Unexpected Effects of a Heterozygous Dnmt1 Null Mutation on Age-Dependent DNA Hypomethylation and Autoimmunity

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DNA methylation modifies gene expression. Methylation patterns are established during ontogeny, but they change with aging, usually with a net decrease in methylation. The significance of this change in T cells is unknown, but it could contribute to autoimmunity, senescence, or both. We examined the effects of a null mutation in DNA methyltransferase 1 (Dnmt1), a gene maintaining DNA methylation patterns, on immune aging. Whereas aged control mice developed hypomethylated DNA, autoimmunity, and signs of immune senescence as predicted, the knockout mice surprisingly increased DNA methylation and developed signs of autoimmunity and senescence more slowly. To identify potential mechanisms, we compared transcripts of DNA methyltransferase and methylcytosine binding protein family members in control and knockout mice. McCP2, a methylcytosine binding protein involved in gene suppression and chromatin inactivation, was the only transcript differentially expressed between old knockout mice and controls, and thus it is a candidate for a gene product mediating these effects.
of an effect of the Dnmt1 mutation on methylation changes with aging.

To test these hypotheses, we compared the development of histologic and serologic signs of autoimmunity in young, middle aged, and old heterozygous Dnmt1 knockout mice with their wild-type littermates. Selected parameters of T-cell function and gene expression known to change with aging were also compared. Additional studies included a comparison of total genomic d\(^{3}C\) content and expression of DNA MTase and methylcytosine binding protein transcripts between groups. The results support the association between age-dependent, progressive DNA hypomethylation and the development of autoimmunity. Surprisingly, however, the Dnmt1 knockout mice increased genomic d\(^{3}C\) content with aging, and they showed a decline in the development of several age-dependent immune abnormalities. A search for possible secondary effects of the knockout mutation showed that these mice maintained MeCP2 expression with aging, which may maintain patterns of DNA methylation and gene expression with aging. (MeCP2 is a methylcytosine binding protein involved in gene suppression and chromatin inactivation.)

**Materials and Methods**

**Mice**

Heterozygous female Dnmt1 knockout mice, bred onto a C57BL/6 background, and their wild-type littermates were obtained from Jackson Labs (Bar Harbor, ME) and housed in a specific pathogen-free environment in the University of Michigan Unit for Laboratory Animal Medicine. Sentinel mice from this colony were tested every 3 months for antibodies to murine viral pathogens, and all tests were negative during the experimental period. At the time of the study, the groups were aged approximately 6, 11, and 18 months, with a variability of \(\pm 1\) month.

**Histologic Analysis**

Tissues were fixed, embedded in paraffin, sectioned, and stained with hematoxylin and eosin, using previously published protocols (5,6). Slides were read by a pathologist who was blinded to the groups being studied, and they were scored on a 0–4 scale. Activity of glomerulonephritis was scored according to published criteria (15).

**Isolation of Lymphocytes and Measurement of Lymphocyte Function**

Spleens were removed from mice and splenocytes recovered as described (5). Where indicated, CD4\(^{+}\) T cells were enriched by two cycles of treatment with anti-CD8 plus anti-I\(^{a}\)b (Pharmingen, San Diego, CA) and rabbit complement (Pel-Freeze, Brown Deer, WI) and previously published protocols (5). This typically resulted in a twofold to threefold increase in the percentage of CD4\(^{+}\) cells. Proliferative and IL-2 responses were measured by using flat-bottomed microtiter wells (Costar, from Corning; Corning, NY) and protocols described by others (16). Briefly, 50 \(\mu\)l of anti-CD3 (10 \(\mu\)g/ml in phosphate-buffered saline; 2C11, from Pharmingen) were added to the microtiter wells, and allowed to bind overnight at 4\(^{\circ}\)C. The wells were then washed three to four times with phosphate-buffered saline (PBS), and 10\(^{5}\) cells were added to each well in 200 \(\mu\)l of Roswell Park Memorial Institute 1640 (RPMI) supplemented with 10\(^{\circ}\) fetal calf serum (FCS) and 50 \(\mu\)M of 2-mercaptoethanol. Where indicated, anti-CD28 (Pharmingen, 2.25 \(\mu\)g/ml) was also added; 150 \(\mu\)l of media was removed at 48 hours, saved for enzyme-linked immunosorbent assays (ELISAs), and replaced with an equal volume of fresh media. At 54 hours, 1 \(\mu\)Ci of tritiated thymidine (\(^{3}\)H-TdR) was added, and the cells were harvested 2 hours later and proliferation measured by \(^{3}\)H-TdR incorporation. IL-2, IL-4, IL-10 and interferon gamma (IFN-\(\gamma\)) in culture supernatants were detected by two-site ELISA, using matched pair antibodies (Pharmingen) according to the manufacturer’s instructions. Levels were determined graphically by using a standard curve generated with recombinant murine cytokines (Genzyme, Cambridge, MA).

