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STAT4 and T-bet Are Required for the Plasticity of IFN-γ Expression across Th2 Ontogeny and Influence Changes in Ifng Promoter DNA Methylation

Christopher L. Williams,*† Marcia M. Schilling,*† Sung Hoon Cho,*† Keunwook Lee,*† Mei Wei,*† Aditi,*† and Mark Boothby,*†‡

CD4⁺ T cells develop toward a Th2 fate express IL-4, IL-5, and IL-13 while inhibiting production of cytokines associated with other Th types, such as the Th1 cytokine IFN-γ. IL-4-producing Th2 effector cells give rise to a long-lived memory population committed to reactivation of the Th2 cytokine gene expression program. However, reactivation of these effector-derived cells under Th1-skewing conditions leads to production of IFN-γ along with IL-4 in the same cell. We now show that this flexibility (“plasticity”) of cytokine expression is preceded by a loss of the repressive DNA methylation of the Ifng promoter acquired during Th2 polarization yet requires STAT4 along with T-box expressed in T cells. Surprisingly, loss of either STAT4 or T-box expressed in T cells increased Ifng promoter CpG methylation in both effector and memory Th2 cells. Taken together, our data suggest a model in which the expression of IFN-γ by Th2-derived memory cells involves attenuation of epigenetic repression in memory Th2 cells, combined with Th1-polarizing signals after their recall activation. The Journal of Immunology, 2013, 191: 000–000.

Christopher L. Williams,*† Marcia M. Schilling,*† Sung Hoon Cho,*† Keunwook Lee,*† Mei Wei,*† Aditi,*† and Mark Boothby,*†‡

CD4⁺ T cells play central roles in the ability of the immune system to adapt the nature of its responses to different types of pathogens. Upon exposure to their cognate Ag, signals from the TCR and the local cytokine milieu drive naive CD4⁺ T cells to develop into one of several effector programs. Each effector type, commonly referred to as a lineage or subset, produces a set of hallmark cytokines while inhibiting the expression of cytokine genes characteristic of other effector types (1). Development along an effector lineage is, in large part, directed by cytokines signaling through their membrane-bound receptors at or around the time of Ag encounter (2, 3). The cell surface receptors for cytokines that can polarize populations of Th cells activate immediate-early transcription factors in the family of STAT proteins (4, 5). These, in concert with other transcription factors and signaling pathways, induce subset- or lineage-specific transcription factors sometimes considered master regulators (6, 7). The combined signals from the TCR, cytokine receptors, and the activity of the master regulator transcription factors lead to the subset-specific expression of cytokines that characterize the CD4 effector cells.

Two of the best studied effector programs, both in terms of physiological impact and the mechanisms leading to their development, are Th1 and Th2 (8, 9). Th1 effectors produce IFN-γ, which activates macrophages to promote clearance of intracellular pathogens (10, 11) and is involved in the pathogenesis of autoimmune diseases such as type 1 diabetes (12). The importance of IFN-γ in human health is illustrated by the increased susceptibility to mycobacterial infections in patients lacking a functional IFN-γR (13). Th1 polarization requires IL-12R signaling via STAT4 and an induction of T-box expressed in T cells (T-bet) expression (4, 6, 7). These transcription factors direct histone posttranslational modifications (14) along with chromatin remodeling of the Ifng gene (15) to allow for efficient gene transcription. In contrast, the Th2 effector program is characterized by repression of Ifng gene expression along with production of IL-4, IL-5, and IL-13 (8, 16). These Th2 cytokines direct responses against helminthic pathogens (17) and contribute to atopic diseases such as allergic asthma (18). Th2 polarization involves IL-4R signaling though STAT6 (19, 20), followed by induction of the transcription factor GATA3 (21, 22), to enable transcription of the Th2 cytokine genes.

Beyond the activation of cytokine gene expression, each polarized Th program also involves the silencing of genes from opposing transcriptional programs (23). For instance, GATA3 mediates the silencing of the genes encoding IFN-γ, IL-12Rβ, and STAT4 via repressive histone modifications during the course of Th2 polarization (24). Conversely, cells developing toward Th1 effector function inhibit the production of IL-4 through inhibition of GATA3 transcription (23, 25). The silencing of cytokines associated with other Th subsets also involves repressive DNA methylation. Thus, the proximal promotor of the Ifng gene is CpG methylated in Th2 clones (26) and primary effector cells (27–29) when compared with Th1 counterparts. Moreover, methylation of the evolutionarily conserved CpG at −53 in this proximal Ifng promotor sufficed to abrogate its activity (29). Together, these studies indicated that DNA methylation, especially at the −53
CpG of that Ifng promoter is a key aspect of repressing expression of this Th1 cytokine in Th2 effector cells. Immunological memory is a key feature of the adaptive immune system and provides protection against reinfection after a first exposure to a pathogen (30). After an Ag has been cleared, a fraction of responding cells survives as a long-lived population and appears to acquire a memory program differing from the effector state (31). Because cytokine production by memory cells upon Ag exposure can instruct a new generation of immune effectors, the profile of cytokines produced by recall responses of a memory CD4+ T cell can have a profound impact on the function of memory Th2 cells. However, the mechanisms underlying this plasticity of cytokine expression are not well understood. Further, we analyzed memory Th2 cells to express T-bet or IFN-γ to understand the epigenetic modifications of the Ifng gene that underlie the repression of this Th1 cytokine in Th2 effector cells.

