3-20-2017

Efficient Remyelination Requires DNA Methylation

Sarah Moyon  
*Icahn School of Medicine*

Dan Ma  
*University of Cambridge*

Jimmy L. Huynh  
*Icahn School of Medicine*

David J.C. Coutts  
*University of Cambridge*

Chao Zhao  
*University of Cambridge*

*See next page for additional authors*

Follow this and additional works at: [https://academicworks.cuny.edu/asrc_pubs](https://academicworks.cuny.edu/asrc_pubs)

Part of the [Neurology Commons](https://academicworks.cuny.edu/asrc_pubs)

**Recommended Citation**

Moyon, Sarah; Ma, Dan; Huynh, Jimmy L.; Coutts, David J.C.; Zhao, Chao; Casaccia, Patrizia; and Franklin, Robin J. M., "Efficient Remyelination Requires DNA Methylation" (2017). CUNY Academic Works.  
[https://academicworks.cuny.edu/asrc_pubs/14](https://academicworks.cuny.edu/asrc_pubs/14)

This Article is brought to you for free and open access by the Centers & Institutes at CUNY Academic Works. It has been accepted for inclusion in Advanced Science Research Center by an authorized administrator of CUNY Academic Works. For more information, please contact AcademicWorks@cuny.edu.
Disorders of the Nervous System

Efficient Remyelination Requires DNA Methylation

Sarah Moyon,1,* Dan Ma,4,* Jimmy L. Huynh,1,2 David J.C. Coutts,4 Chao Zhao,4 Patrizia Casaccia,1,2,3 and Robin J.M. Franklin4

DOI: http://dx.doi.org/10.1523/ENEURO.0336-16.2017

1Department of Neuroscience, Icahn School of Medicine at Mount Sinai, New York, NY 10029, 2Department of Genetics and Genomic Sciences, Icahn School of Medicine at Mount Sinai, New York, NY 10029, 3Neuroscience Initiative Advanced Science Research Center, CUNY, New York, NY 10031, and 4Wellcome Trust-Medical Research Council Cambridge Stem Cell Institute and Department of Clinical Neurosciences, University of Cambridge, Cambridge, CB2 0AH, UK

Visual Abstract

Oligodendrocyte progenitor cells (OPCs) are the principal source of new myelin in the central nervous system. A better understanding of how they mature into myelin-forming cells is of high relevance for remyelination. It has recently been demonstrated that during developmental myelination, the DNA methyltransferase 1 (DNMT1), but not DNMT3A, is critical for regulating proliferation and differentiation of OPCs into myelinating oligodendrocytes.

Significance Statement

The regenerative therapy of enhancing remyelination is the subject of much current investigation for a number of central nervous system disorders. However, its mechanisms remain incompletely understood. A recent study identified a distinct role of the DNA methyltransferase 1 (DNMT1), but not DNMT3A, is critical for regulating proliferation and differentiation of OPCs into myelinating oligodendrocytes after lysolecithin-induced demyelination. Overall, this is of high relevance, as it indicates that neonatal and adult oligodendrocyte progenitor cells might be characterized by distinct epigenetic landscapes that may need to be taken into consideration for the development of future therapeutic strategies.
(OLs). However, it remains to be determined whether DNA methylation is also critical for the differentiation of adult OPCs during remyelination. After lysolecithin-induced demyelination in the ventrolateral spinal cord white matter of adult mice of either sex, we detected increased levels of DNA methylation and higher expression levels of the DNA methyltransferase DNMT3A and lower levels of DNMT1 in differentiating adult OLs. To functionally assess the role of DNMT1 and DNMT3 in adult OPCs, we used mice with inducible and lineage-specific ablation of Dnmt3a and/or Dnmt1 (i.e., Plp-creERT2;Dnmt3a-flox, Plp-creERT2;Dnmt1-flox, Plp-creERT2;Dnmt1-flox;Dnmt3a-flox). Upon lysolecithin injection in the spinal cord of these transgenic mice, we detected defective OPC differentiation and inefficient remyelination in the Dnmt3a null and Dnmt1/Dnmt3a null mice, but not in the Dnmt1 null mice. Taken together with previous results in the developing spinal cord, these data suggest an age-dependent role of distinct DNA methyltransferases in the oligodendrocyte lineage, with a dominant role for DNMT1 in neonatal OPCs and for DNMT3A in adult OPCs.

