Development of a unique epigenetic signature during \textit{in vivo} Th17 differentiation

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ABSTRACT

Activated naive CD4\textsuperscript{+} T cells are highly plastic cells that can differentiate into various T helper (Th) cell fates characterized by the expression of effector cytokines like IFN-\(\gamma\) (Th1), IL-4 (Th2) or IL-17A (Th17). Although previous studies have demonstrated that epigenetic mechanisms including DNA demethylation can stabilize effector cytokine expression, a comprehensive analysis of the changes in the DNA methylation pattern during differentiation of naive T cells into Th cell subsets is lacking. Hence, we here performed a genome-wide methylome analysis of \textit{ex vivo} isolated naive CD4\textsuperscript{+} T cells, Th1 and Th17 cells. We could demonstrate that naive CD4\textsuperscript{+} T cells share more demethylated regions with Th17 cells when compared to Th1 cells, and that overall Th17 cells display the highest number of demethylated regions, findings which are in line with the previously reported plasticity of Th17 cells. We could identify seven regions located in \textit{Il17a}, Zfp362, Ccr6, Acsbg1, Dpp4, Rora and Dclk1 showing pronounced demethylation selectively in \textit{ex vivo} isolated Th17 cells when compared to other \textit{ex vivo} isolated Th cell subsets and \textit{in vitro} generated Th17 cells, suggesting that this unique epigenetic signature allows identifying and functionally characterizing \textit{in vivo} generated Th17 cells.

INTRODUCTION

After egress from the thymus, naive CD4\textsuperscript{+} T cells circulate through secondary lymphoid organs via the blood stream and lymphatics. Unless being stimulated, these cells remain in a naive state. However, activation by antigen-presenting cells (APC) offering their cognate antigen plus appropriate co-stimulatory signals initiates a differentiation program, leading to the development of highly specialized T helper (Th) cell lineages (1). Initially, two subsets named Th1 and Th2 were identified (2,3), which are involved in the induction of cellular and humoral immune responses to eliminate intracellular and extracellular pathogens, respectively. Th1 cells are generated in a microenvironment containing the cytokines interleukin (IL)-12 and interferon-\(\gamma\) (IFN-\(\gamma\)), which causes the upregulation of the lineage specification factor T-bet and finally results in the expression of high levels of the effector cytokine IFN-\(\gamma\) at the end of the differentiation process (4). In contrast, Th2 differentiation is initiated via triggering of the IL-4 receptor or via Notch-driven signals (5). After upregulation of the lineage specification factor GATA3, Th2 cells start to produce the effector cytokines IL-4, IL-5 and IL-13. More recently, Th17 cells were identified as a novel Th cell subset (6,7) that is regulated by the transcription factors, ROR\(\gamma\)t and ROR\(\alpha\) (8). Th17 cells secrete several cytokines, including IL-17A, IL-17F and granulocyte-macrophage colony-stimulating factor (GM-CSF), are involved in the defence of extracellular bacterial infections and together with Th1 cells can cause autoimmune disorders (9,10).

Fully differentiated Th1 and Th2 cells show a remarkable memory of their cytokine expression patterns (11). Detailed studies of the corresponding cytokine and lineage specification factor loci revealed that this stability is achieved by epigenetic processes (12). In Th1 cells, IFN-\(\gamma\) expression is promoted by permissive histone modifications and DNA demethylation of \textit{Ifng} and \textit{Tbx21} (13–18), whereas expression of the Th2-specific gene cluster (\textit{Il4}, \textit{Il5}, \textit{Il13} and \textit{Rad50}) is suppressed by repressive histone modifications as well as DNA methylation (16,19). In contrast, Th2 cells display permissive histone modifications and DNA demethylation at the Th2-specific gene cluster as well as repressive histone modifications and DNA methylation of \textit{Ifng} and \textit{Tbx21} (16,20–22). Similarly, in Th17 cells the promoter regions of \textit{Il17a}, \textit{Il17f} and \textit{Rora} are associated with permissive histone modifications and show signs of pronounced

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DNA demethylation (16,17,23–25), which is in line with the reported stability of IL-17A expression in ex vivo isolated Th17 cells (26). However, in contrast to Th1 and Th2 cells, where the differentiation from naive T cells is considered to be an irreversible event, accumulating evidence suggests that Th17 cells have a greater degree of flexibility in their differentiation options and are more plastic (27). Particularly under inflammatory conditions, Th17 cells can further differentiate and switch toward Th1-and Th2-like cells (co)expressing IFN-γ and IL-4, respectively (28–33).