Although production of IL-4 remains part of the programming for Th2-derived memory cells, reactivation under Th1 conditions also drove these cells to produce substantial amounts of IFN-γ (35–37). These findings revealed that the nature of gene silencing as part of the Th program could be changed in memory cells, so that IFN-γ and the Th2 cytokine genes can be coexpressed within an individual CD4 lymphocyte. However, almost nothing is known about the molecular mechanisms for this plasticity of programming. Recent work indicated that, in addition to the Th1 master regulator T-bet, IL-12 was required for the induction of Ifng gene expression after reactivation of memory Th2 populations (38). The signal or signals downstream from IL-12 and essential for plasticity of Ifng regulation are not established. Moreover, a key unanswered question regarding the mechanisms permitting IFN-γ production by Th2-derived memory cells is whether repressive epigenetic modifications of the Ifng promoter that occur during Th2 polarization are maintained in the memory phases. In this article, we have tested whether STAT4 affects the ability of memory Th2 cells to express T-bet or IFN-γ in Th1 recall conditions. Further, we analyzed Ifng promoter DNA methylation in naive, Th1-, Th2-, and Th2-derived memory CD4+ T cells, and explored the relationship between promoter methylation and the Th1-determining transcription factors STAT4 and T-bet.

Materials and Methods

Mice

BALB/c or DBA/2 mice were bred with BALB/c-Tbx21−/− mice to obtain Tbx21−/− mice (The Jackson Laboratory) or BALB/cStat4−/− KO mice (The Jackson Laboratory) and H2−/− mice (The Jackson Laboratory) provided by Dr. M. Lotz (University of Nebraska Medical Center, Omaha, NE). The upper-strand oligonucleotides were designated as unmethylated, hemimethylated (meC at 5′- and 3′-unmethylated); and trihemimethylated (meC at 5′- and 3′-unmethylated and hemimethylated, respectively) (29, 30). Each was annealed to an unmethylated lower-strand oligonucleotide after radioactive labeling with [α-32P]-dCTP.

Reagents

Fluorophore-conjugated and purified mAbs were obtained from BD Pharmingen (Franklin Lakes, NJ), eBioscience (San Diego, CA), and Invitrogen (Santa Cruz, CA). Oligonucleotides were synthesized by Invitrogen (Grand Island, NY) unless otherwise stated. Cell culture and purification of GFP+ IL-4–producing effectors and adoptive transfers

DO11.10 cells were activated with OVA323–339 peptide, and all cells were cultured as described (35), with the following modifications. For Th1 culture conditions, cells were plated at 7 × 10^6 cells per well in 96-well plates and received 100 ng/ml OVA peptide, 5 ng/ml IL-12, and 3 ng/ml anti-IL-4 Ab 11B11. For Th2 cell cultures, cells were plated at 3.5 × 10^6 cells per well in 96-well plates and received 0.5 μg/ml OVA peptide, 7.5 ng/ml IL-4, 3 μg/ml anti-IFN-γ Ab, and 2 μg/ml anti-IL-12 Ab. Both Th1 and Th2 cell cultures were supplemented with IL-2 (50 U/ml) and 24 h after activation. GFP+ Th2 effector cells were purified for transfer as described (35). After 4 d of culture in Th2 conditions, 4get, DO11.10 cells (Tbx21−/−, Stat4−/−, or transcriptionally wild-type (WT)) were transferred with APC-conjugated anti-CD4 and PE-conjugated KJ1-26 (anti-DO11.10 TCR) Abs and sorted on a FACSAria (BD, Franklin Lakes, NJ) to purify (>98.5%) viable DO11.10 KJ1-26+ CD4+ GFP+ cells. Prior to transfer or DNA isolation for methyl-CPG analyses, these cells were cultured in Th2 conditions for 9–10 d after reactivation with APCs (4:1 with T cells) and 0.25 μg/ml OVA323–339 (13–14 d total).

Quantitation of cytokine production

Th cell cultures plated with APCs at a 1:4 ratio, and single-cell suspensions of recipient spleens, were stimulated with 1 μg/ml OVA323–339. Cytokine concentrations in supernatant collected after 36 h were quantified using a flow cytometric kit (Th1/Th2/Th17 cytokine bead array; BD Pharmingen). Intracellular cytokines were quantified by stimulating cells 18 h with OVA323–339 (1 μg/ml) in the presence of APCs, followed by GolgiStop (BD) (2–3 h), and staining in the presence of anti-CD16/32 (Fc Block; BD Pharmingen), as previously described (35). Viable cells were selected based on forward and side scatter characteristics, and fluorescence signals representing intracellular cytokines were determined in cells positive for the DO11.10 TCR and CD4.

Bisulfite analysis of DNA methylation

DNA isolated from flow-purified naive, effector (Th1, Th2, 13 d), and memory CD4 T cells, or from tissues, was digested with BamHI (New England Biolabs, Ipswich, MA), bisulfite modified using the Imprint bisulfite modification kit (Sigma-Aldrich, St. Louis, MO), then used as template in quadruplicate PCR performed using primer pairs specific for each modified strand sequence in the Ifng promoter (Supplemental Table I) (29). The nondescoding side of the Ifng promoter was amplified with a single reaction, whereas the coding strand was amplified using a nested PCR. After pooling four tubes of separate amplification for each sample, specific PCR products were identified on agarose gels, extracted using the QIAquick Gel Extraction Kit (Qiagen, Valencia, CA), ligated with T Easy vector (Promega, Madison, WI), and then transformed into JM109 cells (Agilent, Santa Clara, CA). For each of three independent biological replicate cell samples and for each strand, 8–10 clones derived from each reaction pool were sequenced and scored for the frequency of unmethylated C residues in the CpG dinucleotides; the modification frequency for C residues outside of CpG dyads was verified as >99% for all sample sets.

EMSA

EMSA were performed as reported (29, 39), except that extracts of Th1 cells developing from primary mouse CD4+ T cells were used. Methylated upper-strand oligonucleotides were synthesized by Invitrogen (Grand Island, NY). The upper-strand oligonucleotides were designated as unmethylated, methylated (meC–5′- and 3′-hemimethylated), and trihemimethylated (meC at 5′, 3′, and 3′-hemimethylated) (29, 34) (Supplemental Table I). Each was annealed to an unmethylated lower-strand oligonucleotide after labeling with γ-[32P]-ATP (Perkin-Elmer, Waltham, MA) and T4 polyuridylate kinase (New England Biolabs). For competition assays, unlabeled competitor was added simultaneously with the labeled probe at molar ratios (competitor: probe) of 100:1, 10:1, and 1:1. Abs used for the supershift assays were CREB1 (sc-186), ATF2 (sc-187), and c-Jun (sc-45) (Santa Cruz Biotechnology, Santa Cruz, CA).

