Promoter Hypomethylation Results in Increased Expression of Protein Phosphatase 2A in T Cells from Patients with Systemic Lupus Erythematosus

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Promoter Hypomethylation Results in Increased Expression of Protein Phosphatase 2A in T Cells from Patients with Systemic Lupus Erythematosus

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The catalytic subunit α isofrom of protein phosphatase 2A (PP2Acα) activity, protein, and mRNA have been found increased in systemic lupus erythematosus (SLE) T cells and to contribute to decreased IL-2 production. The PP2Acα promoter activity is controlled epigenetically through the methylation of a CpG within a cAMP response element (CRE) motif defined by its promoter. We considered that hypomethylation may account for the increased expression of PP2Acα in patients with SLE. Using bisulfite sequencing, we found that SLE T cells displayed decreased DNA methylation in the promoter region compared with normal T cells. More importantly, we found that the CRE-defined CpG, which binds p-CREB, is significantly less methylated in SLE compared with normal T cells, and the levels of methylation correlated with decreased amounts of DNA methyltransferase 1 transcripts. Methylation intensity correlated inversely with levels of PP2Acα mRNA and SLE disease activity. Chromatin immunoprecipitation assays revealed more binding of p-CREB to the CRE site in SLE T cells, resulting in increased expression of PP2Acα. We propose that PP2Acα represents a new methylation-sensitive gene that, like the previously reported CD70 and CD11a, contributes to the pathogenesis of SLE. The Journal of Immunology, 2011, 186: 000–000.

Systemic lupus erythematosus (SLE) is an autoimmune disease primarily affecting women and is characterized by autoantibody formation against a host of nuclear Ags and immune complex deposition in multiple organ systems such as the kidney and blood vessels (1, 2). Although multiple genetic loci have been reported to be involved in determining SLE susceptibility, incomplete concordance in monozygotic twins who carry the same SLE-susceptibility genes suggests that environmental factors are also important for its pathogenesis (3–5). Established examples of exogenous agents affecting lupus include drugs like procainamide and hydralazine that cause lupus-like symptoms (6, 7) and exposure to UV light, which may initiate disease flares (8, 9). Several studies have shown that these agents may induce DNA demethylation, which plays an important role in transcriptional regulation by altering the accessibility of several transcription factors to the targeted gene-encoding promoters, genomic imprinting, and X-chromosome inactivation (10–13). Therefore, study of epigenetic mechanisms may provide important clues on how environmental factors may contribute to the expression of autoimmune related pathology.

Indeed, several studies have suggested that impairment of DNA methylation may account for several T cell abnormalities in patients with SLE and to be involved in the pathogenesis of the disease (14). Treatment of normal T cells with DNA methylation inhibitor 5-azacytidine (5-azaC) induces overexpression of several methylation-sensitive genes, such as LFA-1 (CD11a/CD18) (15, 16), CD70 (17), which is known as a member of TNF superfamily member 7 as well as a ligand for B cell CD27, and CD40L (18), all of which are hypomethylated and overexpressed in T cells from SLE patients (19). Abnormal enhancement of costimulatory signaling pathways initiated or modulated by these molecules may contribute to autoimmunity. Some other methylation-sensitive genes, like perforin 1 (20), or cytokines (IL-4, IL-6, and IFN-γ) have been implicated in the expression of autoimmune disease like SLE (21–25). In addition, defective signaling through ERK-1/ERK-2 in lupus T cells has been claimed to contribute to DNA hypomethylation (25–27) because of the reduction of DNA methyltransferase subsequently. Decreased expression of DNA methyltransferase 1 (DNMT1), which is responsible for the methylation of newly replicated daughter DNA strands during mitosis, has been also linked to hypomethylation and SLE expression (8, 27, 28).