Although genome-wide histone modification maps of naive CD4+ T cells and in vitro generated Th cell subsets were previously generated to better understand the complexity of T cell differentiation (16), a global analysis of epigenetic changes at the DNA methylation level during these processes is still missing. Thus, we here performed a genome-wide methyleome analysis of naive CD4+ T cells, Th1 and Th17 cells. Since previous studies have revealed significant differences between the methylomes of ex vivo isolated Foxp3+ regulatory T cells (Tregs) and in vitro generated, TGF-β-induced Tregs (34,35), we solely used ex vivo isolated Th cell subsets for the epigenetic profiling. While we could demonstrate that the methyleome of naive CD4+ T cells shows closer similarity with Th17 cells when compared to Th1 cells, we also observed that Th17 cells display an even increased number of demethylated regions when compared to naive CD4+ T cells, suggesting that epigenetic processes at the DNA methylation level control the high plasticity of Th17 cells. Seven Th17-specific epigenetic signature genes could be identified, showing pronounced demethylation only in ex vivo isolated Th17 cells, but neither in other ex vivo isolated Th cell subsets nor in in vitro generated Th17 cells, suggesting that these genes play an important role for the functional properties of in vivo generated Th17 cells.

MATERIALS AND METHODS

Mice

Aged female Balb/c mice (>6 months) or female C57Bl/6 mice (6–8 weeks old) were purchased from Charles River and Janvier, respectively. Foxp3-IREs-mRFP (FIR) mice (36) (6–12 weeks old) were bred in-house (Helmholtz Centre for Infection Research, Braunschweig, Germany). All animal experiments were performed under specific pathogen-free conditions and in accordance with institutional, state and federal guidelines.

Flow cytometry

Flow cytometric analyses were performed on a LSR II or LSR Fortessa (BD Biosciences). Dead cells were excluded from analyses by using LIVE/DEAD fixable Blue dead cell stain kit (Invitrogen) according to the manufacturer's instructions. Data were analyzed using the FlowJo software (Tree Star, Inc.).

Ex vivo isolation of naïve T cells, cytokine-producing Th cell subsets and Tregs

CD4+ T cells were enriched from spleen and lymph nodes of aged female Balb/c mice by magnetic-activated cell sorting (MACS) using anti-CD4 MicroBeads and the autoMACS magnetic separation system (Miltenyi Biotec). Enriched CD4+ T cells were stimulated for 3 h with phorbol 12-myristate 13-acetate (PMA; 10 ng/ml, Sigma-Aldrich) and ionomycin (500 ng/ml, Sigma-Aldrich), followed by the labeling of IL-17A and/or IFN-γ-secreting cells using the IL-17A and IFN-γ secretion assay kit (Miltenyi Biotec) according to the manufacturer’s instructions. Subsequently, the cells were stained with fluorochrome-conjugated anti-CD3 (145-2C11), CD4 (RM4-5) and CD45RB (C363.16A) antibodies. Th17 cells (CD3+CD4+CD45RBlowIL-17A+IFN-γ−/−), Th1 cells (CD3+CD4+CD45RBlowIL-17A+IFN-γ−/−), Th-mm cells (CD3+CD4+CD45RBlowIL-17A+IFN-γ−/−) and naive CD4+ T cells (CD3+CD4+CD45RBhighIL-17A+IFN-γ−/−) were sorted by fluorescence-activated cell sorting (FACS) on a FACSArria II (BD Biosciences). Purities of sorted populations ranged between 97% and 99%. Tregs were sorted from the same source as CD3+CD4+CD25high cells (anti-CD25 antibody PC61.5) and subsequently stimulated with the same concentration of PMA/ionomycin for 3 h. Treg purity was confirmed by intracellular staining for Foxp3 (FJK-16S), IL-17A (eBio17B7) and IFN-γ (XMGl.2) using the Foxp3 transcription factor staining buffer set (eBioscience).

Ex vivo isolation of immune cell subsets

CD11b+ or CD11b− cells were separated from spleen and lymph nodes of aged female Balb/c mice using APC-conjugated anti-CD11b (M1/70), anti-APC MicroBeads and the autoMACS magnetic separation system (Miltenyi Biotec). MACS-separated CD11b+ cells were labeled with antibodies against CD3 (145-2C11), CD4 (RM4-5), CD8 (53–67), B220 (RA3–6B2), γδTCR (eBioGL3) and sorted into B cells (CD3−B220−), CD8+ T cells (CD3+B220−CD4−CD8+), CD4+ T cells (CD3+CD4+CD8−) and γδ T cells (CD3+CD4−CD8−γδTCR−). MACS-separated CD11b+ cells were stained with antibodies against CD11b, CD11c (N418), CD49b (DX5), Ly6C (HK1.4), Ly6G (1A8), F4/80 (BM8), CD3, CD19 (MB19–1) and sorted into conventional dendritic cells (cDCs) (CD3−CD19−CD11bdimCD11c+), neutrophils (CD3−CD19−CD11b+CD11c+Ly6G−), monocytes (CD3−CD19−CD11b+CD11c−Ly6G+Ly6C+), macrophages (CD3−CD19−CD11b+CD11c−Ly6G−Ly6C−F4/80+), and natural killer (NK) cells (CD3−CD19−CD11b+CD11c−Ly6G−Ly6C−F4/80−CD49b+).