Transfection and reporter assays

Nucleofection was carried out via the Amaxa T cell kit (Lonza, Basel, Switzerland) using a minimal Ifng promoter reporter P1P2-Luc (40) along with pCMV-Sport6-CREB1 or pCMV-Sport7. All results were normalized to GFP expression from the pCMV-GFP plasmid (Lonza) measured via flow cytometry. Luciferase activity was measured using the Dual-Glo Luciferase Assay System (Promega) according to the manufacturer’s protocols.

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Chromatin immunoprecipitation assays

Chromatin immunoprecipitation (ChIP) assays were performed essentially as described previously (15). After cross-linking with formaldehyde, primary Th1 and Th2 cells were sonicated in a Bioruptor (Diagenode, Denville, NJ) to produce an average sheered DNA length of 400 bp. Immunoprecipitation was carried out using anti-AcH3(K9) (acetyl-lysine 9 of histone H3; #DAM1813175; Millipore), or CREB1 (sc-186X; Santa Cruz.), and the precipitates were analyzed by PCR using primers shown in Supplemental Table I.

Proliferation in vitro and in vivo

Proliferation studies using CFSE partitioning and BrdU incorporation were carried out as described (39). For CFSE partitioning in vivo, Th2 cells were grown for 5 d, labeled with 5 (and 6)-carboxyfluorescein diacetate-succinimidyl ester (CFDA-SE; Invitrogen) (2.5 μM, 15 min) following manufacturer instructions, and then transferred into BALB/c recipients. Fluorescence was measured on donor-derived cells recovered 12 d after transfer, with gating as described above. For CFSE partitioning assays in vitro, DO11.10 splenocytes were either labeled, Ag-stimulated, and cultured 2 d, or activated with Ag, cultured in Th2 conditions (11 d, with one interim Ag stimulation, as for cells used in adoptive transfers), labeled with CFDA-SE as above, and then cultured 2 d in IL-2–supplemented medium before analysis by flow cytometry. For assays of BrdU incorporation into donor cells in vivo, recipient mice were injected twice (72 h, 24 h before harvest; 3 mg i.p. per injection) with BrdU (Sigma-Aldrich) in sterile saline. Cells harvested 12 d posttransfer were then processed as described (39) to detect Alexa-647 anti-BrdU (Invitrogen) in donor- (KJ1-26+) and recipient-derived CD4+ T cells by flow cytometry. For in vitro proliferation studies using CFSE partitioning and BrdU incorporation were carried out as described (39). For CFSE partitioning in vivo, Th2 cells were grown for 5 d, labeled with 5 (and 6)-carboxyfluorescein diacetate-succinimidyl ester (CFDA-SE; Invitrogen) (2.5 μM, 15 min) following manufacturer instructions, and then transferred into BALB/c recipients. Fluorescence was measured on donor-derived cells recovered 12 d after transfer, with gating as described above. For CFSE partitioning assays in vitro, DO11.10 splenocytes were either labeled, Ag-stimulated, and cultured 2 d, or activated with Ag, cultured in Th2 conditions (11 d, with one interim Ag stimulation, as for cells used in adoptive transfers), labeled with CFDA-SE as above, and then cultured 2 d in IL-2–supplemented medium before analysis by flow cytometry. For assays of BrdU incorporation into donor cells in vivo, recipient mice were injected twice (72 h, 24 h before harvest; 3 mg i.p. per injection) with BrdU (Sigma-Aldrich) in sterile saline. Cells harvested 12 d posttransfer were then processed as described (39) to detect Alexa-647 anti-BrdU (Invitrogen) in donor- (KJ1-26+) and recipient-derived CD4+ T cells by flow cytometry. For in vitro proliferation studies using CFSE partitioning and BrdU incorporation were carried out as described (39). For CFSE partitioning in vivo, Th2 cells were grown for 5 d, labeled with 5 (and 6)-carboxyfluorescein diacetate-succinimidyl ester (CFDA-SE; Invitrogen) (2.5 μM, 15 min) following manufacturer instructions, and then transferred into BALB/c recipients. Fluorescence was measured on donor-derived cells recovered 12 d after transfer, with gating as described above. For CFSE partitioning assays in vitro, DO11.10 splenocytes were either labeled, Ag-stimulated, and cultured 2 d, or activated with Ag, cultured in Th2 conditions (11 d, with one interim Ag stimulation, as for cells used in adoptive transfers), labeled with CFDA-SE as above, and then cultured 2 d in IL-2–supplemented medium before analysis by flow cytometry. For assays of BrdU incorporation into donor cells in vivo, recipient mice were injected twice (72 h, 24 h before harvest; 3 mg i.p. per injection) with BrdU (Sigma-Aldrich) in sterile saline. Cells harvested 12 d posttransfer were then processed as described (39) to detect Alexa-647 anti-BrdU (Invitrogen) in donor- (KJ1-26+) and recipient-derived CD4+ T cells by flow cytometry. For in vitro

![Figure 1](http://www.jimmunol.org/) Asymmetrical increase in CpG methylation of the Ifng promoter in Th2 cells. Methylation of CpG residues was determined by sequencing individual subcloned products from strand-specific PCR of bisulfite-modified DNA from naive CD4+ T cells (A) and Th1 and Th2 cells (B). Shown are diagrams illustrating representative individual sequences, from biological replicates for each type of sample, generated from naive (A) or Th1 and Th2 cells (B). Filled circles (●) represent methylated cytosine, and open circles (○) the unmethylated residue. Analyses included at least eight independent clones from each of three independent biological replicates per sample. (C) Data for the coding (left) and noncoding (right) strands are shown, with each bar representing the mean (± SEM) number of methylated CpGs per clone in all surveyed upstream CpGs (six total), the CpGs at −205, −190, −170, or the CpG triad at −53, −45, and −34. (D) Comparison of coding and noncoding strand methylation in Th2 effectors. (E) Methylation frequencies at the −53 CpG dinucleotide. (F) CFSE partitioning was measured 48 h after labeling cells that were either acutely stimulated (2 d total), or from 11-d Th2 cultures (13 d total). (G) Cells cultured under Th2 conditions for 2 d or 13 d were pulsed with BrdU for 4 h. The incorporation of BrdU into cellular DNA was measured by intracellular staining. Cells grown continuously in BrdU or unexposed to BrdU were used as staining controls. Results (F and G) are representative of two independent experiments. *p < 0.05, **p < 0.01, ***p < 0.001.  