The catalytic subunit of protein phosphatase 2A (PP2Ac) is overexpressed in SLE T cells (29). It is a highly abundant and ubiquitously expressed serine-threonine protein phosphatase in eukaryotic cells with various important roles including cell cycle progression and signal transduction (30–32). p-CREB, which is an important transcription factor in the regulation of the expression of IL-2, is a well-known PP2Ac substrate (33). We have shown that increased PP2Ac expression suppresses IL-2 production in SLE T cells by decreasing binding of p-CREB to IL-2 promoter (29). Recently, we identified a core promoter region of the α isofrom of PP2Ac (PP2Acα), which contains a cAMP response element (CRE) motif flanked by three GC boxes. The fact that p-CREB can only bind to demethylated CRE motif in the PP2Acα promoter revealed that transcriptional regulation is tightly coordinated in an epigenetic manner (34).
In this study, we investigated DNA methylation patterns in the PP2Ac promoter region in SLE T cells and compared it to that in normal T cells. We show evidence that the PP2Ac promoter is hypomethylated in SLE T cells due to reduced DNMT1 expression and allows enhanced binding of p-CREB, which results in the overexpression of this molecule. Thus, PP2Ac represents a new methylation-sensitive gene, which, like the previously reported CD70, CD40L and CD11a, and probably others, contributes to the pathogenesis of SLE.

Materials and Methods

Patients and T lymphocyte purification

A total of 24 SLE patients (23 female and 1 male) who fulfilled at least 4 of the 11 revised criteria of the American College of Rheumatology for the classification of SLE (35) were enrolled in this study. The demographics of the patients are shown in Table I. Nine patients were studied at different time points, and their demographics are shown in Table II. The patients shown in Table II were studied in multiple occasions. Thus, total sample number from lupus patients studied in this work is 34. SLE disease activity was assessed by the SLE disease activity index (SLEDAI) (36). Age ranged between 19 and 49 y (average: 35), and SLEDAI ranged between 0 and 36 (average: 7). We classified samples from patients into two groups: the high disease activity group was defined when the SLEDAI score was >6 (n = 19), and the low disease activity group was defined when the SLEDAI score was ≤6 (n = 15). Appropriate age-, ethnicity-, and sex-matched 16 healthy volunteers were also used as controls. Studies were approved by the Human Use Committee of our institution.

CD3+ T lymphocytes were purified using a rosette T cell purification kit (Stem Cell Technologies) as described before (34). Subsequently, both RNA and DNA were extracted from T cells (3 × 10^6) using the AllPrep RNA/DNA-Protein mini kit (Qiagen) according to the manufacturer’s protocol.

DNMTs plasmid transfection

After the purification of CD3+ T lymphocytes from normal individuals’ peripheral blood, a plasmid encoding DNMT1 (Invivogen) and DNMT3a (Invivogen) or corresponding empty vector (pORF9) were transfected into primary T cells. The plasmid DNA isolated from T cells of three lupus patients and three SLE patients was purified and treated with 5-azaC, a DNA methylation inhibitor, and induced increased activity (34). In this study, we examined whether DNA methyltransferase DNMT1 (maintenance methyltransferase) and DNMT3a (de novo methyltransferases) regulate the core promoter region. First, we confirmed that the DNA methyltransferase DNMT1 (Invivogen) and DNMT3a (Invivogen) or corresponding empty vector (pORF9) were transfected into primary T cells. The total amount of plasmid used in each sample was 6 μg per 6 × 10^6 T cells. Following transfection, 6 × 10^6 T cells were resuspended into 1 ml RPMI 1640 medium (Mediatech) supplemented with 10% heat-inactivated FBS (Quality Biological) and 2 mM l-glutamine, placed onto 12-well plates, and harvested after 24 h incubation for several experiments.

Bisulfite sequencing

Genomic DNA isolated from T cells of three lupus patients and three matched control subjects was bisulfite converted using the EpiTect kit (Qiagen) following the manufacturer’s protocol. The fragments of 547 bp PP2Ac promoter were amplified by nested PCR and cloned into a pCR 2.1-TOPO vector using the TOPO TA Cloning kit (Invitrogen) after the PCR amplitcons were gel purified. Ten clones from each sample were selected by blue/white screening, and plasmid DNA was extracted using the 2 μg DNA–protein complexes were immunoprecipitated with anti–p-CREB Ab (Upstate Biotechnology) or its control Ab (rabbit normal IgG; Santa Cruz Biotechnology), and, after a series of washing steps, the cross-linking was reversed, and the protein was digested with proteinase K (Qiagen). The DNA was extracted by the QIAquick PCR Purification kit (Qiagen). Immunoprecipitated and purified DNA was analyzed by PCR using the primers F (−468) and R (−83) described as above, which are specific for the human PP2Ac promoter and were used to amplify a fragment containing a CRE motif. The corresponding nonimmunoprecipitated DNA (input DNA) was also analyzed. PCR products were semiquantified using the same method as above in the methylation-specific PCR.

