[ \text{FIGURE 2.} \text{ In vitro inflammatory stimuli change pDC phenotype and function. A.} \text{ Freshly isolated pDCs were incubated with CpG}\_A \text{(solid line), CpG}\_B \text{(gray line), and IFN-}\beta \text{(dashed line) for 48 h, and the expression of CD58 was checked on different pDC subpopulations. The frequency of pDC1 and pDC2 based on CD58 expression is shown (one representative experiment), the black vertical line divides pDC1 (left) and pDC2 (right). Filled histograms show the isotype-matched control Ab when gated on pDC1 (black) and pDC2 (gray). B.} \text{ FACS isolated BDCA-4}^+ \text{ pDCs were cell-sorted into pDC1 (CD123}^+\text{CD58}^+\text{), and pDC2 (CD123}^+\text{CD58}^-\text{) and cocultured with allogeneic naive CD4}^+ \text{T cells. The secretion of IL-17 and IL-10 by T cells was analyzed after 7 d in vitro by intracellular cytokine staining and the} \]

\[ \text{right panels} \text{ show dot plots gated on CD4}^+ \text{T cells, where the numbers demonstrate the percentage of IL-10 secreting cells. Data acquired are representative of five independent experiments performed.} \]

pDC1/pDC2 distribution influences the generation of IL-10–producing T cells versus Tr1/

We next investigated the influence of prestimulated total pDCs (containing pDC1 and pDC2 subsets) on T cell priming in vitro to corroborate our previous observations. Total pDCs were isolated and treated with CpG\_A or CpG\_B for 48 h prior to coculture with allogeneic naive T cells. After 7 d, the cells were collected and analyzed for the expression of T cell-secreted cytokines (Fig. 2C). After showing that CpG\_A does not alter the composition of pDCs (Fig. 2A), we compared how in vitro-shifted pDCs differed in the T cell priming assay. CpG\_B-treated pDCs (therefore mainly con-sisting of pDC2; Fig. 2C, left panel) induced no Tr1 (Fig. 2C, right panel), and IFN-\beta–driven pDCs (therefore mainly consisting of pDC1) induced Tr1.

Moreover, we challenged the capability of general pDCs as well as pDC1 versus pDC2 differentially to induce FoxP3 regulatory T cells, as previously suggested (20). As a positive control, we used TGFB, which has been reported to induce FoxP3-expressing cells under in vitro conditions (21). In our experimental settings, we did not observe the induction of FoxP3-expressing cells by pDC (data not shown).

The ratio of pDC1 versus pDC2 is inverted in peripheral blood-derived pDCs of patients with MS

To investigate whether MS might be associated with a disturbance of the pDC1/pDC2 ratio, we next evaluated phenotype and distribution of pDC1/pDC2 in peripheral blood of patients with MS. pDCs isolated from human peripheral blood of stable, untreated, relapsing-remitting MS cases were compared with HDs and another autoimmune disease (OD). MG. In HDs, the ratio of pDC1 to pDC2 was rather stable at an average number of 4.4 to 1 (pDC1 to pDC2: n = 21, range, 0.6:1–18.2:1; Fig. 3A). Interestingly, pDCs of patients with MS showed a reversed ratio of pDC1 to pDC2 (n = 16; average, 0.69:1; range, 0:1–1.81:1), which was not observed in OD. Patients with MG (n = 15), a prototypic Ab-mediated neurologic disorder, had a slightly altered pDC1/pDC2 balance in the same direction as MS (average ratio, 0.9:1), but this ratio did not reach the level of significance and the pDC1/pDC2 distribution was not as apparent as in MS blood samples (Fig. 3A). In addition, we investigated several patients with rheumatoid arthritis, where the pDC1/pDC2 ratio was not altered (data not shown). We did not observe significant differences in cell surface markers expression for both pDC1 and pDC2 when compared between HD and MS (Supplemental Fig. 3).

pDC derived from patients with MS induce more Th17 in comparison with HD controls

To address whether the inverted pDC1-to-pDC2 ratio in the total pDCs from patients with MS might have consequences for the balance of primed immune responses—similar to our in vitro experiments (Fig. 2)—we compared the properties of HD- and MS-derived pDCs in coculture assays with naive allogeneic T cells.