In vitro generation of Th cell subsets

Naive CD4+ T cells (CD4+CD25−CD62L+) were isolated from spleen and lymph nodes of female C57Bl/6 mice. Briefly, CD25+ cells, labeled with anti-CD25-APC (PC61.5) and anti-APC MicroBeads (Miltenyi Biotec), were magnetically removed from cell suspension by using the autoMACS magnetic separation system (Miltenyi Biotec). CD4+ cells were isolated from the CD25− population by magnetic sorting, using anti-CD4-FITC (RM4-5) and anti-FITC MultiSort MicroBeads (Miltenyi Biotec). After release of the
MicroBeads from the positive population, addition of anti-CD62L. MicroBeads and sorting via the autoMACS magnetic separation system resulted in CD4⁺/CD25⁻/CD62L⁻ naive T cells. Differentiation of naive CD4⁺ T cells into Th1 or Th17 cells was performed as recently described (37). For the in vitro differentiation into induced Tregs (iTregs), sorted naive CD4⁺ T cells were stimulated with plate-bound anti-CD3 (145-2C11; 5 μg/ml) antibody in the presence of soluble anti-CD28 antibody (37.51; 1 μg/ml), recombinant human IL-2 (200 U/ml; Roche) and recombinant TGF-β (1 ng/ml; Peprotech). IL-2 (200 U/ml) was added every second day to the culture. On day 4, cells were harvested and dead cells were removed as described (37). An aliquot of Th1 and Th17 cells was stimulated for 4 h in the presence of PMA (10 ng/ml) and ionomycin (500 ng/ml) with addition of Brefeldin A (10 μg/ml; Sigma-Aldrich) after 2 h. Th1, Th17 cells and an aliquot of iTregs were fixed and permeabilized as described above and analyzed for IL-17A, IFN-γ and Foxp3 expression by flow cytometry. The phenotype of in vitro generated Th1 cells, Th17 cells and iTregs is shown in Supplementary Figure S1.

Preparation of genomic DNA

Genomic DNA was isolated from ex vivo sorted or in vitro cultivated T cells, as well as other ex vivo isolated immune cell subsets by using the NucleoSpin® Tissue XS kit (Macherey-Nagel) or DNA/RNA AllPrep Kit (Qiagen) according to the manufacturer’s protocols.

Methyl-CpG binding domain protein sequencing (MBD-seq)

Genomic DNA for MBD-seq was obtained from 168 mice and several independently performed FACS experiments. Material from the individual sort was pooled and the MBD-seq was performed once at NXT-DX (Gent, Belgium). Genomic DNA (3 μg) was fragmented by using a Covaris S2 system (130 μl volume, duty cycle 10%, intensity 5, 200 cycles per burst during 190 s) to obtain fragments with an average length of 200 base pairs (bp). The size of the fragments was controlled with an Agilent 2100 system (Agilent Technologies). Methylated DNA was enriched by using a MethylCap kit (Diagenode) according to the manufacturer’s protocol. The concentration of fragmented and captured DNA was determined on a Fluorost Optima plate reader (BMG Labtech) with the Quant-iTTM Picogreen® dsDNA assay kit (Invitrogen). We used a modified ‘multiplexed paired end ChIP protocol’ (Illumina) to generate a library for next-generation sequencing from 250 ng precipitated DNA. Briefly, we used the DNA Sample Prep Master Mix Set (New England Biolabs) in combination with the Multiplexing Sample Preparation Oligo Kit (Illumina). The preparation was performed on an Apollo 324 (IntegenX) with PrepX DNA or PrepX-32-DNA Library Kit according to the manufacturer’s protocol. Small DNA fragments were removed from the samples by separation on an agarose gel. Fragments between 250 and 350 bp were excised and purified by using a Gel Extraction Kit (Qia-gen). Samples were adjusted to 10 nM, pooled according to the index and sequenced with an Illumina HiSeq 2000. The FASTQ sequence reads were generated using the Illumina Casava pipeline version 1.8.0. Reads containing adapters and/or Phix control signals were removed. The paired end 51 bp sequence reads were mapped using the bowtie (v0.12.7) software (38). The bowtie parameters were set to 0 mismatches in the seed (first 28 nucleotides). Differences in sequencing depth and mapping efficiency among the MBD-seq samples were compensated by using the library size normalization (39). Every value is normalized on the total amount of mapped reads. Only uniquely mapped reads were retained and both paired end-sequencing reads must be located within 400 bp from each other on the mouse reference genome build NCBI37/mm9. DNA fragments were constructed as a genomic DNA sequence bounded by a read pair. Identical fragments, i.e. those starting and ending at the same positions, were classified as polymerase chain reaction (PCR) artifacts and removed. Overlapping fragments were joined into a larger fragment, called region and the maximum ‘height’ of overlapping fragments represent the activity value for the region. For example, fragments within the Xist gene in naive T cells shown in Figure 4A have maximum activity of two, but in Th17 cells it is four. The activity value was used to rank the identified regions according to their DNA methylation.