Key words: Adult oligodendrocyte progenitor cells; DNA methylation; remyelination

Introduction

In demyelinating disorders, such as multiple sclerosis (MS), loss of myelin sheaths disturbs axonal conduction and trophic support, eventually leading to irreversible axonal loss and disease progression (Trapp et al. 1998; Nave and Trapp, 2008; Franklin et al. 2012). Remyelination, which restores myelin sheaths to demyelinated axons and thereby restores both axonal function and protection, is regarded as a promising way to prevent disease progression (Dubois-Dalcq et al. 2008; Franklin and Ffrench-Constant, 2008). Oligodendrocyte progenitor cells (OPCs) have been identified as the main source for new myelin formation in the adult central nervous system (CNS; Zawadzka et al. 2010). Therefore, a better understanding of the molecular mechanism regulating their differentiation into myelin-forming cells is highly desirable. It has been proposed that after demyelination, adult OPC differentiation recapitulates developmental myelinization to a large extent, and the expression of well-established differentiation regulatory transcription factors (e.g., Myrf, Nkx2.2, Tcfl4, Sox2) has been shown to change during remyelination (Fancy et al. 2004, 2009; Koening et al. 2012; Moyon et al. 2015; Zhao et al. 2015).

The importance of posttranslational histone modifications during remyelination has previously been reported (Shen et al. 2008). Recently, it has been shown that DNA methylation mediated by the DNA methyltransferase DNMT1 is essential for developmental myelination, where it controls the transition from the proliferative OPC stage to differentiating oligodendrocytes (OLs; Moyon et al. 2016). In this study, we asked whether similar epigenetic mechanisms might be involved in the regulation of adult OPC differentiation during remyelination. Transcriptomic data gathered from laser microdissected regions of CNS white matter at various times after acute experimentally induced demyelination indicate that the expression of Dnmt1 and Dnmt3a are differentially regulated during remyelination (Huang et al. 2011). Both enzyme levels were higher at 5 days post-lesion (dpl), during the early stages of remyelination, and lower at 14 and 28 dpl, suggesting that DNA methylation might also play a role in the transition from adult OPCs to myelinating OLs. A recent study has previously reported genome-wide DNA methylation changes in postmortem brain samples from MS patients compared with controls, suggesting an underlying dysregulation of DNA methylation in MS brains (Huynh et al. 2014).

This study directly addresses the role of DNA methylation in oligodendrogial lineage cells during remyelination in the adult spinal cord. Here we show that DNA methylation and DNA methyltransferase levels are differentially regulated during remyelination. We use lineage-specific inducible genetic ablation of Dnmt1 or Dnmt3a in adult mice to address the functional relevance of DNA methylation perturbations for adult OPC differentiation and the efficiency of remyelination after experimentally induced demyelination.

Materials and Methods

Animals

All experiments were performed according to institutional animal care and use committee–approved protocols and mice were maintained in a temperature- and humidity-controlled facility on a 12-h light-dark cycle with food and water ad libitum. Dnmt1<sup>fl/fl</sup> (Fan et al. 2001; Jackson-Grusby et al. 2001, RRID:MMRRC_014114-UCD) and Dnmt3a<sup>−/−</sup> (Kaneda et al. 2004, RRID:MG:3718448) mice on a C57BL/6 background were crossed with Plp-creERT2 (The Jackson Laboratory, RRID:MG:3696409; Doerflinger et al. 2003).