**Flow Cytometric Analysis**

Phenotypic characterization was performed by using anti-CD4-fluorescein isothiocyanate (FITC), anti CD8-FITC, anti-CD11a-FITC, and anti-CD44-phycocerythrin (PE) (all from Pharmingen) as described by Quddus and colleagues (5). Controls included MS Ig-PE and mouse serum immunoglobulin (MS Ig)-FITC. All samples were analyzed by using a Coulter ELITE flow cytometer.

**Autoantibodies**

Sera were diluted 1:200 with PBS, and then they were added to Immulon 4 flat-bottomed microtiter wells (Dynex Technologies, VA) coated with ssDNA or dsDNA as described (5,6). The plates were then washed and bound immunoglobulin (Ig) detected with horse radish peroxidase (HPO)-conjugated polyclonal goat antimouse IgM or IgG (Sigma, St. Louis, MO) as described (5,6). All determinations were performed in quadruplicate and repeated at least once. A reference standard consisting of pooled sera from mice with lupus (17) was included on each plate, and results are expressed relative to this standard. Total IgG and IgM were also measured by ELISA, using previously published protocols (5,6).

**Quantitation of Genomic Deoxymethylcytosine Content**

The d\(^{3}C\) content was compared between groups by using SssI methylation assays (18). Briefly, 500 ng of genomic DNA from CD4-enriched T cells was incubated 37\(^{\circ}\)C for 4 hours with 4 U of SssI CpG methytransferase (New England BioLabs, Beverly, MA), 1.5 \(\mu\)M of S-adenosyl-L-[methyl-\(^{3}\)H] methionine (\(^{3}\)H-SAM) (77 Ci/mmol; Amersham, Arlington Heights, IL), and 1.5 \(\mu\)M of nonradioactive S-adenosylmethionine (New England BioLabs) in buffer provided by the manufacturer. Five \(\mu\)l of 2.5-mM nonradioactive SAM was then added and the reaction mixture was spotted on Whatman GF/C 2.4-cm\(^{2}\) filter disks, which were air dried for 15 minutes. The filters were washed with 6 ml of 5% TCA followed by 6 ml of 70% ethanol, and they were air dried overnight; \(^{3}\)H incorporation was measured by using a scintillation spectrometer. All determinations were performed in triplicate, and results were normalized to the young control.
group, arbitrarily defined as 100%. Similar studies were performed on brain tissue from old mice.