In silico analyses

Classification of DNA regions by methylation status was performed as follows. Let \( a_{i,j} \) be an activity value that is equal to the count of overlapped fragments for a DNA region \( j \) in \( i \)th cell population \((i = 1, 2, 3, 4) \) and \( N_{CPG}^{i,j} \) be a number of CpG motifs contained in that region. Throughout this work, the numbering of cell populations will be: 1 = Th17, 2 = Th1, 3 = Th-mem and 4 = Th-naive. Thus, a methylation status of any DNA region in these cell subsets can be described by a quadruple \((a_{1,j}, a_{2,j}, a_{3,j}, a_{4,j})\). We denote as \( C(i, N_{CPG}^{i,j}, a) \) the number of regions in the cell subset \( i \) that have \( N_{CPG}^{i,j} \) CpG motifs and showed an activity value equal to \( a \):

\[
C(i, N_{CPG}^{i,j}, a) = \#(DNA region j|N_{CPG}^{i,j} = N_{CPG}^{i,j} \text{ and } a_{i,j} = a).
\]

Then the empirical point probability (probability density function) of activity values is given by

\[
\rho(i, N_{CPG}^{i,j}, a) = C(i, N_{CPG}^{i,j}, a) / \sum_{a=0,\ldots,\infty} C(i, N_{CPG}^{i,j}, a)
\]

The empirical probability distribution function (cumulative distribution) is given by

\[
P(i, N_{CPG}^{i,j}, a) = \sum_{x=0,\ldots,a} \rho(i, N_{CPG}^{i,j}, x)
\]

Several example distributions are presented in Figure 2A. We define that a DNA fragment is in a demethylated state in cell population \( i \) if the probability \( P(i, N_{CPG}^{i,j}, a_{i,j}) \) is below a threshold \( P_{Thr} \). If this probability is above 1-\( P_{Thr} \), the fragment is supposed to be in methylated state. In other cases \((P_{Thr} < P(i, N_{CPG}^{i,j}, a_{i,j}) < 1-P_{Thr})\) a DNA fragment will have an undefined state.
Methylation sensitive high-resolution melting (MS-HRM) analysis

Genomic DNA from ex vivo isolated T cell subsets was bisulfite converted by using the EZ DNA Methylation Kit (Zymo Research). Candidate regions showing a high activity from MBD-seq in naive T cells, Th1 cells and Tregs, but not in Th17 cells were chosen and primers were designed (Supplementary Table S1). In a subsequent qPCR on a LightCycler®480 System (Roche), 10 ng of converted DNA was mixed with 12.5 μl of 2× EpiTect HRM PCR Master Mix (Qiagen), 1 μl of 25 mM MgCl₂, 9.5 pmol each of forward and reverse primers in a final volume of 25 μl. After the amplification phase (95°C for 15 min; 45 cycles: 95°C for 30 s, 55°C-60°C for 1 min, 72°C for 1 min), the HRM analysis was performed between 65°C and 95°C with a final cooling step at 40°C for 1 s. Melting curves were analyzed by the Gene Scanning Analysis Software Module (Roche). According to the manufacturer’s recommendations, the relative signal differences between various samples were plotted after normalizing the raw melting curve data and shifting the normalized curves along a temperature axis.

Pyrosequencing

Genomic DNA from ex vivo isolated or in vitro cultivated T cells, as well as other ex vivo isolated immune cell subsets was bisulfite converted by using the EZ DNA Methylation Kit (Zymo Research). Validated candidate regions from MS-HRM analysis were amplified by PCR containing 10 ng of bisulfite-converted genomic DNA, HotStar Taq PCR buffer (Qiagen), 1 U HotStar Taq DNA polymerase, 2.5 mM MgCl₂ and 0.38 μM each of forward and reverse primers (Supplementary Table S1) in a final volume of 50 μl (95°C for 15 min; 50 cycles: 95°C for 30 s, 57°C for 1 min, 72°C for 1 min; 72°C for 7 min). The PCR product was analyzed by gel electrophoresis. 20-40 μl of the PCR product, Pyromark Gold Q96 reagents (Qiagen), Pyromark buffers (Qiagen), Streptavidin Sepharose (GE Healthcare) and sequencing primers (Supplementary Table S1) were used for pyrosequencing on a PSQ96MA (Qiagen) according to the manufacturer’s protocol. Significance of methylation rate differences between compared subsets was calculated using Prism (GraphPad Software) and a two-way ANOVA with Bonferroni’s multiple comparisons test. Locations of analyzed CpG motifs in mouse genome GRC38m are listed in Supplementary Table S2.

