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Localized DNA Demethylation at Recombination Intermediates during Immunoglobin Heavy Chain Gene Assembly

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Abstract

Multiple epigenetic marks have been proposed to contribute to the regulation of antigen receptor gene assembly via V(D)J recombination. Here we provide a comprehensive view of DNA methylation at the immunoglobin heavy chain (IgH) gene locus prior to and during V(D)J recombination. DNA methylation did not correlate with the histone modification state on unarranged alleles, indicating that these epigenetic marks were regulated independently. Instead, pockets of tissue-specific demethylation were restricted to DNase I hypersensitive sites within this locus. Though unarranged diversity (DH) and joining (JH) gene segments were methylated, DJH junctions created after the first recombination step were largely demethylated in pro-, pre-, and mature B cells. Junctional demethylation was highly localized, B-lineage-specific, and required an intact tissue-specific enhancer, Eq. We propose that demethylation occurs after the first recombination step and may mark the junction for secondary recombination.


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Abbreviations: CGI, CpG islands; DH, IgH diversity region; DHS, DNase I hypersensitive sites; DP, double positive; H3K4me3, histone H3 trimethylated at lysine 4; H3K9me, histone H3 methylated at lysine 9; H3K9me2, H3 dimethylated at lysine 9; IgH, immunoglobin heavy chain; JH, IgH joining region; VH, IgH variable region.

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Introduction

Tissue-specific gene expression requires multiple epigenetic changes. These include nuclear location, chromatin remodeling, covalent histone modifications, and DNA methylation [1–4]. Recent genome-wide analyses reveal several important correlations between gene activity and epigenetic modifications. Transcriptionally inactive genes are marked by histone H3 methylation at lysines 9 and 27 (H3K9me, H3K27me), whereas histone acetylation and H3K4 methylation are associated with gene activity [5]. H3K9 acetylation and H3K4 methylation have been inversely correlated with CpG methylation, consistent with the long-established view that transcriptionally active promoters are hypomethylated [6].

Most studies of CpG methylation vis-à-vis transcription have focused on gene promoters, particularly those that contain CpG islands (CGI). Such promoters are typically unmethylated and are transcriptionally active; conversely, methylated CGI promoters are usually transcriptionally silent. The role of CpG methylation in non-CGI promoters is less clear [7]. Many tissue-specific promoters fall in this category and, in a limited number of cases where examined, such promoters also have reduced CpG methylation in tissues where they are active. Most recently, the advent of whole genome CpG mapping has drawn attention to possible functions of CpG methylation within gene bodies [8,9]. Proposed functions for such CpGs include transcription elongation and the regulation of splicing. The lack of a coherent picture for the role of CpG methylation in non-CGI contexts indicates an ongoing need for analysis of CpG methylation, particularly in tissue-specific genes that lack CGIs.

Antigen receptor genes of B and T lymphocytes serve as excellent paradigms for developmentally regulated gene expression. Immunoglobin heavy chain (IgH) genes are assembled during B lymphocyte development by juxtaposition of variable (VH), diversity (DH), and joining (JH) gene segments by a process known as V(D)J recombination [10]. The mouse genome contains approximately 150 VH gene segments, 10 to 13 DH gene segments, and four JH gene segments, dispersed over 2 Mb [11,12]. DH to JH recombination occurs first, followed by VH recombination to the rearranged DJH junction (Figure 1). These two steps produce a
DNA methylation at CpG dinucleotides is implicated in the regulation of gene expression in mammals. However, the regulation of DNA methylation itself is less clear despite recent advances in identifying enzymes that add or remove methyl groups. We have investigated the dynamics of DNA methylation during genome rearrangements that assemble antigen receptor genes in developing B lymphocytes to determine whether methylation status correlates with rearrangement potential. Two recombination events generate immunoglobulin heavy chain (IgH) genes. The first step brings together diversity (D<sub>H</sub>) and joining (J<sub>H</sub>) gene segments to produce DJ<sub>H</sub> junctions. We show that both gene segments are methylated prior to rearrangement, whereas the DJ<sub>H</sub> product is demethylated.

The DJ<sub>H</sub> junctional demethylation is tissue-specific and requires an enhancer, E<sub>μ</sub>, located within the IgH locus. The latter observations indicate that localized demethylation of the DJ<sub>H</sub> junction occurs after the first recombination step and thus does not guide this first step of IgH gene assembly. Our working hypothesis is that recombination induces demethylation of recombinant product and may mark the junction for the second step of IgH rearrangement, juxtaposition of variable (V<sub>H</sub>) gene segments to rearranged DJ<sub>H</sub> products to produce fully recombined V(D)J alleles.

fully recombined V(D)J allele, with the potential to encode heavy chain protein. IgH expressing cells develop into pre-B cells where immunoglobulin κ or λ light chain genes rearrange. Cells that make both IgH and IgL polypeptides express cell surface immunoglobulin, and are exported out of the bone marrow to become mature functional B cells.