Chromatin immunoprecipitation assays

Chromatin immunoprecipitation (ChiP) analysis was done using ChiP Assay kit (Upstate Biotechnology) according to the manufacturer’s instructions. T cells (3 × 10^6) were used per immunoprecipitation Ab. The cells were fixed with 1% formaldehyde for 10 min, lysed, and sonicated. The DNA–protein complexes were immunoprecipitated with anti-p-CREB Ab (Upstate Biotechnology) as a control Ab (rabbit normal IgG; Santa Cruz Biotechnology), and, after a series of washing steps, the cross-linking was reversed, and the protein was digested with proteinase K (Qiagen). The DNA was extracted by the QIAquick PCR Purification kit (Qiagen). Immunoprecipitated and purified DNA was analyzed by PCR using the primers F (−468) and R (−83) described as above, which are specific for the human PP2Ac promoter and were used to amplify a fragment containing a CRE motif. The corresponding nonimmunoprecipitated DNA (input DNA) was also analyzed. PCR products were semiquantified using the same method as above in the methylation-specific PCR.

Data are presented as mean value ± SEM. The paired two-tailed Student t test and the Pearson product moment correlation coefficient were used for statistical analysis. Statistical significance was defined as p < 0.05.

Results

Cotransfection of DNMT1 and DNMT3a into normal T cells reduced mRNA expression of PP2Ac by blocking p-CREB binding to methylated promoter region

We previously showed that 5-azacytidine (5-azaC), a DNA methylation inhibitor, influenced the methylation pattern in PP2Ac promoter region and induced increased activity (34). In this study, we examined whether DNA methyltransferase DNMT1 (maintenance methyltransferase) and DNMT3a (de novo methyltransferases) regulate PP2Ac expression by modifying the methylation pattern on the PP2Ac core promoter region. First, we confirmed that the DNA methylation levels at a specific site that is essential for the binding of transcription factor p-CREB were significantly elevated when the DNMTs were transfected into normal T cells (Fig. 1A). We compared the methylation effect in T cells with DNMT1 or DNMT3a alone or in combination. Cells transfected with both DNMTs produced the strongest methylation effect, and these were used in all subsequent experiments.

Next, we determined the levels of p-CREB binding to the CRE motif in the PP2Ac core promoter region in T cells transfected with DNMTs. As shown in Fig. 1B, using ChiP assay, we found that overexpression of DNMTs inhibited p-CREB binding to the region. We also quantified PP2Ac mRNA expression levels and

Reverse transcription and real-time PCR

Total RNA (300 ng) was transcribed in cDNA in a conventional thermocycler using AMV reverse transcriptase and oligo(dT) primer (RT-PCR kit; Promega). Real-time RT-PCR was performed for every sample with a LightCycler 480 System by adding SYBR green (Roche) to the reaction mixture. Primers used were: DNMT1 forward 5′-GGGTTGGAGCTTGTTCCTGTC-3′ and reverse 5′-TGAAAGCTGTGGTGCTCTAC-3′; PP2Ac forward 5′-TGTAAGCTGGTTGTTGGAGGAGAG-3′ and reverse 5′-CGTACAAGCTTGTAACGTGTTCA-3′; and GAPDH forward 5′-CAACTCATGGTTAACATGTTCCC-3′ and reverse 5′-GGACTGTTGTCAGTTGTC-3′. The averaged cycle threshold values of each reaction derived from the target gene, determined with LightCycler 480 System software (Roche), were normalized to GAPDH levels. Cycle threshold values were used to calculate relative mRNA expression by the ΔΔCt relative quantification method.

Chromatin immunoprecipitation assays

Chromatin immunoprecipitation (ChiP) analysis was done using ChiP Assay kit (Upstate Biotechnology) according to the manufacturer’s instructions. T cells (3 × 10^6) were used per immunoprecipitation Ab. The cells were fixed with 1% formaldehyde for 10 min, lysed, and sonicated. The DNA–protein complexes were immunoprecipitated with anti-p-CREB Ab (Upstate Biotechnology) as a control Ab (rabbit normal IgG; Santa Cruz Biotechnology), and, after a series of washing steps, the cross-linking was reversed, and the protein was digested with proteinase K (Qiagen). The DNA was extracted by the QIAquick PCR Purification kit (Qiagen). Immunoprecipitated and purified DNA was analyzed by PCR using the primers F (−468) and R (−83) described as above, which are specific for the human PP2Ac promoter and were used to amplify a fragment containing a CRE motif. The corresponding nonimmunoprecipitated DNA (input DNA) was also analyzed. PCR products were semiquantified using the same method as above in the methylation-specific PCR.