Lysolecithin injections

Injections were conducted in the ventrolateral spinal cord white matter of 8-week-old animals of either sex, as previously described (Fancy et al. 2009). Briefly, anesthe-
formed on 12-embedded in OCT. Immunohistochemistry was per-
dissected, cryoprotected in sucrose solutions, and frozen
14, or 21 dpl with 4% paraformaldehyde and postfixed
Immunohistochemistry 9 (21 dpl analysis) after lysolecithin injection (day 0).
70°, and 1
needle was advanced through the spine, at an angle of
bral space, and the dura was pierced. A pulled-glass
was exposed, tissue was cleared overlying the interverte-
metal bars on stereotaxic apparatus. The spinal vertebra
rane/oxygen. The vertebral column was fixed between
sia was induced and maintained with inhalational isoflu-
rane/oxygen. The vertebral column was fixed between
normal donkey serum in PBS/Triton X-100 0.3%). After
bating slides in subboiling (94°C) citrate buffer (pH 6.0) for
15 min. Slides were incubated in blocking buffer (5% normal donkey serum in PBS/Triton X-100 0.3%) for 1 h at
room temperature and then overnight at 4°C with the
primary antibodies diluted in a similar blocking buffer (5% normal donkey serum in PBS/Triton X-100 0.3%). After
rinning with PBS 1×, sections were incubated with the Alexa Fluor secondary antibodies and then washed with PBS 1×. Cell nuclei were counterstained with DNA fluo-
scent dye Hoechst 33342 (Sigma B2261) in PBS. Stained tissue or cells were coveredslipped in FluorSave
ning medium (Millipore 345789) and examined on a
Zeiss Axio Observer fluorescence microscope. To quan-
tify the data generated by immunohistochemical staining,
counts were undertaken by an observer who was blinded
to the experimental group from which the sample being analyzed was taken. Counts were made throughout the
entire lesion area which was scanned using the 20× objective of the fluorescence microscope. Labeled cells
were manually counted from the images captured under the
same exposure conditions. AxioVision Rel4.8 software
was used for colocalized color identification and area measurement. Quantification of total cell number, as defined by nuclear (DAPI) staining, was assessed both within the lesion area and within the cor-
responding region of white matter in unlesioned tissue.
sia was induced and maintained with inhalational isoflu-
rane/oxygen. The vertebral column was fixed between
metal bars on stereotaxic apparatus. The spinal vertebra
was exposed, tissue was cleared overlying the interverte-
metal bars on stereotaxic apparatus. The spinal vertebra
rane/oxygen. The vertebral column was fixed between
sia was induced and maintained with inhalational isoflu-
rane/oxygen. The vertebral column was fixed between
normal donkey serum in PBS/Triton X-100 0.3%). After
bating slides in subboiling (94°C) citrate buffer (pH 6.0) for
15 min. Slides were incubated in blocking buffer (5% normal donkey serum in PBS/Triton X-100 0.3%) for 1 h at
room temperature and then overnight at 4°C with the
primary antibodies diluted in a similar blocking buffer (5% normal donkey serum in PBS/Triton X-100 0.3%). After
rinning with PBS 1×, sections were incubated with the Alexa Fluor secondary antibodies and then washed with PBS 1×. Cell nuclei were counterstained with DNA fluo-
scent dye Hoechst 33342 (Sigma B2261) in PBS. Stained tissue or cells were coveredslipped in FluorSave
ning medium (Millipore 345789) and examined on a
Zeiss Axio Observer fluorescence microscope. To quan-
tify the data generated by immunohistochemical staining,
counts were undertaken by an observer who was blinded
to the experimental group from which the sample being analyzed was taken. Counts were made throughout the
entire lesion area which was scanned using the 20× objective of the fluorescence microscope. Labeled cells
were manually counted from the images captured under the
same exposure conditions. AxioVision Rel4.8 software
was used for colocalized color identification and area measurement. Quantification of total cell number, as defined by nuclear (DAPI) staining, was assessed both within the lesion area and within the cor-
responding region of white matter in unlesioned tissue.