**RT-PCR Amplification of DNA Methyltransferase and Methylcytosine Binding Protein Families**

Tissue stored in liquid nitrogen was rapidly thawed, placed in Trizol (GIBCO-BRL, Gaithersburg, MD) and homogenized. Total RNA was purified according to the manufacturer’s protocol. Real-time reverse transcription polymerase chain reaction (RT-PCR) was performed with a LightCycler (Roche, Indianapolis, IN). With the use of a One-Step RNA Amplification Kit with SYBR Green I (Roche), 200 ng of total RNA was converted to cDNA and then amplified in one step. Conditions for the reactions were as follows: reverse transcription at 55°C for 10 minutes; denaturation at 95°C for 30 seconds; amplification at 95°C for 1 second, 56°C for 10 seconds, and 72°C for a period determined by the product length (1 second per 25 nucleotides) for a total of 45 cycles. At the completion of amplification, melting characteristics of the product were determined. In each experiment, water was included as a negative control to rule out primer dimer formation. A series of five dilutions of one RNA sample were also included to generate a standard curve, and this was used to obtain relative concentrations of the transcript of interest in each of the RNA samples. A curve, and this was used to obtain relative concentrations of one RNA sample were also included to generate a standard curve, and this was used to obtain relative concentrations of the transcript of interest in each of the RNA samples. A standard curve was generated during each experiment by using one of the primer pairs. Relative concentrations were then determined by the second derivative method with the LightCycler computer software. Amplification of GAPDH was performed to confirm that equal amounts of total RNA were added for each sample and that the RNA was intact and equally amplifiable among all samples.

Primer sequences were as follows, listed as forward; reverse:

- **GAPDH**: 5′-TTG AAG GGT GGA GCC AAA CG; 5′-TGG GAG TTG CTG TTG AAG TCG
- **Dnmt1**: 5′-AGG ATG AGA GGG AGG AGA AGA GAC; 5′-GGT GGA GTC GTA GAT GGA CAG TTT C
- **Dnmt3a**: 5′-CAC CAG CCA AGA AAC CCA GAA AG; 5′-TCC CAT CAA AGA GAG ACA GCA CG
- **Dnmt3b**: 5′-CAA ACC CAA CAA GAA GCA ACG AG; 5′-CCA GAC ACT CCA CAC AGA AGC ATC
- **Mbd1**: 5′-CTG TTG GAC GCT CAG ACA TC; 5′-TCC TCT TTT ACC ACC CAA GC
- **Mbd2**: 5′-CAC GAA CCC GAC GAG CAA TAA G; 5′-TCA GTG CCT CCT CCA GTT TCT TG
- **Mbd3**: 5′-ACC CCA GCA ACA AGG TCA AG; 5′-TTT GGA AAG GAG GTG GAC G
- **Mbd4**: 5′-ACT CGG CTT GCT TGC TAT TG; 5′-TGA AGG ATT TGC GTC TTG GG
- **MeCP2**: 5′-CAA CCT TCA GCC CAC CAT TC; 5′-TCT CCA GGA CCC TTT TCA CC.

**Statistical Analysis**

The difference between means was tested by using the unpaired Student’s t test with pooled variance, calculated with Systat and Sigmastat software (SPSS Science, Chicago, IL). Linear regression and analysis of variance was similarly calculated with Systat and Sigmastat software. Differences between grouped assays were tested by using Fisher’s Method of Combining Independent Tests (19). Fisher’s Exact Test was used to test the significance of histologic data.

**RESULTS**

**Development of Autoimmunity**

The effect of the Dnmt1 null mutation on the long-term health of mice is unknown, so weights and overall health were compared among young, middle aged, and old knockout mice and controls. No differences in weights, general health, or mortality were observed among groups during the duration of this study. Complete autopsies were performed on 6 mice from each of the 6 groups (young, middle aged, and old; knockout and control), and no evidence for malignancy was identified. No splenomegaly was identified in any of the groups, and total numbers of splenocytes were similar between the control and old knockout mice (6.92 ± 0.48 × 10^7 vs 6.54 ± 0.98 × 10^7, mean ± SEM of six mice/group, control vs knockout). This suggests that the Dnmt1 mutation has no major effect on the health of the mice at these ages.