Statistics

Data are presented as mean value ± SEM. The paired two-tailed Student t test and the Pearson product moment correlation coefficient were used for statistical analysis. Statistical significance was defined as p < 0.05.
found them decreased in cells transfected with DNMTs (Fig. 1C). These results showed that DNMTs have an important role in promoting hypermethylation in the promoter region and silencing the methylation-sensitive gene PP2Ac.

Several studies have demonstrated that DNMT1 is reduced in SLE patients (25–27), but we confirmed this observation using T cells from SLE patients and corresponding control subjects. The demographics of the patients used in the experiments are all shown in Tables I and II. We divided the samples from patients into two groups: the high disease activity group included patients with an SLEDAI score of >6, and the low disease activity group included patients with an SLEDAI score of ≤6. Fig. 1D showed that T cells from patients with active disease have a reduced amount of DNMT1 compared with inactive patients or normal subjects. There was a negative correlation between SLEDAI and DNMT1 expression ($r = -0.398, p = 0.0192; n = 34$).

These data suggested that decreased levels of DNMT1 in SLE T cells may account for the global DNA hypomethylation and contribute to regulation and expression of the methylation-sensitive gene.
SLE T cells display a highly hypomethylated pattern around the CRE motif defined by the PP2Ac promoter

To investigate PP2Ac transcriptional mechanisms through epigenetic mechanisms, we focused on the essential regulatory region of this gene. As shown in Fig. 2A, the region that started at the −517 position from the translation initiation start site (ATG) was characterized by a high GC content and revealed the existence of several potential stable protein 1 transcription factor sites and a complete CRE motif located around the −238 position. In this region, there are 63 CpG. Among them, one of the CpGs is located at the center of the CRE motif (−238 position).

We first searched for differences in the DNA methylation pattern between T cells from three SLE patients and three matched control subjects. By bisulfite sequence analysis, both groups showed a global hypomethylated pattern; however, SLE T cells displayed a relatively lower methylation pattern than normal T cells, especially around the CRE motif shown in Fig. 2B and 2C. The total percentage of DNA methylated fragments in this region (−519 to +29) was significantly decreased in SLE T cells compared with normal T cells shown in Fig. 2D.

This method, although very useful in determining global gene methylation patterns, is limited when quantification is required. Therefore, we used a methylation-sensitive PCR to quantify the levels of DNA methylation at the CpG in the CRE motif (−238 position). Briefly, we used the methylation-sensitive restriction enzyme AatII, which recognizes only unmethylated CRE motifs, and applied PCR using two sets of primers to distinguish unmethylated and methylated status at this deoxycytosine (dC) in the CRE motif. A band can be detected only when deoxymethylcytosine exists in the CRE motif because it cannot be digested by AatII. A control band was generated by another set of primers defining an area of the PP2Ac promoter, which did not contain any AatII-sensitive motifs. We measured the densitometric intensity for each band, and the ratio of the methylation-sensitive

Table I. Patient demographics and treatment

<table>
<thead>
<tr>
<th>Age (y)</th>
<th>Race</th>
<th>Sex</th>
<th>SLEDAI</th>
<th>Predonisolone (mg)</th>
<th>Others</th>
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<td>17.5</td>
<td>M3</td>
</tr>
</tbody>
</table>

A, azathioprine (mg); C, cyclosporine (mg); Cyc, cyclophosphamide (i.v.); F, female; H, hydroxychloroquine (mg); M, mycophenolate mofetil (g); MTX, methotrexate (mg).