RNA microarray hybridization and analysis

RNA was isolated using the DNA/RNA AllPrep Kit (Qiagen). Quality and integrity of total RNA was controlled on an Agilent 2100 system (Agilent Technologies). Note that 100 ng of total RNA was applied for Cy3-labeling reaction using the one color Quick Amp Labeling protocol (Agilent Technologies). Labeled cRNA was hybridized to Agilent’s mouse 4 × 44k microarrays for 16 h at 68°C and scanned using the Agilent Microarray Scanner. Expression values were calculated by the software package Feature Extraction 10.5.1.1 (Agilent Technologies). Statistical analysis of the expression data was performed using the Gene Spring Software package (Agilent Technologies).

Accession codes

Data sets generated for this study are available from GEO under accession numbers GSE45911 and GSE58152.

RESULTS

DNA methylation pattern of ex vivo isolated naive T cells, Th1 cells and Th17 cells

To obtain a complete overview of the epigenetic changes during Th cell differentiation, we first sought to generate comprehensive profiles of genome-wide DNA methylation patterns of naive CD4⁺ T cells, Th1 cells and Th17 cells by methyl-CpG binding domain protein (MBD) sequencing (MBD-seq). For this study, solely ex vivo isolated CD4⁺ T cell subsets were analyzed since previously published data on Foxp3⁺ Tregs have revealed significant differences between the methylosomes of ex vivo and in vitro generated Tregs (34,35). The CD4⁺ T cell subsets were isolated from secondary lymphoid organs of aged BALB/c mice, harboring a reasonable high frequency of CD45RBlow memory CD4⁺ T cells that contain around 1% IL-17A-producing Th17 cells and around 16% IFN-γ-producing Th1 cells (Figure 1A). We did not observe any IL-17A/IFN-γ-double
producing cells in the secondary lymphoid organs of the healthy donor mice. Th1 cells, Th17 cells, naive CD4+ T cells (CD45RBhigh) and IFN-γ− IL-17A− CD45RBlow CD4+ T cells consisting of a mixture of non-Th1/Th17 memory CD4+ T cells (Th-mem) were sorted to high purity (Figure 1B). Genomic DNA from sorted T cell subsets was fragmented and regions containing methylated CpG motifs were enriched by precipitation using MBD. The resulting DNA fragments were used to generate a library that was subjected to next-generation sequencing. In total 1 497 870 DNA regions (combined overlapping DNA fragments) were identified covering 358 Mb or 10.3% of the genome. Counts of overlapping fragments represented the methylation of a DNA region and were designated as activity (ai,j).

As expected, the mean activity in all T cell subsets increased with an accumulation of CpG motifs (Supplementary Figure S2). However, we did not observe a strict linear relationship, but rather logarithmic shaped curves with a similar course. For further analyses, the identified regions for each T cell population were grouped according to their CpG numbers. Plotting the distribution of activity values in these groups revealed a bell-shaped curve for fragments containing more than three CpG motifs (examplified for Th17 cells in Figure 2A). Most of the fragments with up to three CpG motifs did not show any activity. Therefore, fragments with CpG counts up to three were excluded from the analysis.

Due to the wide range of activity values of sequenced DNA fragments and its dependence from the number of CpG motifs contained within, we decided to associate a probability with each DNA region that will represent its methylated or demethylated state. As such probability, we took the empirical probability distribution function \( P(i, N_{CpG}, a_{i,j}) \). By setting a threshold value for the probability \( P_{Thr} \), we classified the regions as demethylated, methylated or undefined, depending on whether \( P(i, N_{CpG}, a_{i,j}) \) was below \( P_{Thr} \), above \( 1-P_{Thr} \) or between these values. Thus, the probability \( P(i, N_{CpG}, a_{i,j}) \) served to rank DNA regions, where top and bottom ranking were then considered as methylated or demethylated, respectively. Thereby, the differences introduced by CpG counts and experimental settings between T cell subsets were taken into account and absolute values of activity were of no importance for further analysis. We calculated the number of differently methylated regions (DMRs) among the T cell populations for several \( P_{Thr} \). The bars in Figure 2B indicate the percentage of all regions that are methylated in one T cell population, and demethylated in the other three. A non-stringent probability threshold of 50% led to similar frequencies of uniquely methylated DNA fragments. In contrast, a stringent probability threshold of 10% drastically minimized the frequencies of uniquely methylated regions within all subsets. By setting the probability threshold to 25% we obtained the largest differences in frequencies and numbers between naive T cells with 1%, Th-mem cells with 1.6%, Th1 cells with 5.3% and Th17 cells with 1.2%. In summary, methylated regions from ex vivo isolated Th subsets displayed a different activity depending on the number of CpG motifs. Therefore, we classified the sequenced DNA fragments into groups, ranked the fragments within groups and identified the largest differences between cell lines when 25% top and bottom ranking were considered.