Retroviral transduction

Retroviral transduction was carried out using as previously described (15). In brief, retrovirus-containing supernatants from Phoenix packaging cells transfected with MSCV-IRE-5-Thy1.1 (MIT) or MSCV-T-bet-IRE-5-Thy1.1 (MIT-T-bet) were used to transduce established GFP+ DO11.10 Th2 cells 2 d after restimulation. Cells were then cultured under Th1 or Th2 conditions, followed by measurements of Ag-stimulated cytokine production or intracellular cytokines as above.

Results

Strand-biased acquisition of Ifng promoter methylation in Th2 effector cells

The finding that memory Th2 cells, unlike their effector-phase precursors, can respond to an inflammatory milieu by efficient induction of IFN-γ production (35, 36) raises questions about the fate of repressive DNA methylation observed in Th2 effectors once these cells transition to memory status. Accordingly, we used bisulfite modification of DNA followed by strand-specific PCR to analyze CpG methylation in Ifng promoter DNA of naive CD4+ lymphocytes, Th1, and Th2 T cells. Naive CD4+ and Th1 effector cells showed little methylation of either strand of DNA upstream from the transcription start site (Fig. 1), whereas high methyla-
tion densities were found at two dinucleotides in exon 1, independent of T cell differentiation, as expected (41, 42). In effector Th2 cells (Fig. 1B, 1C), we found increased methylation of the coding strand of the Ifng promoter, with a majority of samples exhibiting modification of the key −53 CpG whose modification appeared to abrogate promoter activity (29). Surprisingly, however, the noncoding strand was reproducibly and significantly less methylated in Th2 effector cells relative to the coding strand (Fig. 1D), particularly at the −53 CpG (Fig. 1E). In light of this unexpected result, we tested samples including DNA from a mouse brain and 3T3 cells, both of which would be expected to have symmetrical hemimethylation of the Ifng promoter, along with thymocytes and naive CD4 lymphocytes. Brain and 3T3 cell DNA demonstrated a high density of symmetrical methylation across the surveyed region and in particular at the crucial −53 CpG, whereas thymocytes, like naive CD4 T cells, exhibited little meC (Table I). The frequency of non-coding strand DNA methylation in Th2 cells was too low simply to represent a lack of modification on one chromosome, e.g., from monoallelicism (43). Separate analyses (Table I and later results) exclude a strand bias in the detection method as the basis for the observation. Accordingly, we infer from these data that Ifng promoters were hemimethylated in these Th2 effector cells. The asymmetry of CpG methylation might in principle be observed because a high proportion of the Th2 population was actively in cell cycle and rapidly undergoing DNA synthesis. However, virtually no divisions were observed in CFSE analyses of the effector Th2 cells in the 2 d prior to the time at which DNA samples were prepared (Fig. 1F). Moreover, only a small fraction of the population was in cell cycle, as indicated by a low frequency of BrdU<sup>c</sup> cells at this time 13 d after the initial Ag activation (Fig. 1G). From these low frequencies of cycling cells, we conclude that the slower migrating complex is predominantly formed by CREB1. Consistent with the hemimethylation observed at the Ifng promoter having an impact on CREB1 recruitment in vivo, ChIPs performed using anti-CREB1 Ab showed greater promoter occupancy in Th1 cells than did their Th2 counterparts (Fig. 2E). The decreased binding of CREB1 in effector-stage Th2 cells, in which the Ifng gene is not active, would be consistent with CREB1 function as a trans activator. To test if CREB1 can increase activity of the Ifng promoter in primary Th1 cells, we performed nucleofoctions of developing Th1 cells, using a minimal Ifng promoter reporter construct and either a CREB1 expression vector or an empty vector control (Fig. 2F). We found that CREB1 increased activity of the Ifng reporter construct. In sum, these findings show that upper-strand hemimethylation of the CpG at −53 can impair binding of CREB1, a trans activator of the Ifng promoter.

Table I. CpG methylation in naive CD4<sup>+</sup> T cells, thymus, brain, and NIH 3T3 cells

<table>
<thead>
<tr>
<th>Sample</th>
<th>Strand</th>
<th>−205</th>
<th>−190</th>
<th>−170</th>
<th>−53</th>
<th>−45</th>
<th>−34</th>
<th>16</th>
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<tr>
<td></td>
<td></td>
<td>−205–170</td>
<td></td>
<td></td>
<td></td>
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<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>−53–34</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Naive CD4</td>
<td>Coding</td>
<td>11.4 (3.6)&lt;sup&gt;a&lt;/sup&gt;</td>
<td>11.4 (3.6)</td>
<td>14.4 (3.6)</td>
<td>17.4 (3.9)</td>
<td>14.4 (3.6)</td>
<td>14.4 (3.6)</td>
<td>59.8 (6.1)</td>
</tr>
<tr>
<td></td>
<td>Noncoding</td>
<td>17 (3.6)</td>
<td>10.8 (1.6)</td>
<td>6.25 (2.3)</td>
<td>17 (3.4)</td>
<td>15.3 (2)</td>
<td>15.3 (2)</td>
<td>72.2 (3.5)</td>
</tr>
<tr>
<td>Thymus</td>
<td>Coding</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>71.3 (3.5)</td>
</tr>
<tr>
<td></td>
<td>Noncoding</td>
<td>95 (2.7)</td>
<td>76.7 (3)</td>
<td>86.6 (2)</td>
<td>100</td>
<td>100</td>
<td>100</td>
<td>100</td>
</tr>
<tr>
<td>Brain</td>
<td>Coding</td>
<td>78.9 (3.2)</td>
<td>63.1 (3.8)</td>
<td>52.6 (1.8)</td>
<td>63.1 (0.9)</td>
<td>63.1 (0.9)</td>
<td>52.6 (3.5)</td>
<td>85.5 (4.2)</td>
</tr>
<tr>
<td></td>
<td>Noncoding</td>
<td>62.5 (4.2)</td>
<td>36.3 (6.1)</td>
<td>43.8 (3.0)</td>
<td>56.3 (3.0)</td>
<td>50 (0.0)</td>
<td>50 (0.0)</td>
<td>87.5 (4.2)</td>
</tr>
</tbody>
</table>