Table II. Time course of SLEDAI and treatment from nine different patients

<table>
<thead>
<tr>
<th>Patient No.</th>
<th>Age (y)</th>
<th>Race</th>
<th>Sex</th>
<th>Date</th>
<th>SLEDAI</th>
<th>Predonisolone (mg)</th>
<th>Others</th>
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<tbody>
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<td>M1</td>
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<td>African American</td>
<td>Female</td>
<td>02/11/2009</td>
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<td>M1.5</td>
</tr>
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<td>Female</td>
<td>04/16/2009</td>
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<td>5</td>
<td>M1</td>
</tr>
<tr>
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<td>H200 + Cyc</td>
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<td>Female</td>
<td>10/15/2008</td>
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</tr>
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<td>01/23/2009</td>
<td>10</td>
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</tbody>
</table>

aThis sample was excluded in prospective analysis in Fig. 6.

A, azathioprine (mg); C, cyclosporine (mg); Cyc, cyclophosphamide (i.v.); H, hydroxychloroquine (mg); M, mycophenolate mofetil (g); MTX, methotrexate (mg).
FIGURE 2. Global hypomethylation within the essential PP2Acα promoter region in T cells from SLE patients. A, Nucleotide sequence within bp −517/+29 of the 5′-flanking region of the human PP2Acα gene. The translation initiation codon, ATG, is indicated as +0. The major transcription factor is located at −211 position. Each primer sequence for round II in nested PCR is shown in italics. The essential promoter region for gene regulation, which we previously determined is located from −2280 to −2218, is shown with arrows. At the center, there is a complete CRE motif surrounded by dashed box where the transcription factor CREB/p-CREB can bind. Whole region qualifies as a CpG island using CpG finder at the European Bioinformatics Institute (http://www.ebi.ac.uk/). All dC in CpG included in this region are highlighted with underlining. Within this region, there are 63 dCs in CpG. Among them, a dC in CpG included CRE motif exists at −238 position.

B, One example of PP2Acα promoter methylation pattern in normal (upper panel) or SLE T cells (lower panel). T cells were isolated from a lupus patient and a matched control individual, and DNA was treated by sodium bisulfite. The region shown in Fig. 1A was amplified by PCR, cloned, and 10 colonies were picked up and sequenced from each subject. The fragment number is shown on the y-axis and the location of each CpG pair on the x-axis. Open circles, unmethylated cytosines; closed circles, methylated cytosines.

C, Summary of the promoter DNA methylation pattern in T cells isolated from three different normal individuals (left panel) or three SLE patients (right panel). The value of y-axis showed
product to the control was calculated to semiquantify DNA methylation status within the CRE of the promoter. As shown in Fig. 3A, T cells from SLE patients had significantly lower levels of DNA methylation at this nucleotide than those from healthy controls. This was especially true among patients with high (SLEDAI > 6) disease activity who had significantly lower methylation status compared with patients with low SLEDAI activity (≤ 6) and healthy controls. We could also find a moderate negative correlation between SLEDAI and DNA methylation level ($r = -0.352, p = 0.040; n = 34$).

In addition, we determined whether the expression levels of DNMT1 reflected DNA methylation levels at the PP2Ac promoter (Fig. 3B). The data show that increases in SLE disease activity result in reduction of DNMT1 expression and hypomethylation of the PP2Ac promoter, especially at the site that defines the CRE.

*p-CREB binding to the CRE motif in the PP2Ac promoter was stronger in lupus T cells than in normal T cells*

Next, we investigated predicted differences of p-CREB binding to the PP2Ac promoter in SLE and normal T cells. ChIP assays revealed that p-CREB bound to PP2Ac promoter more intensely in SLE T cells compared with normal T cells (Fig. 4). Previously, we had noted increased p-CREB binding to the PP2Ac promoter (area defining the CRE motif) in T cells treated with the DNA methylation inhibitor 5-azaC (33), suggesting that disease flares initiate a process that leads to inhibition of DNA methylation. In this study, we confirmed the same phenomena between SLE T cells and T cells treated with DNA methylation inhibitor.

The levels of the PP2Ac transcript are increased in T cells from patients with active SLE and reflects DNA methylation of CRE

Previously, we had determined that mRNA and protein levels of PP2Ac were higher in SLE T cells compared with normal T cells, yet we had failed to show a correlation with disease activity (29). In this study, we focused on the major isoform of PP2Ac, PP2Ac1, and re-examined the expression levels of its transcripts. As shown in Fig. 5A, the expression levels of PP2Ac mRNA were significantly higher in the patient group with a high SLEDAI score (> 6), but not in the group of patients with a low SLEDAI score (≤ 6) compared with normal controls. There was a positive correlation between SLEDAI and PP2Ac expression level ($r = 0.369, p = 0.0308; n = 34$). In addition, we noted a significant negative correlation between the levels of transcripts and the levels of DNA methylation (Fig. 5B). Our data, taken together, indicate that disease activity affects DNA methylation status within the PP2Ac promoter, which can result in the upregulation of its expression.