DNA methylation was the earliest epigenetic mark associated with immunoglobulin gene regulation [13,14]. Using a variety of cell lines, these pioneering studies showed that Vk promoters that were rearranged, and therefore transcriptionally active, lacked CpG methylation. Because these studies used restriction enzyme isoschismers, it was difficult to define the extent of demethylation on recombined κ alleles in these studies; however, a site located approximately 10 kb 5′ of the promoter of a rearranged Vk21 remained methylated. Subsequently, studies by Bergman, Cedar and colleagues showed that one κ allele is preferentially demethylated at a site close to the Cκ exons at the pre-B cell stage of B cell differentiation. Preferential Vk recombination of the demethylated allele led them to propose that demethylation permits Vk to Jκ recombination [15]. Analyses of transgenic mice containing synthetic recombination substitutes were also consistent with the idea that demethylated alleles recombine preferentially [16,17]. Additionally, de-methylation state of this site has also been proposed to play a role in somatic hypermutation in germinal centers [18].

Compared to these extensive studies at the κ locus, relatively little is known about developmental regulation of DNA methylation at the IgH locus. Two relatively recent studies evaluated the role of methylation in V<sub>H</sub> gene rearrangements [19,20]. Within the small family of V<sub>H</sub>S107 genes, the methylation status of one CpG in pro-B cells correlated with recombination potential. Both studies also examined the status of the 3′-most V<sub>H</sub> gene segment, V<sub>H</sub> 81X, that rearranges most frequently. Two CpG sites within the coding region remained methylated in pro-B cells whereas a CpG near the recombination signal sequence was demethylated. However, the extent of demethylation of all genes examined was comparable in pro-B cells where V<sub>H</sub> genes recombine and in non-B lineage cells where V<sub>H</sub> genes do not recombine. Thus, methylation status could not be directly correlated with rearrangement potential. More importantly, virtually nothing is known about CpG methylation in DJ<sub>H</sub>–Cκ part of the locus, where V(D)J recombination is initiated [21].

Here we used the bisulfite modification method to assay DNA methylation in the DJ<sub>H</sub>–Cκ domain of the IgH locus prior to the onset of recombination and as recombination proceeds. The only sites of extensive tissue-specific DNA demethylation in the unarranged locus corresponded to a promoter close to DQ52 and the intronic enhancer E<sub>μ</sub>. Additionally, sequences close to the intergenic control region [22], which marks the 5′ boundary of the DJ<sub>H</sub>–Cκ domain, were partially demethylated. These regions correspond to the only known DNase I hypersensitive sites in this part of the IgH locus. All CpGs close to, or within, other rearrangeable DJ<sub>H</sub> or J<sub>H</sub> gene segments remained hypermethylated regardless of whether they were marked with activation or inactivation histone modifications. However, DJ<sub>H</sub> junctions that were generated after the first recombination step were completely demethylated. Junctional demethylation was highly localized, B lineage-specific, and required the presence of an intact E<sub>μ</sub>. These observations suggest that localized demethylation of the DJ<sub>H</sub> junction occurs after the first recombination step and may mark the junction for subsequent V<sub>H</sub> gene rearrangements.

### Results

**Tissue-Specific DNA Demethylation Coincides with DNase I Hypersensitive Sites**

Histone modifications across the unarranged DJ<sub>H</sub>–Cκ domain of the IgH locus show marked heterogeneity. The region encompassing the Jκ gene segments is marked by the highest levels of histone acetylation and histone H3 trimethylation at lysine 4 (H3K4me3) (Figure 1) [23–25]. The 5′- and 3′DJ<sub>H</sub> gene segments, DFL16.1 and DQ52, are also associated with these active modifications, whereas the six to nine DSP gene segments that lie in between are marked by repressive H3 dimethylation at lysine 9 (H3K9me2). Two tissue-specific DNase I hypersensitive sites (DHS) in this part of the locus correspond to a promoter associated with DQ52 and the intronic enhancer E<sub>μ</sub>. A cluster of three DHSs was recently identified just 5′ of DFL16.1 [22]. These latter regions contain binding sites for the transcription factor CTCF [26] and have been proposed to serve as the 5′ boundary of the DJ<sub>H</sub>–Cκ domain [27].

To investigate the DNA methylation state of the unarranged locus, we purified genomic DNA from pro-B cells obtained from the bone marrow of RAG2-deficient mice to use in bisulfite modification assays modified from Frommer et al. [28]. We used at least two independent DNA preparations starting with cells obtained from six mice for each sample. Methylation profiles of the regions amplified from two independent experiments were comparable (Figure S1). We sequenced approximately 12–50 alleles (Table S1), of which 12 representative clones are shown throughout the text. The mb-1 promoter and β-globin locus control region served as positive [29] and negative controls [30], respectively (Figure S2); we used CD4<sup>+</sup> CD8<sup>+</sup> double positive thymocytes (DP) as a lineage control and kidney genomic DNA as a non-lymphoid control. The relative positions of all CpGs are shown in Figure S5.