**Table 1. Statistical analysis**

<table>
<thead>
<tr>
<th>Code</th>
<th>Data structure Type of test</th>
<th>95% CI</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>(Fig. 1C)</em></td>
<td>Normal distribution, equal variances</td>
<td>ANOVA and Bonferroni posttests</td>
</tr>
<tr>
<td><em>(Fig. 1D)</em></td>
<td>Normal distribution, equal variances</td>
<td>ANOVA and Bonferroni posttests</td>
</tr>
<tr>
<td><em>(Fig. 1F)</em></td>
<td>Normal distribution, equal variances</td>
<td>ANOVA and Bonferroni posttests</td>
</tr>
<tr>
<td><em>(Fig. 1G)</em></td>
<td>Normal distribution, equal variances</td>
<td>ANOVA and Bonferroni posttests</td>
</tr>
<tr>
<td><em>(Fig. 1I)</em></td>
<td>Normal distribution, equal variances</td>
<td>ANOVA and Bonferroni posttests</td>
</tr>
<tr>
<td><em>(Fig. 2B)</em></td>
<td>Normal distribution, equal variances</td>
<td>Student’s t-test</td>
</tr>
<tr>
<td><em>(Fig. 2D)</em></td>
<td>Normal distribution, equal variances</td>
<td>Student’s t-test</td>
</tr>
<tr>
<td><em>(Fig. 2F)</em></td>
<td>Normal distribution, equal variances</td>
<td>Student’s t-test</td>
</tr>
<tr>
<td><em>(Fig. 2H)</em></td>
<td>Normal distribution, equal variances</td>
<td>Student’s t-test</td>
</tr>
<tr>
<td><em>(Fig. 2J)</em></td>
<td>Normal distribution, equal variances</td>
<td>Student’s t-test</td>
</tr>
<tr>
<td><em>(Fig. 3B)</em></td>
<td>Normal distribution, equal variances</td>
<td>Student’s t-test</td>
</tr>
<tr>
<td><em>(Fig. 3D)</em></td>
<td>Normal distribution, equal variances</td>
<td>Student’s t-test</td>
</tr>
<tr>
<td><em>(Fig. 3F)</em></td>
<td>Normal distribution, equal variances</td>
<td>Student’s t-test</td>
</tr>
<tr>
<td><em>(Fig. 3G)</em></td>
<td>Normal distribution, equal variances</td>
<td>Student’s t-test</td>
</tr>
<tr>
<td><em>(Fig. 4B)</em></td>
<td>Normal distribution, equal variances</td>
<td>ANOVA and Bonferroni posttests</td>
</tr>
<tr>
<td><em>(Fig. 4D)</em></td>
<td>Normal distribution, equal variances</td>
<td>ANOVA and Bonferroni posttests</td>
</tr>
<tr>
<td><em>(Fig. 4F)</em></td>
<td>Normal distribution, equal variances</td>
<td>ANOVA and Bonferroni posttests</td>
</tr>
<tr>
<td><em>(Fig. 5B)</em></td>
<td>Normal distribution, unequal variances</td>
<td>Nonparametric Mann Whitney test</td>
</tr>
<tr>
<td><em>(Fig. 5C)</em></td>
<td>Normal distribution, unequal variances</td>
<td>Student’s t-test with Welch’s correction</td>
</tr>
<tr>
<td><em>(Fig. 5E)</em></td>
<td>Normal distribution, unequal variances</td>
<td>Nonparametric Mann Whitney test</td>
</tr>
<tr>
<td><em>(Fig. 5F)</em></td>
<td>Normal distribution, unequal variances</td>
<td>Student’s t-test with Welch’s correction</td>
</tr>
<tr>
<td><em>(Fig. 5H)</em></td>
<td>Normal distribution, unequal variances</td>
<td>Nonparametric Mann Whitney test</td>
</tr>
<tr>
<td><em>(Fig. 5G)</em></td>
<td>Normal distribution, unequal variances</td>
<td>Nonparametric Mann Whitney test</td>
</tr>
</tbody>
</table>

- Tamoxifen injections
- 4-Hydroxytamoxifen (Sigma-Aldrich T56-48) was dis-
solved at 40 mg/ml in 10% ethanol and 90% corn oil (Sigma-Aldrich C8267) for 4 h at 37°C with rotation, and
10 mg was administered by gavage to each mouse at
days 3, 5, and 7 (for 14 dpl analysis) or at days 5, 7, and
9 (21 dpl analysis) after lysolecithin injection (day 0).