MS-derived pDCs, predominantly containing the pDC2 subset (Fig. 3A), induced a higher amount of IL-17–secreting T17-type cells in individual experiments in comparison with HD controls (Fig. 3B). In addition, T cells that were double positive for IL-17 and IFN-\gamma secretion were also detected in cocultures with MS-derived pDCs. Interestingly, these cells were not found in assays with HD-derived pDCs (Fig. 3B). Using a Transwell membrane separating pDCs and T cells, we could not detect any induction of IL-17 and IFN-\gamma production by T cells in the absence of pDCs, suggesting that a direct contact, possibly in a form of costimulation, could be required for the instruction of lineage (data not shown).

Immunomodulatory treatment with IFN-\beta reconstitutes the pDC1/pDC2 imbalance in MS

Because an inverted ratio of pDC1 to pDC2 toward pDC2 could be shown for patients with MS (Fig. 3A) and IFN-\beta treatment could induce a pDC1 phenotype in vitro (Fig. 2A), we finally questioned whether immunomodulatory therapy with IFN-\beta, a well-established basic therapy in clinical practice, would exert its effects by influencing the pDC phenotype. We investigated samples from MS cases that were serially acquired before and at different times during clinical treatment. Blood-derived pDCs were analyzed in the samples before IFN-\beta therapy and at 6 and 12 mo after treatment. Analogous to our observations in vitro, systemic IFN-\beta therapy resulted in
a recovery of the underrepresented pDC1 population in MS blood (Fig. 4). In an extreme case, before therapy, there was no detectable pDC1 population (Fig. 4A). The pDC1 population reached 39% after 6 mo and 52% after 12 mo of treatment. We examined five patients in whom this shift could be observed in differing frequencies (Fig. 4B, 4C). The first sign of a recovery of the pDC1-to-pDC2 ratio could be observed as early as after 2 mo of therapy (data not shown). Similar to earlier observations (11), this finding rules out that the subset imbalance is a fixed abnormality not amenable to therapeutic modification.

Discussion

Our study addressed the questions of how human pDCs contribute to the immune regulatory networks and how phenotype and function of blood-derived pDCs might differ in a common autoimmune disorder of the CNS (i.e., MS) from healthy volunteers, thereby providing a further hint to the immunopathogenesis of MS.

We could show that human peripheral pDCs contain at least two major subpopulations, which we propose to be called pDC1 and pDC2 subsets. Under basal conditions, these subpopulations exist in a certain ratio and have different effects on the generation of proinflammatory versus anti-inflammatory or regulatory T cell responses. Although previous reports have recognized differences in the overall pDC population in human blood (15, 22) and MS (11, 23), distinct populations of pDCs as identified by specific markers have not yet been analyzed in detail. Based on the size and activation marker expression of pDCs under basal conditions (24, 25), our data suggest that pDC1 (CD123<sup>high</sup>CD86 MHCI<sup>low</sup>) resemble rather immature DC, whereas pDC2 behave similar to DC showing a mature phenotype.

Accumulating evidence suggests that pDCs exert both immunogenic and tolerogenic properties during various immune responses.

Thus, pDCs can induce Tr1 (26) and FoxP3<sup>+</sup> (20) regulatory T cells in direct coculture assays. Although we could not induce FoxP3 expression in naive T cells by pDC (data not shown), we observed a generation of Tr1-type T cells through direct, cell-to-cell contact dependent pDC interaction. Specifically, our results proved to be in accordance with other work (26) showing that the pDC1 subset could induce Tr1.

It is generally accepted that the functions of pDCs are not fixed, but can be modulated by a variety of environmental factors (e.g., innate stimuli). Thus, pDC act as immune regulators and contain a high percentage of the pDC1 subset under steady-state conditions. However, under pathogenic conditions (e.g., with viral or other inflammatory stimuli resulting in pDC maturation) pDCs effectively switch into pDC2-containing immunogenic cell population to presumably fight pathogens during infection (27).