We found that sequences near DQ52 and E<sub>μ</sub> were substantially demethylated in RAG2-deficient pro-B cell DNA compared to kidney DNA (Figure 2). In contrast, unarranged DFL16.1 and DSP gene segments, which are marked by active and inactive histone modifications [23], respectively, were methylated. While the methylation status of DSP gene segments was consistent with earlier association of H3K9me2 modification with CpG methyl-
The methylated state of DFL16.1 did not follow this paradigm. An amplicon that included the JH1 gene segment located within the peak of active modifications was partially demethylated in pro-B cells compared to kidney. Note that the DQ52 and JH1 amplicons, that are demethylated and partially methylated, respectively, are separated by only about 170 nucleotides that contain two CpGs. These observations indicate that the prominent peak of H3ac and H3K4me3 encompassing the JH gene segments is not sufficient to direct CpG demethylation of this region. Moreover, the JH region has been shown to bind the highest levels of recombinase proteins RAG1 and 2, to form a recombination center at which IgH rearrangement initiates [21]. Clearly, the partially methylated state of this region does not preclude RAG 1/2 recruitment. Additionally, DQ52 and

Figure 1. Immunoglobulin heavy chain locus and B cell development. Schematic of the murine IgH locus showing variable (VH, blue, n represents approximately 150 VH gene segments), diversity (DH, grey, n represents six to nine DSP gene segments), and joining (JH, orange) gene segment [11,12]. Exons encoding the constant regions of IgM and IgD are indicated as Cμ and Cδ. A promoter 5’ of DQ52, the 3′-most DH gene segment, is indicated by the yellow oval and the intronic enhancer Eμ by a teal oval. Top line shows the germline (GL) configuration with associated histone modifications in B lineage precursors [23–25]. Histone H3 and H4 acetylation are shown in orange and presence of heterochromatic H3K9 methylation by the red line. Vertical red arrows represent the tissue-specific DNase I hypersensitive sites in the germline state. Next two lines show sequential stages of VDJ recombination at the IgH locus. DX to JH rearrangement occurs first resulting in a DJH junction and, depending on which DX rearranges, residual upstream unrearranged DXs may be present. VH rearrangement occurs to the DJH junction to generate a VDJH junction; during this process unrearranged DXs are lost from the genome.

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Figure 2. DNA methylation in the ΔH-Cμ domain of the IgH locus. Purified genomic DNA from CD19+ pro-B cells obtained from the bone marrow of RAG2-deficient mice was used in bisulfite modification assays. 400–500-bp amplicons corresponding to ΔH and Jμ gene segments and regulatory sequences (DQ52 and Eμ) as indicated were cloned and sequenced. Each horizontal line represents the methylation status of a sequenced DNA segment.
DFL16.1 have been shown to recombine most frequently among DH gene segments [32–35], yet they had distinctly different methylation states. The methylation status of DH and JH gene segments suggests that the first step of Ig gene assembly may not be regulated by DNA methylation.

Because both DQ52 and Eμ coincide with tissue-specific DHSs, we examined the methylation status of newly identified DHSs located approximately 6, 4, and 1 kb 5′ of DFL16.1. We found two clusters of CpG dinucleotides centered approximately at 6.5 and 4 kb 5′ of DFL16.1. The precise location of these regions and the relative location of CpG dinucleotides within each region are shown in Figure S3. The cluster at ~6.5 was partially demethylated in primary pro-B cells compared to DP thymocytes that served as a non-B lineage control (Figure 3). The cluster at ~4 kb was similarly methylated in both cell types. Because neither location corresponded precisely with the DHSs, we also examined shorter stretches of CpG dinucleotides in this region. Two sites located at ~6 kb were significantly demethylated in pro-B cells compared to DP thymocytes, whereas one out of three CpGs at ~5 kb was completely demethylated in pro-B cells. Two CpGs at ~3 kb were completely demethylated in both pro-B cells and DP thymocytes. Finally, a cluster of CpGs in the ~1.3 kb region was largely methylated in pro-B cells (see below). Overall, the majority of sites in this region remained methylated in pro-B cells, with very specific sites being targeted for demethylation. Possible interpretations of these observations are discussed below.