**Immunohistochemistry**

For immunohistochemistry, animals were perfused at 5,
14, or 21 dpl with 4% paraformaldehyde and postfixed
overnight in the same solution at 4°C. Spinal cords were
dissected, cryoprotected in sucrose solutions, and frozen
embedded in OCT. Immunohistochemistry was per-
formed on 12-μm cryostat sections. Antigen retrieval was
performed for 5-methylcytosine (5mC) staining by incu-

![Fig. 3G](image-url)
Figure 1. DNA methyltransferases are differently expressed in adult OPCs during remyelination. A, Schematic of the lysolecithin-induced focal demyelination and of the area of NWM used for quantification. B, Representative DNMT1, NKX2.2, and CC1 stainings in NWM and at 5, 14, and 21 dpl (white arrowheads indicate double-positive cells). C, Quantification of the number of double DNMT1 \(^+\) and NKX2.2 \(^+\) cells at 5, 14, and 21 dpl, compared with NWM. D, Quantification of the percentage of double DNMT1 \(^+\) and NKX2.2 \(^+\) or CC1 \(^+\) cells at 5, 14, and 21 dpl, compared with NWM. E, Representative DNMT3A, NKX2.2, and CC1 stainings in NWM and at
To assess the levels of 5mC in OLIG2+ cells, arbitrarily defined as being either low, medium, or high, a macro was created in ImageJ (RRID:SCR_003070) that first localized the OLIG2+ (red) nuclei and then measured the intensity of the 5mC (green) staining within the nuclear area. The intensity value was then normalized by deducting the background staining intensity. For all quantifications, a minimum of three sections of 12-μm thickness from each lesion randomly chosen from n = 4–6 mice was examined. The percentage or density of cells was determined per mouse. The average and standard error was then calculated for each group using GraphPad Prism (GraphPad, RRID:SCR_002798).

Electron microscopy
For electron microscopy, animals were perfused at 21 dpl with 4% glutaraldehyde in PBS containing 0.4 mM CaCl₂ and postfixed in the same solution at 4°C. The spinal cord was coronally sliced at 1-mm thickness and treated with 2% osmium tetroxide overnight before being subjected to a standard protocol for epoxy resin embedding (Zhao et al. 2008). Tissues were sectioned at 1 μm and stained with toluidine blue. Remyelination ranking, in which lesions with the greatest extent of remyelination were assigned the highest rank value, was performed under light microscopy (Ibanez et al. 2003). Ultrathin sections of the lesion site were cut onto copper grids and stained with uranyl acetate before being examined with a Hitachi H-600 transmission electron microscope. G-ratio was quantified on 50-nm sections on a minimum of 70 myelinated and remyelinated axons per animal, three to five mice for each genotype.

Statistical analysis
All statistical analyses were done using GraphPad Prism (Table 1). Unpaired Student’s t test was used for every two datasets with equal variances and for which data followed a normal distribution. If data were not normally distributed, nonparametric Mann–Whitney test was used (for rankings analysis), and if the variances were significantly different, the Welch’s correction was applied (for g-ratio analysis). Two-way ANOVA was used to compare three or more sets of data. For all graphs, error bars are mean ± SEM.
crosed the Dnmt1fl/fl and Dnmt3afl/fl lines with the inducible Plp-creER(t), to target specific ablation of Dnmt1, Dnmt3a, or both Dnmt1 and Dnmt3a in proteolipid protein (PLP)-expressing oligodendroglial cells after lyssolecithin-induced demyelination. All three mutants (Plp-creER(t); Dnmt1fl/fl, Plp-creER(t); Dnmt3afl/fl, and Plp-creER(t); Dnmt1fl/fl and control littermates (Plp-creER(t); Dnmt1fl/fl, Plp-creER(t); Dnmt3afl/fl, and Plp-creER(t); Dnmt1fl/fl;Dnmt3afl/fl) were gavaged with tamoxifen at 3, 5, and 7 dpl and then lesion-containing tissue harvested at 14 dpl and processed for immunohistochemistry using antibodies specific for 5mC, for mature oligodendrocytes (CC1), or for all cells within NWM (Plp-creER(t)). We first quantified the number of OLIG2+ cells in tamoxifen-treated Dnmt1fl/fl;Dnmt3afl/fl mutants compared with control littermates (Plp-creER(t); Dnmt1fl/fl, Plp-creER(t); Dnmt3afl/fl, and Plp-creER(t); Dnmt1fl/fl;Dnmt3afl/fl) were gavaged with tamoxifen at 3, 5, and 7 dpl and then lesion-containing tissue harvested at 14 dpl and processed for immunohistochemistry using antibodies specific for 5mC, for mature oligodendrocytes (CC1), or for all cells within the oligodendrocyte lineage (OLIG2).