**Number of demethylated regions increases upon Th17 cell differentiation**

A mapping of all demethylated regions being identified in the T cell subsets analyzed revealed that only very small fractions were found within promoter and 3′ regions and within exons. The vast majority of demethylated regions was found in introns and intergenic regions (Supplementary Figure S3). An initial global inspection of the methylomes already revealed striking differences between Th1 and Th17 cells. Whereas Th1 cells showed a decreased number of demethylated regions (6862) compared to naive T cells (12 710), an increased number of demethylated regions was observed for Th17 cells (17 384) (Figure 3A). Only a rather low number of demethylated regions was found to overlap between naive T cells and Th1 cells (2054), and the
Identification of a Th17-specific epigenetic signature

After having obtained a global overview of the epigenetic changes during Th cell differentiation and having demonstrated that Th17 cells harbor a unique methylome, we next sought to describe the epigenome of Th17 cells in more detail with the aim to identify Th17-specific epigenetic signature genes. In light of the recently reported developmental and functional links between the Treg and Th17 cell lineages (46), we sought to exclude methylation patterns also present in Foxp3+ Tregs. Thus, MBD-seq data from ex vivo isolated Tregs (Supplementary Figure S4) generated as described above were included into the search for Th17-specific demethylated regions.

We first inspected control regions to confirm the validity of the generated MBD-seq data sets. The 5’ end of the Xist allele on the active X chromosome is known to be fully methylated in any somatic tissue (47), and a CpG island in the promoter of integrin alpha 4 (Igα4), although being inactivated by methylation in gastric cancer cells (48), is not regulated in T cells by methylation (unpublished observation). Accordingly, valid signals for Xist and no valid signals for Igα4 were detected in all T cell subsets (Figure 4A).

Next, we analyzed the methylation status of the Ifng and Il17a promoter known to be selectively demethylated in Th1 and Th17 cells, respectively (12, 14, 17, 18, 23, 24, 49). Here, we observed T cell subset-specific methylation patterns with valid MBD-seq signals for the Ifng and Il17a promoter being present in all samples except Th1 and Th17 cells, respectively (Figure 4A). By performing MS-HRM analyses (50), the methylation patterns of the control regions Xist, Igα4,
II17a and Ifng in the different T cell subsets could be validated (Figure 4B). Thus, the inspection of the control regions confirmed the validity of the generated MBD-seq data sets.

Next, we screened the MBD-seq data for regions showing valid signals in all samples except Th17 cells to identify Th17-specific demethylated regions. Note that 195 candidate regions were tested by MS-HRM analyses (data not shown). Highest melting-curve differences between Th17 cells and all other T cell subsets were observed for regions within Zfp362, Ccr6, Acsbg1, Dpp4, Rora and Dclk1 (Figure 5). Most of these regions are located in introns, except for the region from Acsbg1, which covers transcribed exons, and from Ccr6 that spans promoter, start site and the first non-translated exon. To get more detailed information on the methylation status of individual CpG motifs, we performed pyrosequencing for the regions within II17a, Zfp362, Ccr6, Acsbg1, Dpp4, Rora and Dclk1 and could observe a more pronounced demethylation in Th17 cells when compared to naive T cells, Th1 cells and Tregs (Figure 6A, Supplementary Figures S5 and Supplementary Table S3). Interestingly, the regions within II17a, Zfp362, Ccr6, Dpp4 and Rora showed a more or less homogeneous demethylation of the majority of CpG motifs analyzed, whereas the demethylation within Acsbg1 and Dclk1 is restricted to a subpart of the region or even to a single CpG motif, respectively. It is worth mentioning that also ex vivo isolated Th1 cells and Tregs showed signs of demethylation in some of the regions analyzed, but less pronounced when compared to Th17 cells and restricted to individual CpG motifs only (Figure 6A, Supplementary Figure S5 and Supplementary Table S3). Interestingly, in vitro generated Th17 cells did not show any demethylation within Ccr6, Acsbg1, Dpp4, Rora and Dclk1 when compared to naive T cells (Figure 6A and B and Supplementary Table S3). Only II17a and Zfp362 showed some signs of demethylation albeit less pronounced when compared to ex vivo isolated Th17 cells (II17a) or restricted to only subparts of the region (Zfp362). In vitro generated Th1 cells and Tregs, which were analyzed as controls, showed a methylation pattern comparable to naive T cells in any of the regions being analyzed (Figure 6A and B and Supplementary Table S3). Together, these data suggest that

![Figure 5. Candidate regions Zfp362, Ccr6, Acsbg1, Dpp4, Rora and Dclk1 are differentially methylated. Locus organization and CpG motif distribution are shown for six candidate regions. The methylation status of marked CpG motifs (black) was studied by MS-HRM analyses. Relative signal difference at each temperature was calculated and plotted by comparing differences between the melting curves of each subset. Data from one out of two independently performed experiments are depicted.](https://academic.oup.com/nar/article-abstract/43/3/1537/2411744/1543)

![Figure 6. Detailed methylation analysis of Th17-specific epigenetic signature genes in ex vivo isolated and in vitro generated T cell subsets by pyrosequencing. Detailed analysis of the methylation status of the candidate DMRs was performed by pyrosequencing using genomic DNA from the indicated (A) ex vivo isolated and (B) in vitro generated T cell subsets. The methylation rates were translated into a color code from yellow (0%) via green (50%) up to blue (100%). Each rectangle represents the methylation of one CpG motif. Data from three independently performed cell sorts and cultures are depicted.](https://academic.oup.com/nar/article-abstract/43/3/1537/2411744/1543)
genetic signature despite some similarities with γδ T cells is specific to \textit{ex vivo} isolated Th17 cells.