Localized DNA Methylation at Recombination Intermediates

To determine whether DNA methylation was altered by recombination, we examined pro-B cells purified from the bone marrow of wild-type mice, which contain DJH junctions as well as unrearranged alleles. We found that unrearranged DFL16.1, DSP, and JH1 regions were methylated, while Eμ region was demethylated (Figure 4A) as seen in RAG2-deficient pro-B cells (note that un-rearranged DFL16.1 and DSP regions in these cells represent fully germline IgH alleles as well as those in which a downstream DH gene segment has undergone recombination to form a DJH junction). However, DFL16.1/JH1 and DSP/JH1 recombinant junctions were demethylated (Figures 4B and S4). For junctions that involved DFL16.1, demethylation of both parts of the recombination reaction was evident due to the presence of analyzable CpGs in each segment. Many DSP-involving junctions lacked CpG dinucleotides contributed from the DSP part. This is because all DSP gene segments lie within a 4-kb repeat unit [23,36], which is reflected in all DSP family members sharing a common CpG located 3′ of the gene segment. Two DSP gene segments, DSP2.2 and DSP2.3, have a CpG within the gene segment. In addition, the amplicon encompassing DSP2.3, includes a third CpG dinucleotide 5′ of the gene segment (Figure S3). The 3′ CpG is lost during recombination, and deletions that occur during recombination lead to many junctions that have no CpG contribution from the DH part (Figures 4B, 4C, and S4). Yet, demethylation of DSP/JH1 junctions was evident from the state of residual CpGs that fell within the JH1 region.

During B cell development, pro-B cells that contain a functional IgH allele undergo several rounds of cell division and differentiate into small pre-B cells [37]. We found that pro-B cells also contained demethylated DFL16.1/JH1 and DSP/JH1 junctions (Figure 4C). Sequence diversity at recombination junctions provided an unequivocal measure of allelic individuality in our experiments. For example, complete demethylated alleles, such as DFL16.1/JH1 junctions in pre-B cells, could have arisen by aberrant amplification of a single allele. However, analysis of the junctional sequences (Figure S4) showed that each of these represented unique alleles.

Demethylated DJH junctions could arise by preferential juxtaposition of demethylated DH and JH gene segments; alternatively, demethylation could be targeted to the junction after recombination. One prediction of allelic demethylation prior to recombination is that unrearranged DH is located 5′ of the DJH junction (see Figure 1) should be demethylated. To determine whether DNA demethylation was specific to the DJH junction, or occurred more widely over recombinant allele, we used mature B cells. Earlier studies have shown that about 40% of mature B cells from wild-type mice contain VDJH rearrangement on both alleles [37,38]. In such cells, unrearranged DH gene segments are lost from the genome. The remainder contain one VDJH rearranged allele and one DJH rearranged allele; these cells therefore contain unrearranged DH gene segments 5′ to the rearranged DJH junction (Figure 5A). Mature B cells with germline IgH alleles have not been identified in normal mice. First, we determined the methylation state of the DJH junctions in mature B cells. As seen in pro- or pre-B cells, DFL16.1/JH1 and DSP/JH1 junctions were demethylated in mature B cells (Figure 5C). We then analyzed germline DFL16.1 in mature B cells to score for all alleles with downstream DH arrangements. We also analyzed a region approximately 1.3 kb 5′ of DFL16.1 that would be intact on DFL16.1 rearranged alleles. We found that both these regions were hypermethylated in mature B cells approximating that seen in RAG2-deficient pro-B cells (Figure 5B). We conclude that demethylation of recombinant alleles is highly localized to the DJH junction.

DNA Demethylation Requires the Intronic Enhancer Eμ

To understand the basis for localized demethylation, we considered the following possibilities. First, a specific DH gene segment and the JH region could be demethylated immediately after recombination. In this model demethylation would precede rearrangement and could possibly target the recombinase to a pre-selected DH gene segment. Second, demethylation may occur during recombination, after the DNA breaks have been introduced by recombinase. Third, demethylation of the DJH junction could occur after rearrangement. The last model predicts the existence of methylated DJH junctions that are somehow trapped between recombination and demethylation steps. As described below, we found two sources of such DJH recombinant alleles.

The intronic enhancer Eμ controls key features of the IgH locus assembly via its effects on chromatin structure. Of note, Eμ-deleted IgH alleles undergo DH recombination but not VH...
Three newly identified DNase 1 hypersensitive sites are located at approximately 6–6.5, 4–4.5, and 0.4–1.3 kb 5’ of DFL16.1. Genomic DNA from primary RAG-deficient pro-B cells and DP (CD4+ CD8+) thymocytes were used in bisulfite mapping experiments to examine CpG methylation. Five amplicons covering regions between 3 kb and 7 kb 5’ of DFL16.1 were modified, cloned, and sequenced. The distribution of CpG dinucleotides within each amplicon are noted in Figure S3. Filled and open circles represent methylated and unmethylated residues, respectively. Pie charts summarize the percentage of methylated alleles at each position.