The development of autoimmunity in the Dnmt1 knockout mice and their wild-type littermates was compared. At later ages, C57BL/6 mice develop lymphocytic infiltrates of the salivary glands and liver, as well as of other organs (10), so histologic evidence for these lesions was sought in young, middle aged, and old Dnmt1 knockout and control mice. The most consistent abnormalities detected were mononuclear infiltrates of the liver and salivary glands. Figures 1A and 1B show representative histology of these organs from affected mice. By 18 months of age, a majority of mice from both groups had evidence for autoimmune salivary gland lesions. These results compare favorably with those reported by others (10). However, in the 11-month-old age group, significantly (p = .02) more of the control mice had moderate to severe lesions compared with the knockout mice (Table 1). These lesions are typically ~86% T cells and 7% B cells in aged C57BL/6 mice (10), although the composition of the lesions was not determined in the Dnmt1 knockout mice. The liver lesions were observed in 5 of 6 old control mice, whereas only 1 of 6 old knockout mice had the mononuclear cell infiltrates. Four of the six aged control mice had evidence for glomerulonephritis and interstitial inflammation (average activity score 3.8 ± 1.5, mean ± SEM), whereas 2 of the 6 aged knockout mice had similar lesions (activity 1.7 ± 1.1). Three of six of the old control mice had mild to moderate lymphocytic infiltration of the lungs; none of six old knockout mice did. It is noteworthy that in all organs, the controls had greater evidence
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for autoimmunity compared with their knockout littermates (p < .01 overall by Fisher’s method for combining independent tests). Overall the incidence of these lesions is somewhat higher than those reported previously (10). However, in the present study, tissues were counted as positive if lymphocyte aggregates were observed in the sections, whereas in the previous report (10), tissues were only scored as positive if more than 50 mononuclear cells were observed in the center of the tissue at 100× magnification.

Serologic evidence for autoimmunity was also sought. Sera were obtained from young, middle aged, and old knockout and control mice, and they were tested for IgM and IgG anti-ssDNA and anti-dsDNA antibodies (Figure 2). No difference in titer was observed in the young and middle aged mice. However, in all cases, sera from the aged control mice had greater titers of anti-ssDNA (p < .05) and anti-dsDNA (p < .025) antibodies relative to their Dnmt1-deficient littermates (p < .005 overall). Total IgM and IgG were also measured in the aged groups, to exclude the possibility that an increase in autoantibodies reflected a polyclonal increase in immunoglobulin. ELISA assays demonstrated no significant differences in total IgM (OD 0.377 ± 0.007 vs 0.363 ± 0.004, old knockouts vs old controls, mean ± SEM, using a 1:100 serum dilution) or IgG (OD 0.456 ± 0.005 vs 0.447 ± 0.009). No significant differences in total IgG or IgM levels were observed in the young or middle aged groups as well (not shown). Together, these data indicate that the wild-type mice develop anti-DNA antibodies and tissue evidence for autoimmunity more rapidly than the Dnmt1 knockout mice.

Immune Characterization

The observation that autoimmunity developed more slowly in the Dnmt1-deficient mice raised the possibility that the knockout mice had impaired T-cell function, thus preventing the development of autoimmunity. It was also possible that the Dnmt1 null mutation modified the development of immune senescence. As a way to test these possibilities, T-cell subsets, proliferative responses, and cytokine secretion, all reported to change with aging (12), were com-

Table 1. Salivary Gland Inflammation: Middle-Aged Mice

<table>
<thead>
<tr>
<th>Mouse Strain</th>
<th>Negative</th>
<th>Mild</th>
<th>Moderate–Severe</th>
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</thead>
<tbody>
<tr>
<td>Control</td>
<td>1</td>
<td>1</td>
<td>4</td>
</tr>
<tr>
<td>Knockout</td>
<td>4</td>
<td>3</td>
<td>0</td>
</tr>
</tbody>
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*p = .02, negative + mild vs moderate + severe.