| Sample          | Strand  | Total<sup>b</sup> | −205–170 |       |       |       |       |        |
|-----------------|---------|-------------------|----------|-------|-------|-------|-------|        |
|                 |         | −53–34            |          |       |       |       |       |        |
| Naive CD4       | Coding  | 0.9 (0.25)<sup>a</sup> | 0.4 (0.18) | 0.52 (0.2) | 0 (0) | 0.11 (0.07) | 0 (0) |        |
|                 | Noncoding | 0.7 (0.34) | 0.25 (0.14) | 0.45 (0.22) | 0 (0) | 0.11 (0.07) | 0 (0) |        |
| Thymus          | Coding  | 0.11 (0.07) | 0 (0) | 0.11 (0.07) | 0 (0) | 0.11 (0.07) | 0 (0) |        |
|                 | Noncoding | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) |        |
| Brain           | Coding  | 5.7 (0.12) | 2.7 (0.12) | 3 (0) | 0.6 (0.12) | 0 (0) | 0 (0) |        |
|                 | Noncoding | 5.6 (0.16) | 2.6 (0.15) | 2.9 (0.06) | 0 (0) | 0 (0) | 0 (0) |        |
| 3T3             | Coding  | 3.8 (0.45) | 2.1 (0.27) | 1.8 (0.31) | 0 (0) | 0 (0) | 0 (0) |        |
|                 | Noncoding | 2.9 (0.53) | 1.4 (0.26) | 1.5 (0.35) | 0 (0) | 0 (0) | 0 (0) |        |

<sup>a</sup>Position is presented as the distance in bases from the transcription start site.
<sup>b</sup>Data are presented as the mean (±SEM) percentage of samples methylated at a given position.
<sup>c</sup>Cluster of CpG dinucleotides being assayed.
<sup>d</sup>Mean (±SEM) number of methyl-CpGs per clone in a given cluster.

Asymmetrical methylation affects transcription factor binding to the Ifng promoter

On the basis of evidence that the Ifng promoter in many Th2 cells can be in a state of asymmetrical methylation, we investigated whether hemimethylation might affect transcription factor recruitment to the Ifng promoter. EMSA using nuclear extracts of primary Th1 cells were carried out using unmethylated or hemimethylated probes (Fig. 2A). Both hemimethylated probes impaired the formation of the slower migrating complex (indicated by filled arrow, Fig. 2B). Competition assays using unlabeled competitor DNA confirmed that the mobility shift bands represented sequence-specific binding; moreover, 10-fold more cold competitor was needed to attenuate the slower migrating complex to the WT compared with the hemimethylated probe (Fig. 2C). To characterize this complex, we performed Ab blocking/supershift assays with the unmethylated probe and Abs against CREB1/ATF family members. The upper band was impacted by anti-CREB1 (Fig. 2D), whereas Abs against ATF2 and c-Jun had no discernible effect, leading us to conclude that the slower migrating complex is predominantly formed by CREB1. Consistent with the hemimethylation observed at the Ifng promoter having an impact on CREB1 recruitment in vivo, ChIPs performed using anti-CREB1 Ab showed greater promoter occupancy in Th1 cells than did their Th2 counterparts (Fig. 2E). The decreased binding of CREB1 in effector-stage Th2 cells, in which the Ifng gene is not active, would be consistent with CREB1 function as a trans activator. To test if CREB1 can increase activity of the Ifng promoter in primary Th1 cells, we performed nucleofoctions of developing Th1 cells, using a minimal Ifng promoter reporter construct and either a CREB1 expression vector or an empty vector control (Fig. 2F). We found that CREB1 increased activity of the Ifng reporter construct. In sum, these findings show that upper-strand hemimethylation of the CpG at −53 can impair binding of CREB1, a trans activator of the Ifng promoter.

Loss of Ifng methylation in Th2-derived memory cells

Th2-derived memory cells can produce IFN-γ when exposed to Th1-skewing conditions during recall responses (35, 36). To
investigate the relationship between this capacity and the repressive methylation observed in primary Th2 cells, we prepared DNA from purified effector cells and their memory Th2 descendants (Fig. 3A). As expected, cells in the donor-derived memory pool in each type of recipient underwent homeostatic divisions after transfer (Fig. 3B), and these memory cells produced IFN-γings after transfers into normal or lymphopenic BALB/c mice, donor-derived cells were purified from the recipient lymphoid organs. Strand-specific PCR analyses of bisulfite-modified donor-derived cellular DNA showed that methylation of multiple sites decreased (Fig. 4B) and the −53 CpG of the Ifng promoter coding strand was almost completely unmethylated (Fig. 4C). These results were independent of whether the recipients had normal endogenous T cells or were lymphopenic (data not shown). These findings provide evidence of dynamic change in Ifng promoter methylation, as the population of Th2 effectors yields a memory Th2 subset.