**DISCUSSION**

Differentiation of naive T cells into Th cell subsets results in the acquisition of highly specialized functional properties characterized by the expression of unique effector cytokines. It is well known that epigenetic modifications of the corresponding effector cytokine gene loci ensure long-term stability of the respective Th cell phenotypes, however, a comprehensive picture of the epigenetic modifications occurring during Th cell differentiation was by and large lacking. Therefore, we here performed a global analysis of changes at the DNA methylation level upon differentiation of naive CD4+ T cells into IFN-γ-secreting Th1 cells and IL-17A-secreting Th17 cells. Genome-wide MBD-seq data were generated from \textit{ex vivo} isolated T cell subsets and revealed a unique phenotype of Th17 cells harboring the highest number of demethylated regions and showing a larger overlap with naive T cells when compared to Th1 cells. A detailed inspection of the MBD-seq data resulted in the identification of seven CpG-rich regions located in \textit{Il17a}, \textit{Zfp362}, \textit{Ccr6}, \textit{Acsbg1}, \textit{Dpp4}, \textit{Rora} and \textit{Dclk1} that show more pronounced demethylation in \textit{ex vivo} isolated Th17 cells when compared to any other T cell subset. This Th17-specific epigenetic signature allows identifying and functionally characterizing \textit{in vivo} generated Th17 cells.

Interestingly, an initial global assessment of the MBD-seq data revealed that the vast majority of demethylated regions across all T cell subsets mapped to introns and intergenic regions, whereas only a low number was found in promoters. These findings are in line with results from a recent study, in which global changes at the DNA methylation level during differentiation of TCR-transgenic naive T cells into memory T cells were analyzed using a methyl-sensitive cut counting method (51). Also in that study, the majority of DMRs were found to be located in introns, suggesting that epigenetic modifications occurring during Th cell differentiation more frequently affect enhancer rather than promoter activity of immunologically relevant genes. Despite these similarities the study by Hashimoto \textit{et al.} and the present study also exhibit some controversies: Although the authors did not subdivide the memory T cell compartment into different Th cell subsets according to their cytokine expression pattern, but rather analyzed the bulk CD25−CD69−CD127\textit{high}CD4+memory T cell pool (51), this cell population was largely dominated by cells harboring a Th1 phenotype (92% TNF-α+ and 43% IFN-γ+ cells). Nevertheless, they observed an overall increase in the number of demethylated regions upon differentiation of naive T cells into memory T cells (51), whereas in the present study \textit{ex vivo} isolated Th1 cells showed exactly the opposite picture with a substantial decrease in the number of demethylated regions when compared to naive T cells. These somewhat contradicting results might be explained by the different sources of memory T cells used for the global DNA methylation analyses in these two studies. In the present study, cytokine-producing memory T cells were isolated directly \textit{ex vivo}. In contrast, Hashimoto \textit{et al.}
first stimulated naive T cells for 5 days in vitro, followed by an adoptive transfer into recipient mice, from which memory T cells were isolated 4 weeks later (51). It is tempting to speculate that the initial in vitro stimulation step might have resulted in the formation of a methylome that differs from the DNA methylation pattern found in ex vivo isolated Th cell subsets.

This assumption is also supported by our finding that in vitro generated Th17 cells strongly differ in their DNA methylation pattern when compared to ex vivo isolated Th17 cells. Indeed, a lower degree of demethylation at Il17a was identified in in vitro cultivated Th17 cells, and particularly the other Th17-specific epigenetic signature genes showed hardly any signs of demethylation in the cultivated cells. These data suggest that essential signals, e.g. provided by highly specialized APCs or by unique cytokine milieu (52), were lacking under the in vitro culture conditions, thereby leading to the generation of Th17 cells with an unstable phenotype (28,29,53,54). Similar differences were observed for Foxp3+ Tregs, where only ex vivo isolated or in vitro induced, but not in vitro generated cells showed pronounced demethylation of the Treg-specific epigenetic signature, consisting of regions within Foxp3, Tnfsf18, Ctxa4, Il1ra, Iκbκ and Il2ra, which finally resulted in a stably imprinted Treg phenotype (34,35). It has been suggested that several rounds of in vitro restimulation under Th1-polarizing conditions can lead to some stabilization of the Th1 phenotype (55), and that ‘chronic’ TCR-triggering can result in mild demethylation of part of the Treg-specific epigenetic signature (35). However, even repetitive rounds of in vitro restimulation in the presence of TGF-β do not cause demethylation of the Foxp3 locus nor stabilization of Foxp3 expression (56), further supporting the assumption that unique signals being solely present in vivo are critical for the epigenetic imprinting of Th cell phenotypes.