Figure 2. Anti-DNA antibodies in Dnmt1-deficient and control mice. Sera were obtained from Dnmt1-deficient (knockout, or KO; ☐) or wild-type littermates (control; ◆) at the indicated ages, and they were tested for the following autoantibodies: A, IgM anti-ssDNA; B, IgM anti-dsDNA; C, IgG anti-ssDNA; and D, IgG anti-dsDNA. Results represent the mean of quadruplicate determinations performed on 10 mice/group and are expressed relative to a standard consisting of sera from mice with lupus induced with a DNA methylation inhibitor. Standard errors averaged 15.6% of the means.
pared between groups. Flow cytometric analysis was used to compare the percentage of CD4+ and CD8+ T cells in the spleen in the young, middle aged, and old knockouts and controls. No significant differences were observed at any age (not shown). Others have reported that “memory” CD4+ T cells, expressing high levels of CD44, accumulate with age (12), so CD44 expression was compared between groups (Figure 3). Overall, the number of CD4+ memory cells increased with age in both groups (\( p = .001 \) by analysis of variance, or ANOVA). However, T cells from the knockout mice tended to have fewer CD4+, CD44 high T cells than controls (\( p = .031 \) overall by ANOVA), which reached statistical significance in the old group (\( p = .003 \) by \( t \) test), but not at the younger ages, suggesting a more pronounced difference in the older mice.

Proliferative responses were tested by stimulating unfractionated splenocytes and CD4-enriched splenocytes from young and old Dnmt1 knockout mice and controls with immobilized anti-CD3 with and without anti-CD28 (Figure 4). No differences were seen between the young groups with either form of stimulation. The control group showed essentially no change in response to either stimulus with aging. Although murine T-cell proliferative responses usually decline with age by 18 months of age (12), the decline appears to be delayed when immobilized anti-CD3 is used as the stimulus (16), perhaps reflecting a relatively stronger stimulus from immobilized anti-CD3. In contrast, the CD4-enriched population from the knockout mice demonstrated an increased proliferative response with age to anti-CD3 with and without anti-CD28 (\( p < .05 \), young vs old). These responses were significantly greater than those in the age-matched controls (\( p < .005 \) overall).

Cytokine responses were also compared by using CD4-enriched populations from the young, middle aged, and old knockouts and controls. The cells were stimulated with immobilized anti-CD3 and soluble anti-CD28 as in Figure 4, and supernatants harvested 48 hours later. T cells from the control mice showed an age-dependent decline in IL-2 production (Figure 5) as described by others (12; \( p < .005 \) young vs old), whereas no significant decrease was observed in the knockouts. The difference in the slopes (young to old) was significant (\(-0.480 \pm 0.099 \) vs \(-0.029 \pm 0.042\).
0.129, control vs knockout, \( p < .02 \). The amount of IL-2 secreted by T cells from control and Dnmt1 knockout mice was also significantly different in the old group \( (p = .041) \). Although there was a trend for the knockout mice to secrete less IL-2 in the younger age groups, this did not achieve statistical significance. No significant differences were observed in IL-4, IL-10, or IFN-\( \gamma \) production between T cells from both young and old groups (not shown). These results argue against impaired T-cell responsiveness as a mechanism for the protection of autoimmunity developing in the knockout mice. In addition, the observation that the knockout mice develop signs of autoimmunity more slowly, develop fewer “memory” cells, and do not lose IL-2 secretory capacity by 18 months of age suggests that some aspects of the immune system may age more slowly in the knockout mice.

**DNA Methylation Analysis**

The effect of age on genomic d\( ^{30} \)C content was compared in the knockout mice and controls. DNA from the CD4-enriched splenocytes was incubated with \( ^{3} \)H-SAM and S\( _{3} \)SI methylase, and then it was precipitated and washed; \( ^{3} \)H incorporation was compared between groups. S\( _{3} \)SI will methylate all unmethylated CG pairs, so \( ^{3} \)H incorporation is inversely proportional to d\( ^{30} \)C content, with greater \( ^{3} \)H incorporation reflecting a lower d\( ^{30} \)C content. Figure 6A shows that lymphocyte DNA from control mice demethylates in an age-dependent fashion as described by others \((8,20,21)\). In addition, DNA from young Dnmt1 knockout mice is relatively hypomethylated compared with that of age-matched littermates \( (p < .01) \), which is consistent with published reports \((13,22)\). Unexpectedly, however, total d\( ^{30} \)C content increased with age in the knockout mice, so that by 18 months the d\( ^{30} \)C content was significantly greater \( (p < .01) \) than in age-matched littermates, and approximated that of the young wild-type mice. Similar results were observed in the brains of the aged mice \( (p < .02, \text{Figure } 6B) \), suggesting the existence of compensatory mechanisms for Dnmt1 deficiency.