**STAT4 is required for flexible IFN-γ production**

The development of Th1 effector cells from naive CD4+ T cell precursors is highly dependent on IL-12-induced STAT4 and, in most settings, on T-bet (4, 7, 44). IL-12 is required for the facultative induction of IFN-γ production by memory Th2 cells after recall stimulation in vitro and in vivo (35, 36, 38). However, the IL-12R elicits multiple intracellular signals (45, 46), and which of these is essential for the plasticity of gene expression is not known. Accordingly, we compared the amounts of IFN-γ produced after recall stimulation and cultures of memory Th2 cells from Tbx21−/− and Stat4−/− T cells to that derived from parallel controls with normal transcriptional function (Fig. 5A, Supplemental Fig. 1A). When cytokine production was elicited 1 wk after recall restimulation with peptide Ag and culture under Th1 and Th2 conditions, samples of each transcription factor–deficient memory Th2 population produced substantially less IFN-γ than did matched WT controls (Fig. 5A). IFN-γ production elicited after Th1-skewed recall was higher than background with each type of knockout cell type. To assess the extent to which double-producing (IL-4+ IFN-γ+) cells could be generated from memory Th2 cells, we used intracellular staining for these cytokines (Fig. 5B, 5C). Although subject to the likelihood that the limits of detection are more sensitive for secreted cytokine than intracellular staining, these analyses consistently revealed almost no IFN-γ+ donor-derived (KJ1-26+ CD4+) cells in the absence of either Stat4 or T-bet (Fig. 5C). In sharp contrast, ample IL-4+ IFN-γ+ CD4+ T cells were abundant (31% of donor T cells) when controls with normal transcription factor genes were used (Fig. 5C). These data indicate that STAT4 is required in support of the capacity for memory Th2 cells to turn on IFN-γ production to an extent similar to that of T-bet.
T-bet induction in developing Th1 cells is driven by STAT1 and NF-κB (47, 48), but STAT4 regulates a later, IL-12–dependent phase of T-bet expression in the development of primary Th1 responses (49, 50). Therefore, we also tested whether STAT4 is required for Ifng plasticity in memory Th2 cells because it is essential for T-bet induction. Consistent with prior work (49, 50), intracellular stains detected T-bet immunofluorescence in STAT4-deficient Th1 effectors at levels equivalent to those observed for Th2 effectors (Fig. 6A, top panel). After recall activation and culture under Th1 conditions, however, STAT4-deficient memory Th2 cells displayed more T-bet protein expression, with at least half of the cells exhibiting induction to Th1 levels (Fig. 6A, middle panel). This finding indicates that the regulation of T-bet expression by STAT4 in this memory setting was not sufficient to explain the defect in Ifng induction. Together, the data show that the gene expression plasticity of memory Th2 cells—that is, elicitation of IFN-γ—requires independent input from STAT4 as well as T-bet.

T-bet and STAT4 alter Ifng promoter methylation pattern but not homeostatic divisions

Homeostatic divisions of cells in which asymmetrical methyl-CpG marks were present could lead to descendants in which this repressive mark was absent from the Ifng promoter on both chromosomes. Accordingly, we tested whether the rates of division were slower for Tbx21−/− or Stat4−/− Th2 cells in recipient mice. CFSE partitioning assays showed no defect in rates of division for DO11.10 Th2 cells that were T-bet- or STAT4-deficient cells, compared with controls that were WT with respect to the transcription factors (Fig. 6B). To compare proliferation of the transcriptionally deficient memory Th2 cells to WT controls long after the transfer, recipient mice received BrdU and its incorporation into DNA was measured. This analysis provided evidence that the transferred cells almost completely exited the cell cycle and that low rates of S-phase entry were similar for all genotypes (Fig. 6C).

An alternative model is that the absence of T-bet or STAT4 led to a higher or more symmetric density of CpG methylation at the Ifng promoter during the development of Th2 effectors. Significant changes in upper-strand meCpG densities were not observed (Supplemental Fig. 1B), but the methylation frequency of the noncoding strand was strikingly higher for T-bet–null Th2 cells. In addition, STAT4-deficient cells had essentially symmetrical DNA methylation (Fig. 6D) and increased noncoding strand methylation, especially at the crucial −53 CpG (Supplemental Fig. 1C). Moreover, meCpG densities in the Ifng promoter DNA from transcription factor–deficient memory Th2 cells, recovered after several weeks in vivo, were higher than those from WT memory controls (Fig. 6E; Supplemental Fig. 1D). Thus, T-bet and STAT4 each influenced Ifng promoter methylation in memory as well as effector Th2 lymphocytes.

Prior studies have supported several potential relationships between T-bet and the capacity to produce IFN-γ after Th2 differentiation. In one study, most human CD4 T cells could switch from polarized Th2 cytokine gene expression to turn on their IFNG gene; a subset of the helper cells unable to exhibit such flexibility was attributed to lack of T-bet expression (51). Parallel work indicated that differentiation progressively reduced the capacity of such Th2 cells to turn on IFN-γ expression in the presence of forced T-bet expression (52). In light of the failure of T-bet–deficient Th2 cells to exhibit flexibility (Fig. 5A) and their

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**FIGURE 3.** Elicitation of IFN-γ production from memory Th2 cells (A) Schematic overview of the experimental design and generation of Th2-derived memory cells. (B) CFSE partitioning assay for DO11.10 cells transferred into WT (shaded) or nude recipients (outline) and recovered after 2 wk, gated on CD4+ DO11.10 TCR+ cells. (C) IFN-γ secretion data are shown for memory Th2 cells at the time of harvest and after recall activation and growth (6 d) under Th1- or Th2-polarizing conditions, as indicated. Values in each individual sample were normalized to the frequencies of DO11.10 TCR+ CD4+ cell number to account for differences in cell prevalence. Shown are data from a single experiment representative of four independent replicates and consistent with earlier work (35, 36).