Figure 3. DNA methylation status of DNase 1 hypersensitive sites 5’ of DFL16.1. Three newly identified DNase 1 hypersensitive sites are located at approximately 6–6.5, 4–4.5, and 0.4–1.3 kb 5’ of DFL16.1. Genomic DNA from primary RAG-deficient pro-B cells and DP (CD4+ CD8+) thymocytes were used in bisulfite mapping experiments to examine CpG methylation. Five amplicons covering regions between 3 kb and 7 kb 5’ of DFL16.1 were modified, cloned, and sequenced. The distribution of CpG dinucleotides within each amplicon are noted in Figure S3. Filled and open circles represent methylated and unmethylated residues, respectively. Pie charts summarize the percentage of methylated alleles at each position.
Figure 4. DNA methylation status after the first step of IgH locus recombination. Pro-B cells were purified from the bone marrow of wild-type C57BL/6 mice. Data shown are derived from two independent preparations of pro- and pre-B cells obtained from six to eight mice in each experiment. This cell population contains a mix of germline and partially rearranged IgH alleles. After bisulfite modification, the genomic DNA was used to amplify unrearranged (A) and DJH rearranged junctions containing DFL16.1 and DSP gene segments (B). Cytosines derived from DJ and JH gene segments are marked as circles and squares, respectively. Filled and open circles, or squares, indicate methylated and unmethylated cytosines, respectively. Numbers within regions marked as DFL16.1, DSP and JH in (B) denote CpG dinucleotides corresponding to the configuration of these residues at the respective unrearranged gene segments. For example, of the five CpGs at unrearranged DFL16.1 only the first two are retained in DFL16.1/JH1 junctions. The total numbers of CpG dinucleotides are reduced in junctional sequences because some residues are lost during VDJ recombination as described in the text. Additional heterogeneity is due to the imprecise nature of recombination. Pie charts summarize the percentage of methylated cytosines at each position, except where the number of alleles falls below 12 (indicated by asterisks). (C) Methylation state of rearranged DJH alleles in purified pro-B cells. This population contains a mix of VDJH recombined and DJH recombined IgH alleles (see Figure 5A). Note that the number of circles and squares representing DJ or JH-associated CpGs differed in the DJH junctions compared to the corresponding unrearranged regions due to junctional variability.
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Figure 5. DNA methylation state of unrearranged and DJ\textsubscript{H} recombined alleles in mature B cells. (A) Mature B cells were purified from spleens of C57BL/6 mice, and the genomic DNA was subjected to bisulfite modification assays. 40% of these cells contain two VDJ\textsubscript{H} recombined alleles and the remainder contains one VDJ\textsubscript{H} and one DJ\textsubscript{H} recombined allele. (B) Amplicons corresponding to unrearranged DFL16.1 gene segment.
and a region centered 1.3 kb 5' to DFL16.1 were cloned and sequenced. For comparison, methylation of the same region in pro-B cells derived from RAG2-deficient bone marrow was shown in the bottom panel. Filled and open circles indicate methylated and unmethylated cytosines. Pie charts summarize the percentage of methylated cytosines at each position; data are derived from two independent spleen B cell preparations with two to four mice in each experiment. (C) DjH junctions were amplified from bisulfite-modified DNA, followed by cloning and sequencing. Circles and squares represent cytosines from Dj and JH1 gene segment, respectively. Filled and open circles, or squares, indicate methylated and unmethylated cytosines, respectively. Numbers within regions marked as DFL16.1, DSP, and JH1 denote CpG dinucleotides corresponding to the configuration at the respective unrearranged gene segments. For example, of the five CpGs at unrearranged DFL16.1, only the first two are retained in DFL16.1/JH1 junctions. Variations in the total number of cytosines are due to imprecise joining during VDJ recombination. Pie charts summarize the percentage of methylated cytosines. The asterisk indicates positions where less than 12 CpGs were observed due to reduced representation caused by junctional diversity.

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Discussion

Systematic analysis of DNA methylation of unrearranged and partially rearranged IgH alleles in primary cells revealed several interesting features. First, the lack of correlation between histone modifications and DNA methylation status indicates that these marks are independently regulated. This was most clearly evident in the JH region that is marked with the highest levels of histone acetylation and H3K4me3 in the unrearranged state, yet remains hypermethylated. Furthermore, germline DFL16.1 and the DSP gene segments were comparably methylated despite being differentially marked at the level of histone modifications. These observations appear to be at odds with genomic studies that show a correlation between histone acetylation and DNA demethylation, and H3K9 methylation and DNA methylation [31,44,45]. We suggest that the results from genome-wide studies may be skewed towards promoter-based CGIs. Instead, the sites we analyzed were largely non-CGIs and included enhancers (such as Eμ, promoters (such as DQ52), cryptic promoters (such as DSP and DFL16.1, see below), and regions that cannot be categorized as any of these.