**Expression of DNA Methyltransferase and Methylcytosine Binding Protein Families**

Because brain tissue from the aged knockout mice demonstrated greater amounts of d\( ^{30} \)C than did age-matched controls, similar to lymphocytes, levels of DNA MTase and methylcytosine binding protein transcripts were compared by real-time RT-PCR in brains from young and old knockout and control mice, using 3 mice/group. There was a small and statistically insignificant decrease in Dnmt1 mRNA in brains from young knockout mice relative to controls \((96 \pm 5 \text{ vs } 132 \pm 16, \text{mean } \pm \text{SEM, knockout vs control}) \), and similarly no significant difference in the brains from old mice \((106 \pm 25 \text{ vs } 112 \pm 27) \). Similar results were found for Dnmt3b, whereas Dnmt3a mRNA was barely detectable in all groups, requiring \( \approx 30 \) cycles of amplification for detection. Methylcytosine binding proteins have been implicated in modifying chromatin structure and gene expression \((1,23)\), so expression of MBD1–4 and MeCP2 transcripts were compared. No significant differences in MBD1, MBD2, or MBD4 mRNAs were found between groups as well. MBD3 mRNA demonstrated a significant decrease with aging in the control \( (p = .03) \) and knockout \( (p = .008) \) groups (Figure 7A). However, because the change was identical in both groups, it is unlikely that this gene product contributes to the phenotypic differences between the controls and knockout mice. In contrast, although MeCP2 decreased with age in the control mice \( (p = .001) \), no decrease was observed in the knockout mice, and the difference in MeCP2 levels between old control and knockout mice was significant \((p = .03, \text{Figure } 7B) \). GAPDH was run as a control and showed no significant differences between groups.

**DISCUSSION**

These experiments were designed to determine the effects of heterozygous Dnmt1 deficiency on lymphocyte DNA methylation with aging, and to correlate the results with the development of autoimmunity and immune senescence. Four significant observations were made. First, whereas lymphocyte DNA from the young Dnmt1 knockout mice was hypomethylated relative to age-matched controls, total d\( ^{30} \)C content increased with age in the knockouts. This is in contrast to the wild-type littermates, which demonstrated the expected age-dependent decrease. Second, the onset of age-dependent autoimmunity was delayed in the knockout mice compared with controls. Third, characteristics of T-cell aging, in particular development of the memory subset and the rate of decrease in IL-2 secretion, showed altered developmental patterns in the knockout mice. Fourth, levels of MBD3 mRNA decreased with age in both control and knockout mice, whereas MeCP2 mRNA decreased only in the control mice.

![Figure 6. Genomic DNA methylation in CD4-enriched T cells from Dnmt1-deficient and control mice.](https://academic.oup.com/biomedgerontology/article-abstract/56/6/B268/526413)
The relative hypomethylation of lymphocytes from the young knockout mice was not unexpected, because others have reported similar findings (22). However, the observation that knockdown levels of Dnmt1 transcripts in the knockouts were identical to controls was surprising. Because Dnmt1 levels are decreased in the Dnmt1 knockout embryonal stem cells (13), it is possible that a decrease in Dnmt1 exists during development, resulting in hypomethylation that is maintained at least through 6 months of age despite higher levels of Dnmt1 transcripts. This is consistent with the observation that the increase in methylation is delayed and not observed until 11 months of age.

The changes in genomic d\textsuperscript{4}C content observed in both groups could potentially affect gene expression. However, phenotypic changes occurred largely in the control group. Therefore, it seems reasonable to propose that the changes in the control group occur in transcriptionally relevant regions of the genome. Other work from our group demonstrates that in mice, age-dependent methylation changes occur outside of CpG islands (manuscript in preparation), suggesting the changes in methylation occur in promoters lacking islands. Slightly less than half of murine genes lack CpG islands (24), so the changes could potentially affect a large number of genes. In contrast, the paucity of functional changes in the knockout group suggest that the increases in d\textsuperscript{4}C may occur largely outside of regulatory regions.