IFN-β, an approved immunomodulatory drug for MS (28), had a long-lasting effect on the pDC1 to pDC2 distribution, shifting the ratio of the two subsets to a pDC1 phenotype in MS blood samples. IFN-β–modulated pDCs with enhanced CD123 expression and IL-10 production were previously described as a subset of myeloid DCs (29–31). Interestingly, these cells resemble the pDC1 subset described in this study and suggest that both pDC1 and pDC2 are a subset of plasmacytoid DCs and not, as hypothesized earlier (22), a possible subtype of myeloid DCs.

An impaired maturation profile and a lower cytokine secretion in response to innate stimulation of pDCs derived from patients with MS have been demonstrated recently (11, 23). However, the factors responsible for this impairment remained elusive, as was the link with the disordered immunoregulation in MS. We found a remarkable imbalance in the distribution of pDC1 versus pDC2 subsets in MS. Although the overall frequency of pDCs in peripheral blood did not differ between MS and HDs, and the cell
surface markers on both pDC1 and pDC2 between MS and HDs proved to be similar, the functional consequences of pDC–T cell interactions were significantly different. Thus, the number of T<sub>H17</sub> after pDC interaction was clearly higher in the presence of MS-derived pDCs. In addition, unlike pDCs from HD controls, MS-derived pDCs induced double-positive IFN-γ-IL-17<sup>T</sup> T cells in vitro, which are believed to represent a highly proinflammatory and, in the proper antigenic setting, encephalitogenic subpopulation of CD<sub>4</sub><sup>+</sup> T cells. The generation of these cells has recently been reported (32), suggesting a synergistic action of two cytokines. As a side note, our results differ in one data point from those of Stasiôłeök et al. (11); whereas they found CD8<sub>D</sub> to be expressed less in MS pDCs ex vivo, we observed that pDC2 is CD8<sub>D</sub><sup>+</sup> and patients with MS have a much higher percentage of pDC2. Other discrepancies between our studies can be attributed to cell preparation (PBMCs versus leukaphereses) and general differences in scientific questioning (cocultures versus monocultures).

The description of two phenotypically and functionally different pDC populations in conjunction with their alteration in MS raises several important questions, such as: 1) is the imbalance between pDC1/pDC2 a phenomenon associated with autoimmune conditions in general or is it specifically associated with MS, and 2) could the reversion of the pDC1/pDC2 imbalance be a strategy of reconstituting parts of the disordered immunoregulatory networks in MS? First, the significant imbalance in pDC1 to pDC2 subset distribution could be observed only in MS and not in MG, which we used as a neurologic autoimmune disease control. This finding suggests that the detected imbalance of pDC1/pDC2 is characteristic of MS. Therefore, it is tempting to speculate about specific pathogenetic conditions that might induce this phenomenon in MS. For example, through its stimulation, a viral infection present in patients with MS could drive the pDC maturation toward the pDC2 phenotype. Indeed, the contribution of viruses (e.g., herpesviruses) to the development of MS (33, 34) and modulation of pDC subpopulations in blood and tissue under human CMV (HCMV) infection (35) have been described. Thus, the expression of cell surface markers on pDCs was shown to be differently regulated in response to HCMV infection (35). These results imply that, similar to HCMV infection, a yet unidentified low-virus infection persistency in patients with MS could selectively target pDC population in the blood, changing their phenotype and function. However, from the observations in the current study, it is not possible to determine whether pDC maturation in the blood of patients with MS is occurring before the disease develops as a phenotypic variant or during the course of disease. This question is possibly addressed by assessing very early MS (e.g., pDCs from juvenile cases of MS), in which the number of environmental triggers influencing the immunoregulatory networks is lower than in cases of adult MS.

The fact that systemic therapy with IFN-β had an effect on the pDC1-to-pDC2 shift in MS blood samples not only corroborates our findings on pDC1/pDC2 shifting in vitro, but also strengthens the notion of its pathogenic relevance. Despite the fact that IFN-β therapy acts at various levels within the putative pathogenesis of MS (36), the examples how IFN-β enhances interferon-producing cells in human blood. Science 284: 1835–1837.


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