An important corollary of this observation is that pre-rearrangement DNA methylation status correlates poorly with recombination potential. Recent studies identified the JH region as a RAG1/2-rich recombination center [21]. Our observation suggests that DNA demethylation is not required to generate the recombination center. Additionally, DFL16.1 and DQ52 gene segments that rearrange most frequently [32–35] have very different levels of DNA methylation prior to rearrangement; conversely, DSP gene segments that rearrange relatively less frequently have comparable levels of DNA methylation as DFL16.1. Taken together, our working model is that DNA methylation status does not guide the first step of IgH gene assembly.

We note, however, that we cannot unequivocally rule out the possibility that selective demethylation of specific D1H and JH segments occur in a subset of cells just prior to recombination. For example, while the JH1 region that we analyzed was largely methylated in pro-B cells prior to rearrangement, we observed that a minority of alleles were demethylated in both RAG-sufficient and RAG-deficient pro-B cells. These demethylated JH1 alleles may represent a subset of cells in which DNA recombination will occur preferentially to the JH1 gene segment. It will be interesting to determine whether other JH gene segments are similarly singled out for demethylation in subsets of pro-B cells.

Second, sites of maximal tissue-specific CpG demethylation in the germline IgH locus corresponded to the two strongest DNase I hypersensitive sites in the 70-kb D1H-Cμ domain, DQ52 and Eμ.
Because these regions share transcriptional regulatory properties, it is likely that their demethylation is linked to transcription or transcription-associated chromatin changes. Additionally, we noted highly selective CpG demethylation of some sequences and partial demethylation of others 5' of DFL16.1 where three additional DNase 1 HSs have been recently identified. Though these observations link DNase 1 hypersensitivity to DNA methylation, this doesn’t seem to be always the case. For example, JH region is known to be highly sensitive to DNase 1 digestion [46] (without being associated with “classical” DNase 1 hypersensitive sites), yet it is not demethylated. A possible model for this pattern of methylation emerges from the recent demonstration that Eμ is...
in spatial proximity to the cluster of DHSs 5’ of DFL16.1 [27,47,48]. Since \(E_m\) itself has a demethylating potential (\(E_m\) flanking regions are methylated on \(E_m\)-deficient alleles), perhaps \(E_m\) looping to 5’ DFL16.1 sites “delivers” demethylating activities to this region. The partial demethylation observed at 5’ DFL16.1 sites may reflect that such loops are present in only a fraction of pro-B cells at any given time. Consistent with the idea that \(E_m\) induces demethylation in a subset of cells, the form of partial

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**Figure 7. DNA methylation of IgH alleles in thymocytes.** CD4⁺CD8⁺ thymocytes from C57BL/6 mice were enriched by adsorption to PNA-coated plastic plates. Genomic DNA purified from these cells was used in bisulfite modification analysis. Amplicons corresponding to unrearranged parts of IgH allele (A) and DJ₉ junctions (B) were cloned and sequenced. Circles and squares depict CpGs corresponding to \(\alpha\) and \(J_\mu\) cytosines, respectively. Filled circles/squares correspond to methylated cytosines; pie charts summarize the percentage of methylated cytosines at each position except where the number of sequenced alleles falls below 12, indicated by asterisks. Untemplated CpGs incorporated during VDJ recombination were found to be methylated (filled diamonds). Data shown were obtained from two independent preparations of thymocytes, using one mouse per experiment.

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demethylation seen at DFL16.1 (−6.5) involves extensive demethylation of some alleles and essentially complete methylation of others (Figure 3). Eβ has also been proposed to loop to DHS5-7 of the 3′ regulatory region at the 3′ of the IgH locus. Interestingly, earlier studies by Giambra et al. [49] showed that DHS5-7 was partially demethylated in a pro-B cell line in a manner similar to the methylation state 5′ of DFL16.1. This pattern may be the consequence of Eβ looping to DHS5-7 in a subset of pro-B cells. Overall, we propose that the pattern of DNA demethylation in the germline IgH locus is determined by spatial proximity to Eβ.

Third, we found that DJH junctions were extensively demethylated. Though we cannot discount the possibility that germline Dα1 and Jα1 gene segments were demethylated just before recombination, we favor the hypothesis that demethylation of DJα1 junction occurred after recombination. The reasons for this are two-fold: first, DJα1 junctions remain methylated in Eβ-deficient pro-B cells and in CD4+CD8+ thymocytes. Our interpretation is that these DJα1 alleles are caught in an intermediate stage where recombination has occurred but demethylation has not. Second, we think it is unlikely that demethylation occurred prior to recombination followed by re-methylation of DJα1 junctions based on the state of DQ52/Jα1 junctions. In both Eβ-deficient pro-B cells and DP thymocytes the methylation status of DQ52/Jα1 junctions was such that the DQ52 portion was demethylated and the Jα1 portion was methylated. If demethylation preceded rearrangement, generation of each hybrid junction would require re-methylation of a subset of closely associated CpGs.