The age-dependent increase in DNA methylation observed in the knockout mice could be viewed as paradoxical, because expression of only one Dnmt1 allele would be expected to lead to a more pronounced decrease in DNA methylation with age. However, the increase in DNA methylation observed in the knockout mice may represent a compensatory mechanism, for which there is precedent. Our group has reported that inhibiting T-cell DNA methylation with pharmacologic inhibitors such as 5-azacytidine or procainamide results in a compensatory increase in Dnmt1 mRNA expression and increased DNA MTase enzyme activity (18,25). This is supported by our observation that brain Dnmt1 mRNA levels were not significantly different between groups. It is thus possible that similar regulatory mechanisms lead to overexpression of the remaining Dnmt1 allele. Two additional DNA MTases with de novo methyltransferase capabilities, Dnmt3a and Dnmt3b, have recently been described (26), but minimal Dnmt3a mRNA was detectable in the brains of the mice, and no significant differences in Dnmt3b mRNA were observed. However, as gene expression at the protein level was not measured, it is possible that differential expression in the activity of one or more of these enzymes might be responsible. It is also possible that a relative increase in a demethylase in the control mice could account for progressive hypomethylation in this group. A recent report suggests that methylcytosine binding domain 2 (MBD2) might have demethylase activity, although others have been unable to confirm this result (27–29). It is thus relevant to note that there were no differences in MBD2 transcripts between groups. Others have described a ribonucleoprotein complex with glycosidase activity in chickens, which results in DNA demethylation (30). The differential expression of a similar enzyme in mammals might account for the decrease in d\textsuperscript{4}C content observed in the control mice. Future experiments will have to compare expression of these enzymes at the protein level in various tissues from young, middle aged, and old Dnmt1 knockout mice and controls under both quiescent and mitogen-stimulated conditions, to test these possibilities.

Comparison of transcripts of the methylcytosine binding protein family demonstrated that MBD3 decreased with age in both controls and knockouts, and thus is unlikely to contribute to the differences in age-dependent DNA methylation between the groups. However, MeCP2 transcripts decreased in the controls but not the knockouts. This protein binds methylcytosine and contains a transcriptional repression domain that interacts with a transcriptional corepressor complex containing histone deacetylases (31). MeCP2 can also suppress gene expression through mechanisms independent of histone deacetylases (32). A decrease in this protein could potentially lead to abnormal expression of genes repressed by both mechanisms, contributing to the aging process. It is also possible that persistence of its expression may contribute to an increase in d\textsuperscript{4}C with age in the knockout mice by promoting chromatin inactivation. This hypothesis is indirectly supported by the observation that the knockout mice are phenotypically unchanged with aging despite increasing d\textsuperscript{4}C levels, consistent with progressive methylation and inactivation of transcriptionally silent regions. However, as noted above, a number of other mechanisms could also account for the difference in DNA methylation between the two groups. Future studies will be required to clarify the significance of these changes in these transcripts. Such studies would include confirmation of differences at the protein level, effects of overexpression and underexpression of the relevant proteins on DNA methylation, and studies on how the Dnmt1 mutation leads to preservation of its expression.
The observation that DNA hypomethylation occurs after 11 months of age in the control mice and correlates with the development of autoimmunity is consistent with the previously noted association between T-cell DNA hypomethylation and autoimmunity. In this case hypomethylation was caused by aging of the control mice, rather than pharmacologic treatment of T lymphocytes. This association is supported by the delayed appearance of autoimmunity and the progressive increase in DNA methylation in the knockout mice. It is also of interest that the relatively hypomethylated young knockout mice did not develop autoimmunity. This suggests either that autoimmunity develops slowly and was prevented by the compensatory methylation, or that the methylation status of genes crucial to the development of autoimmune status is tightly regulated, and is methylated normally despite a total decrease in genomic d^5C content.