**FIGURE 4.** Altered DNA methylation of the Ifng promoter in effector-derived memory Th2 cells. (A) Representative bisulfite sequencing results from freshly isolated memory cells are diagrammed as in Fig. 1A. (B) Mean methylated CpG dinucleotides per clone are shown as in Fig. 1C. The Th2 effector results are taken from Fig. 1 and are shown for comparison. (C) Methylation of the Ifng promoter −53 CpG in effector versus memory Th2 cells is compared as in Fig. 1E. *** p < 0.001.
Ifng promoter methylation pattern, we explored the impact of forcing expression of this transcription factor after Th2 differentiation in its absence. Thbx21−/− Th2 cells were transduced with a bicistronic retrovector (“MiT”) directing T-bet expression linked to a bicistronic retrovector without T-bet cDNA. After culture in Th1 conditions and reactivation of the coding strand by memory Th2 cells. Consistent with this finding, restimulation elicited substantial IFN-γ production by established Th2 cells. Consistent with this component of our overall model, methyltransferase inhibitors in the developing Th2 cell.

Discussion
The capacity of memory cells derived from Th2 effectors to produce IFN-γ in recall responses represents a naturally occurring form of cellular reprogramming. Apart from a requirement for IL-12, type I IFNs, and the transcription factor T-bet (35, 38), nothing is known about the molecular mechanisms by which this plasticity of gene expression is exerted. We have found that the Ifng promoter exhibits asymmetrical methylation in committed Th2 effectors. The coding strand DNA preferentially acquires significantly increased methylation relative to the low frequency of Cpg methylation in naive CD4+ T cells and on the noncoding strand. A hemimethylated state created by such asymmetry suffices to impair CREB1 binding to an Ifng promoter sequence that is highly conserved and strongly required for promoter activity. Consistent with these data, nucleofection assays provide evidence that CREB1 is a trans activator of the Ifng promoter, and that this ubiquitously expressed transcription factor preferentially binds to the promoter in Th1 cells as compared with Th2 counterparts. Strikingly, Cpg methylation of the Ifng promoter in memory Th2 cells was observed at a frequency little different from that of the naive progenitor. Inasmuch as promoter methylation is a strongly repressive mark, these findings suggest that loss of Cpg methylation contributes to the plasticity of Ifng gene expression upon recall activation. In investigating the transcription factor requirements for this facultative production of IFN-γ, we found that the IL-12–induced factor STAT4 is required along with T-bet. Surprisingly, increased densities of Cpg methylation were observed in T-bet−/− deficient Th2 cells relative to WT controls, as well as in memory Th2 cells deficient in either of these essential transcription factors. We suggest that changes in the frequency of this repressive mark at promoters forms one—but not the only—part of the molecular basis for reprogramming of gene expression in memory Th2 cells after recall activation.

Consistent with this component of our overall model, methylation of the coding stand of the Ifng promoter inhibited CREB1 binding, as well as CREB1 trans-activated Ifng promoter activity in primary Th1 cells. Previous work showed that Ifng promoter DNA methylation inhibited mobility shift complexes of the CREB/ATF family, and a more recent study used ChIP of the Th1 clone AE7 to implicate ATF2 as a major factor in this scenario (29, 53). One likely factor in a difference of results is the use of a clone AE7 to implicate ATF2 as a major factor in this scenario (29, 53). One likely factor in a difference of results is the use of a clone AE7 to implicate ATF2 as a major factor in this scenario.
As in previous reports (26, 28, 29), our analyses indicate that thymocytes and naive CD4 T cells have quite low levels of CPG methylation at the *Ifng* promoter. Thus, molecular processes that are part of Th2 differentiation include direction of de novo DNA methylation to this site. In general, DNA methyltransferases (DNMTs) of the DNMT3 family (DNMT3a, b) appear to execute the process of adding new marks. T cell activation via TCR engagement increased DNMT3a expression, and a conditional loss-of-function study indicated that DNMT3a was important for repression of inappropriate cytokine genes in Th differentiation (58). Intriguingly, although memory cell generation and maintenance were not analyzed, in vitro analyses of DNMT3a-deficient cells detected plasticity of cytokine production somewhat akin to what memory Th2 cells are able to execute naturally (35, 36). Further analysis of this *Dnmt3a* model indicated that, similar to the low density of meCpG marking of the *Ifng* promoter in memory Th2 cells in our analyses, the de-repressed in vitro effectors lacking DNMT3a had levels of *Ifng* promoter methylation similar to those of naive CD4 T cells (59). DNA replication naturally creates hemimethylation of Cpg dyads, and establishment or enforced symmetry is predominantly executed by DNMT1 (60). Deletion of this DNMT early in T cell development led to a CD4 T cell population that produced >10-fold more IFN-γ upon primary ex vivo activation (61), underlining the importance of DNA methylation in the restriction of cytokine expression in CD4+ T cells to a specific effector program. Surprisingly, we found that even among cells under Th2-differentiating conditions, absence of T-bet led to increased methylation of the coding strand and substantially greater symmetry (i.e., increased noncoding strand meCpG). These results suggest that, surprisingly, the low level of T-bet present early after activation of naive CD4+ lymphocytes under Th2 conditions (6, 7, 44) directly or indirectly impedes access of DNMTs to the *Ifng* promoter. Beyond this unexpected function, we infer there is an additional aspect of T-bet in the molecular events underlying plasticity of *Ifng* gene expression. Although the promoter methylation and its symmetry increased in T-bet–deficient Th2 cells, a second impediment to IFN-γ production lies in a block to expression of T-bet when Th2 effectors are switched to Th1-promoting conditions without a period as memory cells. This idea would be consistent with the correlative data from switching experiments and measurements after single-cell cloning of human memory-phenotype CD4 T cells (51) as well as results of T-bet transduction [Fig. 6F (52)].