Recent studies on Foxp3+ Tregs by others and us have demonstrated that it is possible to identify and quantify stable Tregs by methylation analysis of a single region within the Foxp3 locus (34,57–59). In the present study, however, we could show that none of the individual regions of the Th17-specific epigenetic signature were sufficient to unequivocally identify Th17 cells on its own. In particular, Ccr6 was found to be fully demethylated in B cells and to a lesser extent in NK cells and γδ T cells, which is in line with the previously reported expression profile of CCR6 on these cell subsets (60–62). Furthermore, γδ T cells showed a high degree of similarity with ex vivo isolated Th17 cells on the DNA methylation level. Although demethylation of Il17a, Zfp362, Ccr6, Acsbg1, Rora and Dclk1 was slightly less pronounced in γδ T cells when compared to ex vivo isolated Th17 cells, the overall pattern was very similar except for Dpp4 which did not show overt signs of demethylation in γδ T cells. This pattern similarity might be explained by the fact that a significant fraction of γδ T cells express the transcription factor RORγt and can produce IL-17A (62–64). From these results we hypothesize that some of the epigenetic changes in Th17 cells and γδ T cells are linked to RORγt-dependent transcriptional regulation.

Despite the fact that none of the individual regions of the Th17-specific epigenetic signature genes was sufficient to unequivocally identify Th17 cells on its own, the whole signature was unique to ex vivo isolated Th17 cells and one might speculate that these genes are of functional importance for Th17 cells and contribute to their unique phenotype. Indeed, transcriptomic profiling of ex vivo isolated Th cells revealed an increased expression of Il17a, Zfp362, Ccr6, Acsbg1, Dpp4 and Rora in Th17 cells when compared to Th1 cells, in line with previously published data showing a high expression of Ccr6, Dpp4 and Rora in Th17 cells (8,65,66). Only Dclk1 displayed an increased expression in Th1 cells when compared to Th17 cells, suggesting that the demethylation of the single CpG motif within Dclk1 does not foster expression of the kinase under these experimental conditions. In contrast, the region within Ccr6 is known to control stable Ccr6 expression via epigenetic mechanisms (67). It is selectively demethylated in CCR6+ T cells and was reported to display transcriptional activity in CCR6+ T cells in a methylation-sensitive manner. Similar mechanisms were also shown for Il17a, where the region around the transcriptional start site was described to be selectively demethylated in Th17 cells when compared to other Th cell subsets (17,23,24). This demethylation of the Il17a promoter is of utmost importance for the induction of Il17a expression since methylation of STAT3 consensus elements within the promoter were reported to directly inhibit STAT3 binding as well as transcriptional activity (17), suggesting that Il17a expression is under direct epigenetic control.

According to the MBD-seq analysis from the present study, the Th17-associated genes Rorc, Iil7f, Il21, Il22, Il1r1, Il23r and Ahr did not show a specific methylation pattern in ex vivo isolated murine Th17 cells. However, in a previously published study, a selective demethylation of several CpG motifs downstream of the transcriptional start site of the human RORγt promoter were observed in RORγt+ cells (25). This discrepancy can be either explained by a low degree of homology for this region between mice and men or by a too low number of CpG motifs within this region. Similarly, the specific demethylation of two CpG motifs within the Il17f promoter in Th17 cells (17) was not detected by our MBD-seq approach, suggesting that the resolution of this technique is insufficient to detect minor differences. In contrast, the recently described demethylation of a CpG-rich region at the transcriptional start site of Il17a and at promoter position −166/−144 (17) could be confirmed by our study (see Figures 4 and 6 and data not shown). Studies on 5-azacytidine treated tumor cells revealed a possible epigenetic regulation of Il21, Il23r and Ahr (68–70). So far, we did not detect any differential methylation within these loci in immune cells.

Although in vivo generated Th17 cells are engraved with unique epigenetic marks that partially enable stable expression of key genes of the Th17 phenotype, recent reports about the plasticity and flexibility of Th17 cells particularly under inflammatory conditions raised the question about stability of the lineage itself (32,71). Th17 cells can easily convert into T cells expressing effector cytokines different from the Th17 phenotype (10,27,72,73). While it has to be clarified whether the converted T cells derive from effector or memory cells, adaptation to an inflammatory environment seems to be a key feature of Th17 cells. The higher number of demethylated regions found in ex vivo isolated Th17 cells when compared to naive T cells might be the
molecular basis for the high plasticity and flexibility of Th17 cells.

In conclusion, the genome-wide DNA methylation analyses of ex vivo isolated Th cell subsets reinforced the finding that Th cell differentiation is associated with massive epigenetic changes at the DNA methylation level. Subset-specific methylation patterns like the Th17-specific epigenetic signature can be used to identify and functionally characterize the highly diverse Th cell subsets.

SUPPLEMENTARY DATA
Supplementary Data are available at NAR Online.

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