It is possible that DNA hypomethylation contributes to autoimmunity in normal aging and our drug-induced model, because similar features are seen in both models, including the development of anti-DNA antibodies and an autoimmune liver disease with a chronic, focal inflammatory infiltrate. Renal and lung lesions were also more common in the control mice, and they are seen in the drug-induced DNA hypomethylation model (6). The features of autoimmunity in C57BL/6 mice are more pronounced when they are at 24 months of age (10), suggesting that examination of older mice might give further evidence of autoimmunity. The aged C57BL/6 mice also developed sialadenitis, which is in contrast to the drug-induced model. It is possible that the sialadenitis is a strain-specific feature, and C57BL/6 mice have not been studied in the drug-induced lupus model. Alternatively, other changes in methylation patterns associated with aging but not produced in the drug-induced model may contribute, or methylation change in the salivary glands themselves might participate.

There were also several observations indicating that the development of age-dependent changes in the immune system are different between the Dnmt1 knockout mice and controls. The memory subset, which increases with age, developed more slowly in the knockout mice. Similarly, IL-2 responses decreased more slowly with age in the knockout mice. The mechanisms causing the appearance of the memory subset and the decrease in IL-2 production with aging are unknown. A decrease in T-cell proliferative capacity in the knockout mice could explain both observations, but proliferative capacity was actually greater in the knockouts than in controls at 18 months, arguing against this interpretation. The observation that the decrease in IL-2 production and development of the memory subset is delayed in the knockout mice suggests that changes in DNA methylation may be responsible for their appearance in the control mice, and that preventing DNA hypomethylation slows their development, although other mechanisms are possible, including increased genomic instability caused by DNA hypomethylation (33). If the alterations caused by the mutation prevent or delay the development of immune senescence, an important test of this hypothesis will be to determine if mice with heterozygous Dnmt1 deficiency live longer and are more disease resistant than their wild-type littermates. These studies are in progress.

The identity of the lymphocyte genes affected by age-dependent changes in DNA methylation is of interest and highly relevant to these studies. Future studies will have to address this question. However, to approximate the number of genes affected, our group has treated human CD4+ T-lymphocyte lines with the DNA methylation inhibitor 2-deoxy-5-azacytidine, and we have compared gene expression in treated and untreated cells by using Affymetrix oligonucleotide arrays. Approximately 619 out of 7000 genes tested demonstrated a twofold or greater change in their level of expression (unpublished results). Furthermore, our group has reported that ~15% of human T-lymphocyte genes with CpG islands are variably methylated on a clonal basis by middle age (34). These observations suggest that a relatively large number of genes could be modified by age-dependent changes in DNA methylation.

An alternative interpretation of these results is that effects of the Dnmt1 mutation on nonlymphoid tissues are responsible for the immunologic effects, preventing the development of autoimmunity and immune senescence indirectly. This seems unlikely, because adoptive transfer studies demonstrate that lymphocytes from young mice will restore immune responses in old recipients (35), and that lymphocytes from old mice will induce autoimmunity in young recipients (36). This suggests that these age-dependent phenomena are unique to the lymphocytes and are not affected by the host. Exclusion of this possibility will require adoptive transfer experiments, in which lymphocytes from the control group are transferred into the knockout mice, and retention of phenotype assessed.

In summary, in this study, wild-type control mice demonstrated an age-dependent decrease in T-cell genomic d^5C content and developed autoimmunity similar to that reported by our group to be induced by hypomethylated T cells, whereas the Dnmt1 mice increased lymphocyte d^5C content with age and demonstrated delayed development of autoimmunity. This supports the proposed association between DNA hypomethylation and autoimmunity (5,6). The observation that d^5C content increased with aging in the knockout mice also suggests that counteracting DNA hypomethylation may prevent immune changes with aging. Persistence of high expression of MeCP2 may also help maintain methylation levels with aging. Immune senescence is a complex area, with many potential abnormalities noted, and multiple mechanisms possible. The data presented in this report suggest that one mechanism might be changes in DNA methylation patterns, with subsequent effects on gene expression and chromatin structure.

Acknowledgments

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