Though our data clearly demonstrate that DNA demethylation of associated gene segments is not essential for DJα1 to Jα1 recombination, we note that the two instances of methylated DJα1 junctions identified in this study involve circumstances where the frequency of DJα1 recombination is lower than in wild-type pro-B cells. DJα1 recombination has been estimated to be 5–10-fold lower in Eβ-deleted pro-B cells [39] and only about 30%–50% of IgH alleles in DP thymocytes [42] have DJα1 junctions. We cannot rule out, therefore, that gene segment demethylation may increase the efficiency of DJα1 recombination in wild-type pro-B cells. Because Eβ deletion also leads to loss of other accessibility-associated epigenetic marks in the unrearranged locus, it is difficult to deconvolute the contribution of each mark to recombination efficiency.

How might DNA demethylation be targeted to DJα1 junctions? We have previously shown that DJα1 recombination activates cryptic bi-directional promoters associated with most Dα1 gene segments [23]. Transcriptional activity and associated RNA polymerase II recruitment is restricted to the DJα1 junctions, and drops off before the unrearranged Dα1 segments located 5′ of the junction. These changes require Eβ and the simplest interpretation is that recombination places cryptic Dα1 promoters under the influence of Eβ. Our working model is that DJα1-promoter/Eβ interaction brings Eβ-associated demethylating activity to DJα1 junctions, thereby resulting in Eβ-directed demethylation. Because Eβ’s influence does not extend to the next upstream Dα1 gene segment, DJα1 demethylation is highly localized. In this model the substantial demethylation of DJα1 junctions compared to partial demethylation of looping sites may be due to stronger interaction of Eβ with DJα1 promoters compared to Eβ interaction with the 3′ RR or 5′ of DFL16.1 sequences.

Does DJα1 demethylation serve a function? In this regard it is interesting to note that Vα1 recombination is significantly reduced in both instances where DJα1 junctions remain methylated (Eβ-deleted alleles and in DP thymocytes). Though this is consistent with the view that DJα1 demethylation facilitates Vα1 recombination, we think that the regulation of Vα1 recombination is more complex. The highly localized Eβ-dependent DJα1 demethylation that we describe in this report adds to the emerging evidence that DJα1 junctions are distinguished from un-rearranged Dα1 gene segments by several forms of epigenetic changes [41]. These include activation-associated histone modifications, such as H3 acetylation and H3K4me3 and increased sensitivity to DNase I. Like DJα1 demethylation, these alterations are also restricted to DJα1 junctions and are Eβ dependent. Taken together, our working model is that all these DJα1-restricted epigenetic changes work in concert to promote the timing and precision of Vα1 recombination.

Materials and Methods

Mice

Rag2-deficient and C57BL/6 mice were obtained from Jackson Laboratory (Bar Harbor, Maine) and housed in pathogen-free facilities at the NIA or at the University of Massachusetts Medical School. Eβ-deficient mice were generated and maintained in the facilities at Children’s Hospital (Boston, Massachusetts). Mouse experiments were approved by the Animal Care and Use Committees at the NIA, Harvard Medical School, and the University of Massachusetts Medical School.

Cell Purification

A magnetic cell-sorting system was used to purify pro-B and mature B cells as previously described [25]. Briefly, to obtain pro-B cells with IgH in germline configuration bone marrow cells were recovered from 6-8-wk-old Rag2-deficient mice by flushing the femur and tibia with 10% calf serum in PBS. CD19+ cells were purified from single cell suspension of bone marrow by positive selection using paramagnetic microbeads (Miltenyi Biotech). To obtain mature B cells, the same procedure was followed using cells obtained from the spleen of C57BL/6 mice. The resulting cells were greater than 90% CD19+ by flow cytometry.

FACS Sorting of Pre-B Cells and Pro-B cells from C57BL/6 Mice

Freshly isolated bone marrow cells were re-suspended to 6×107/ml in staining media containing biotin-, flavin-, and phenol red-deficient RPMI 1640 (Irvine Scientific), 10 mM Hepes, pH 7.2, 0.02% sodium azide, 1 mM EDTA, and 3% newborn calf serum, and treated with Fc block for 10 min on ice. Cells were incubated with primary antibodies for 20 min and then washed three times, incubated with SA-Cy5PE for 15 min, and then washed three more times. After the final wash, samples were re-suspended in 1 μg/ml propidium isothio to exclude dead cells. Primary antibodies included B220 APC; CD43 (clone S7) PE; IgM FITC; Ly6C FITC; BP-1 (clone 6C3) biotin. Antibodies were purchased from BD Biosciences/Pharmingen, eBioscience, or CALTAG. FACS Sorting was performed on a 3-laser, 9-detector MoFlo. Data were analyzed for presentation purposes with FlowJo software (Tree Star).