A complementary finding of our work identifies a functional importance of STAT4 equal to that of T-bet in allowing memory Th2 cells to produce IFN-γ along with Th2 cytokines after recall activation. The initial discovery of this flexibility indicated that IL-12 was a crucial factor for the process (35, 38). The IL-12R signals through both STAT4-dependent (4) and -independent mechanisms (45, 62), each of which can promote *Ifng* gene expression. STAT4 is vital for Th1 differentiation, but IL-12 also activates a PI 3-kinase–mTOR–FoxO (Forkhead box O-class) signaling pathway that culminates in de-repression of the *Tbx21* promoter DNA methylation in Th2 ontogeny.
gene encoding T-bet (46). Studies using conditional alleles will be needed to test whether there is an additional contribution from the mTOR–Akt–FoxO pathway, but our data establish that STAT4 is required for the flexible production of IFN-γ by Th2-derived memory cells. Of interest, this mechanism appears distinct from the primary effector phase, as we confirmed a vital role for STAT4 in maintaining T-bet protein levels in late (day 5) effector cells under Th1 conditions (49) but found little such effect in the memory Th2 cells. Thus, the requirement for STAT4 in the plasticity of memory Th2 cells is independent of an effect on T-bet expression.

A key finding of the work presented in this article was the unexpected dynamism in methylation density of promoter DNA as effector Th2 cells became a population with the low frequency of replicating (BrdU+) cells characteristic of the memory subset. Previous work on Ifng promoter regulation in memory or memory-phenotype T cells as compared with their naive or effector counterparts has focused mostly on the CD8 lineage. Pioneering work indicated that a low level of CpG methylation present in naive cells was lost upon cell activation (63–65). Surprisingly, resting memory-phenotype (total CD44hi) CD8 T cells had substantial CpG methylation at their Ifng promoters, which was quickly lost upon recall stimulation (65). One potential model, which cannot be rigorously tested for a population of effector cells yielding memory, would involve active demethylation of the meCpG. Although remaining a controversial area, especially from the standpoint of molecular mechanisms, rapid loss of H2A promoter DNA methylation scored by endonuclease sensitivity was found to occur without CD4 cell division (66), and other work also supports the existence of active DNA demethylation (67). Nonetheless, our findings suggest a straightforward passive mechanism by which the observed dynamism can be effected. Although Th2 clones were reported to exhibit almost uniform methylation of CpG at the Ifng promoter (26), under the conditions used for the current study we observed meCpG frequencies well below 100% at every site on the coding strand and an asymmetry in which a high fraction of coding strand meCpG dinucleotides exist in a base quartet in which the coding strand is paired with an unmethylated CpG. This finding indicates that the functional capacity of DNMT1 to establish symmetry after initial deoxycytosine methylation was insufficient.

Memory cell homeostasis is maintained by periodic divisions after DNA replication. As a consequence, the frequency of daughter straands lacking meCpG at each site would, in the setting of hemimethylation, increase as divisions progressed. Although likely not the entire mechanistic explanation, the greater symmetry of Ifng promoter DNA methylation observed in the absence of T-bet or STAT4 in the primary Th2 effectors is associated with higher meCpG densities in the memory population. T-bet–deficient, STAT4–deficient, and WT CD4 T cells had comparable cycling and meCpG densities in the memory population. T-bet–deficient, or STAT4 in the primary Th2 effectors is associated with higher Ifng promoter DNA methylation observed in the absence of T-bet and without CD4 T cells characteristic of the memory subset. Previous work on Ifng promoter regulation in memory or memory-phenotype T cells as compared with their naive or effector counterparts has focused mostly on the CD8 lineage. Pioneering work indicated that a low level of CpG methylation present in naive cells was lost upon cell activation (63–65). Surprisingly, resting memory-phenotype (total CD44hi) CD8 T cells had substantial CpG methylation at their Ifng promoters, which was quickly lost upon recall stimulation (65). One potential model, which cannot be rigorously tested for a population of effector cells yielding memory, would involve active demethylation of the meCpG. Although remaining a controversial area, especially from the standpoint of molecular mechanisms, rapid loss of H2A promoter DNA methylation scored by endonuclease sensitivity was found to occur without CD4 cell division (66), and other work also supports the existence of active DNA demethylation (67). Nonetheless, our findings suggest a straightforward passive mechanism by which the observed dynamism can be effected. Although Th2 clones were reported to exhibit almost uniform methylation of CpG at the Ifng promoter (26), under the conditions used for the current study we observed meCpG frequencies well below 100% at every site on the coding strand and an asymmetry in which a high fraction of coding strand meCpG dinucleotides exist in a base quartet in which the coding strand is paired with an unmethylated CpG. This finding indicates that the functional capacity of DNMT1 to establish symmetry after initial deoxycytosine methylation was insufficient.

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Disclosures

The authors have no financial conflicts of interests.

References

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PLASTICITY OF Ifng PROMOTER DNA METHYLATION IN Th2 ONTOGENY


Supplemental Table I

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Supplemental Table I. Oligonucleotides used for PCR and EMSA. The oligonucleotides used as PCR primers for amplification of bisulfite modified DNA (first eight entries), amplification of DNA recovered from chromatin IPs (next two entries), and as EMSA probes are listed. For the generation of EMSA probes, one coding strand oligo was annealed with the complementary non-coding strand oligo. Methylated cytosines are denoted as -(Me)C.
Plasticity of Ifng promoter DNA methylation across Th2 ontogeny

A. Interferon Gamma

B. Coding strand

C. -53 CpG effector

D. -53 CpG memory
Supplemental Figure 1. (A) Flexible production of IFN-γ in Th2 memory cells under Th1 recall conditions. Mean (±SEM) IFN-γ production per 1,000 donor-derived cells one week after recall activation and culture in Th1 conditions is shown. Results are the average of eight independent experiments. (B) Increased methylation of the non-coding strand of the Ifng promoter in Th2 effectors deficient in either T-bet or STAT4. As in Fig. 1, the mean (±SEM) number of methylated CpG dinucleotides per clone analyzed is shown for WT Th2 effectors and Th2 effectors deficient in either T-bet or STAT4. Wildtype data are reproduced from Fig. 1. (C) Frequency of CpG methylation at C-53 in STAT4 or T-bet deficient Th2 effector and memory cells. Each bar represents the frequency of methylation (±SEM) of the -53 CpG dinucleotide in Th2 effector (left panel) or memory (right panel) samples. The wildtype effector and memory cell data are reproduced from Fig. 1E and Fig. 4C, respectively. (* p<0.05, ** p<0.01, *** p<0.001)