Prospective study of PP2Ac promoter methylation status in patients with SLE

Because our data pointed out that DNA hypomethylation is primarily observed in patients with active disease, we wanted to confirm this observation in the same patients as their disease activity changed over time. The demographics of nine patients used in this experiment are shown in Table II. We defined the time point at which disease activity was low as phase 1 (SLEDAI was ranged between 0 and 10, average; 1.78) and the time point when the disease activity was relatively high compared with phase 1 as phase 2 (SLEDAI ranged between 4 and 35; average: 15). The difference of SLEDAI between phase 1 and phase 2 was at least 4
levels decrease, whereas the levels of PP2Ac mRNA increase. (shown in Table II). The mean duration between phase 1 and phase 2 was 8.3 mo (ranged between 5 and 13 mo). We compared three independent parameters within same individuals. Two representative patients are shown in Fig. 6A, one experiencing increasing disease activity and the other going into remission. Cumulative data from nine patients (classifying them arbitrarily in phase 1 disease activity and the other going into remission. Cumulative data from nine patients (classifying them arbitrarily in phase 1 [low activity] and 2 [high activity]) are shown in Fig. 6B. Clearly, as disease activity increases, DNMT1 expression and methylation levels decrease, whereas the levels of PP2Ac mRNA increase.

Discussion

In this study, we present the first evidence, to our knowledge, that PP2Ac, a newly identified methylation-sensitive gene, is involved in the pathogenesis of SLE. Specifically, T cells from patients with active SLE display increased binding of the transcriptional enhancer p-CREB to the PP2Ac promoter-defined CRE motif because of its low methylation status, reflected by a decreased amount of DNMT1 transcripts. Importantly, disease activity variation correlated with the methylation pattern and PP2Ac expression.

Epigenetic mechanisms have been implicated in the pathogenesis of various disorders, including cancer, immunodeficiency, and autoimmunity (19, 24, 37). DNA methylation involves the covalent modification of the fifth carbon in cytosine residues of CG dinucleotides. Most CG pairs in mammalian DNA are methylated, with exceptions in areas that are located in or near the promoters of active genes, in which expression requires a chromatin configuration permissive of transcription factor binding (10, 38). Thus, abnormalities in DNA methylation could disturb the normal regulation of gene silencing, X chromosome inactivation, and lineage specification (10–13, 39–41). The relationship between DNA methylation and the immune system has been particularly well studied in SLE because it may account for several T cell abnormalities involved in the pathogenesis of the disease by providing useful clues on the mechanisms whereby environmental factors including UV light and drugs contribute to the expression of autoimmunity and related pathology (19, 26, 42–45).

DNMT1 is a major DNA methyltransferase responsible for DNA methylation following DNA replication during cell division (26, 27, 46), which has been found to be decreased in SLE T cells and claimed to be involved in the immunopathogenesis of the disease. Defective ERK signaling has been demonstrated to account for the decreased DNMT1 expression in SLE T cells (27). In addition, a defect in the phosphorylation of protein kinase Cδ, which is located downstream of ERK, results in DNA hypomethylation and overexpression of methylation-sensitive genes such as CD70 (47). SLE T cells have been reported to express higher amounts of microRNAs 21 and 148a, and these are known to downregulate DNMT1 (48). In addition, DNMT1 polymorphisms, V120L in exon 4, have been associated with the production of anti-La Ab in SLE patients (49).

Several genes involved in the DNA methylation pathway have been linked to the expression of SLE. RFX1, a transcription factor that affects DNA methylation and histone acetylation by recruiting the corepressors DNMT1 and histone deacetylase 1 to the promoters of methylation-sensitive genes, was reported to be decreased in SLE T cells (50). Gene polymorphisms of methionine
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A

FIGURE 6. Prospective analysis of the levels of DNA methylation in the promoter and transcript levels of DNMT1 and PP2Ac. A DNA methylation and transcripts of DNMT1 and PP2Ac were assessed in nine individuals prospectively. The left panel (patient 7 in Table II) is one example of flare during the course. The right panel (patient 9 in Table II) is also the example of well controlled by treatment. The quantification of DNA methylation in the promoter was conducted in a similar method as shown in Figs. 1 and 3. The ratio of methylation band (upper band, M) to control band (lower band, C) represented by lines (right y-axis) in the graph and the change of each transcript level was shown by bars (right y-axis; PP2Ac, white bar; DNMT1, black bar).