CD4+CD8+ Cells

DP thymocytes were purified by PNA agglutination. In brief, equal volumes of cell suspension (7–8×106 cells/ml) and PNA solution (1.5 mg/ml) were incubated for 1 h at 4°C, followed by sedimentation in fetal calf serum (Invitrogen). PNA-agglutinated cell pellet was dissociated by D-galactose treatment resulting in greater than 90% pure CD4+CD8+ cells.

Genomic DNA Isolation and Modification

Genomic DNA was extracted from 1–5×106 cells by using the DNeasy Blood & Tissue Kit (QIAGEN) according to the manufacturer’s protocol.
Sodium bisulfite modification was carried out as described earlier [20] with some modifications. Briefly, 1 μg of genomic DNA was denatured by incubating with NaOH at 37°C for 15 min. Sodium metabisulfite (3 M) and hydriquinone (0.5 mM) were added to the samples together and incubated overnight at 55°C. The reaction was stopped by incubating samples with NaOH 15 min at 37°C. Modified DNA was purified using GeneClean II (MP Biomedicals). Modified DNA was precipitated with NaOH 15 min at 37°C. Sodium metabisulfite (3 M) and hydriquinone (0.5 mM) were added to the samples and incubated overnight at 55°C. The reaction was stopped by incubating samples with NaOH 15 min at 37°C. Modified DNA was purified using GeneClean II (MP Biomedicals). Modified DNA was precipitated and dissolved in 30 μl of 1 mM Tris- HCl (pH 8.0).

Modified templates were amplified by nested PCR using primers listed in Table S2. PCR products were separated by agarose gel electrophoresis, purified using QIAquick gel extraction kit (QIAGEN), and cloned into pCR II-TOPO vector. Mini prep DNA containing amplicon inserts were identified by PCR and sequenced commercially (SeqWright). Sequence analysis showed 99%–100% bisulfite modification efficiency (Figure S6).

Supporting Information

Figure S1 Comparison of DNA methylation status between two independent experiments. For each region analyzed in the paper, we used at least two independent DNA preparations starting with cells obtained from six mice for each sample. Methylation profiles of the regions amplified from two independent experiments were comparable, as shown with the example of the DFL16.1 region in RAG−/− pro-B mice.

Figure S2 DNA methylation state of the mb-1 and β-globin locus activating region in different cell types. For our experiments we have chosen the previously characterized mb-1 gene and its promoter as a positive and β-globin locus activating region as a negative control. Sequences from at least 12 individual colonies were analyzed for each cell type. Consistent with the observations of the Hagman group [29] mb-1 gene and its promoter are hypomethylated in early stages of B cell development. As expected mb-1 and its promoter were methylated in CD4+CD8+ DP thymocytes and kidney cells, which served as a negative control for this region. β-globin locus activating region was methylated in a RAG2-deficient pro-B cell line, primary RAG2-deficient pro-B cells, and kidney.

Figure S3 Relative positions of the CpG dinucleotides in the amplicons analyzed. Amplicons covering 11 regions of the germline IgH locus are depicted. Numbers in circles represent the order of the CpGs in each amplicon. DH gene segments are highlighted in green, JH region is highlighted in orange. Recombination signal sequences (RSSs) with 12- and 23-bp spacers are highlighted in light blue and grey, respectively. Distances (in nucleotides) between CpG dinucleotides and gene segments are indicated.

Figure S4 Analysis of individual sequences at DJH junctions. While analyzing DNA methylation profiles, one question arises especially in the case of demethylated sequences: whether this is a single DNA molecule having been amplified during PCR. To answer that question we have performed a careful analysis of DNA at the joining regions; nucleotides introduced by non-template end-joining permit unequivocal assignment of sequences to individual alleles. Aligned sequences of a representative cell type, pre-B cells, are shown here.

Figure S5 DNA methylation state of the Eμ region in Eμ− pro-B cells. The schematic representation of the Eμ region in Eμ− cells is represented on top. CpGs are depicted as vertical bars, those CpGs that correspond to the ones in the wild-type sequence adjacent to the Eμ deletion sites, are depicted in blue color, the ones that are introduced during cre-deletion in brown.

Figure S6 Bisulfite modification efficiency. We compared each modified sequence with the genomic DNA sequence to determine the efficiency of cytosine conversion. Sequences used in the analysis showed 99%–100% modification efficiency.

Table S1 Summary of bisulfite modification analysis. Number of sequences analyzed for each amplicon (gene segment) in each cell type (cell type) are indicated (number of sequences).

Table S2 Primer sequences used to amplify indicated amplicons for bisulfite modification analysis.

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Author Contributions

The author(s) have made the following declarations about their contributions: Conceived and designed the experiments: RSeimlyan, RSen. Performed the experiments: RSeimlyan, II, PP. Analyzed the data: RSeimlyan, II, PP. Wrote the paper: RSeimlyan, RSen.