B. We defined relatively inactive time point as a phase 1 and active time point as a phase 2. The difference of SLEDAI between phase 1 and phase 2 was at least 4. The demographics of all patients used this experiment are shown in Table II. Each parameter was measured at two time points and set as 1.0 at phase 1. DNMT1 transcripts level (left panel) and DNA methylation level (middle panel) were significantly decreased when disease was active. PP2Ac transcript levels (right panel) displayed the opposite trend. The results represent the mean ± SEM of nine independent experiments. *p < 0.0001 (left), *p < 0.0001 (middle), *p = 0.00012 (right).

DNA methylase (30–32). PP2Ac has two isoforms, a catalytic regulatory subunit (B subunit) to form a heterotrimeric holenzyme (30–32). PP2Ac has two isoforms, a catalytic subunit and b regulatory subunit (A subunit). To gain full activity toward serine/threonine phosphatase with complex composition and is involved in many essential aspects of cell function. The heterodimeric PP2A core enzyme consists of a well-conserved 36-kDa catalytic subunit (C subunit; PP2Ac) and a 65-kDa scaffold subunit (A subunit). To gain full activity toward specific substrates, the PP2A core enzyme associates with a variable regulatory subunit (B subunit) to form a heterotrimeric holoenzyme (30–32). PP2Ac has two isoforms, α and β, but α represents the major isoform because of the evidence that the activity of the PP2Aα isoform (60). The PP2Aα gene is composed of seven exons and six introns encoded on chromosome 5q23-q31. It is characterized by an extremely GC-rich sequence...
and the lack of TATA and CCAAT boxes that are frequently found in many housekeeping genes (61). The expression of PP2Ac is tightly controlled through autoregulation to ensure the presence of relatively constant levels of PP2Ac (62). One mechanism of this autoregulation involves p-CREB, which regulating gene expression and is also dephosphorylated by PP2Ac itself (34, 63, 64). However, the autoregulation of PP2Ac appeared to be disturbed in T cells from SLE patients because the expression levels of this molecule are significantly higher in SLE T cells than in normal T cells. The control of the expression of PP2Ac levels in SLE T cells is broken at the methylation level of the CRE motif of its promoter. In addition, because PP2A can dephosphorylate p-ERK and p-JNK, which control DNMT1 expression, it may lead to further positive regulation of itself (positive feedback) (65). We previously reported that total PP2Ac (PP2Ac and PP2Acβ isoforms) is increased in SLE T cells compared with T cells from healthy individuals; yet, we had failed to find a correlation with disease activity. In the current study, we have focused on the regulation of the promoter activity in the PP2Ac, the major isoform of the enzyme, and we have recorded its levels rather than total levels of PP2Ac. The fact that the levels of PP2Ac correlate with disease activity suggests the importance of this isoform in the expression of the disease and that our previous data (29) were confined by the indiscriminate determination of both isoforms together. In addition, in the current study, we used mRNA samples to examine the correlation between expression levels of PP2Ac and disease activity because we focused on the regulation of the transcription of the PP2Ac gene rather than on the translation of the gene. The regulation of PP2Ac mRNA translation is still unclear and remains to be investigated fully in future (29). In this work, we demonstrated that abnormal hypomethylation of this promoter in lupus T cells allows the overexpression of this molecule by increasing accessibility of p-CREB to the CRE motif in the promoter.

In conclusion, we presented the evidence that hypomethylation of the CRE site of the PP2Ac promoter enables ample binding of p-CREB, which results in increased expression of PP2Ac in SLE T cells. Our results add PP2Ac to the list of genes that are altered epigenetically in patients with SLE. The fact that PP2Ac promoter methylation paralleled disease activity urges a larger prospective study to explore its potential to serve as a disease bio-marker.

Disclosures

The authors have no financial conflicts of interest.

References