We first quantified the number of OLIG2+ and CC1+ cells in NWM to address the effect of Dnmt1 and/or Dnmt3a ablation itself on the generation of OPCs and OLs (Fig. 2A–F). We detected no difference in the number of OLIG2+ and CC1+ cells in any knock-out compared with control NWM (Fig. 2B, D, F). Moreover, there was no difference in 5mC expression levels in OLIG2+ cells in knock-out compared with control NWM (Fig. 2G–J). At 14 dpl, there was no difference in the number of OLIG2+ and CC1+ cells in the lesion or in the percentage of CC1+ differentiated OL among the OLIG2+ oligodendroglial cells between Plp-creER(t); Dnmt1fl/fl controls and Plp-creER(t); Dnmt1fl/fl mutants (Fig. 3A, B). Ablation of Dnmt3a resulted in a significant decrease of the percentage of CC1+ differentiated OL among the OLIG2+ oligodendroglial cells (Fig. 3C, D). This indicated that OPC differentiation was altered in mutants lacking Dnmt3a, whereas OLIG2+ proliferation and recruitment to the lesion was not affected (Fig. 3D). It was noteworthy that increased DMT1 levels were detected in CC1+ cells in Plp-creER(t); Dnmt3afl/fl mutant spinal cords, suggesting that in the absence of Dnmt3a there might be a compensatory increase in Dnmt1 (Fig. 3G). To offset this possible effect, we performed a similar analysis on double knockout mice lacking both Dnmt1 and Dnmt3a. Both the number of CC1+ cells in the lesion and the percentage of CC1+ differentiated OL among the OLIG2+ oligodendroglial cells were decreased in the double (Plp-creER(t); Dnmt1fl/fl;Dnmt3afl/fl) mutants, and to a greater extent than we observed in the Dnmt3a-only ablated (Plp-creER(t); Dnmt3afl/fl) mutants (Fig. 3E, F).

There were no changes in 5mC expression levels in OLIG2+ cells in Plp-creER(t); Dnmt1fl/fl and Plp-creER(t); Dnmt3afl/fl mutants (Fig. 4A–D). However, there was an increase in the percentage of low-5mC–expressing OLIG2+ cells, associated with a decrease of medium-5mC–expressing OLIG2+ cells in the double Plp-creER(t); Dnmt1fl/fl;Dnmt3afl/fl mutants (Fig. 4E, F). This suggested an increase in low-methylated and a decrease in medium-methylated oligodendroglial cells in Dnmt1/Dnmt3a-ablated mutants, which contrasted with the increased methylation previously observed in control animals (Fig. 1H, I).

These data indicate a role for Dnmt3a in adult OPC differentiation during remyelination that can be compensated for by Dnmt1.

**Ablation of Dnmt1 and Dnmt3a impairs remyelination in the adult spinal cord**

To establish whether the impaired differentiation of OPC lacking DNMTs affected remyelination, we used a similar experimental design where we killed lesioned control and mutant mice at 21 dpl and evaluated remyelination by light microscopic examination of semithin sections stained with toluidine blue and by electron microscopy. Comparison of control and mutant NWM revealed no abnormalities in myelination in the three knockout mouse lines (data not shown). Ranking of remyelination on semithin sections (Fig. 4A, B, D, E) and quantification of the g-ratio (Fig. 4C, F) did not reveal any differences from controls for either Dnmt1- or Dnmt3a-ablated mice. In contrast, despite a similar ranking of remyelination in sections from controls and double mutants (both Dnmt1 and Dnmt3a ablated; Fig. 3G, H, J), the quantification of the g-ratio revealed thinner myelin in mutants, likely suggesting delayed remyelination in the absence of Dnmt1 and Dnmt3a (Fig. 3I). This suggests that if Dnmt3a-only ablation is sufficient to reduce adult OPC differentiation in a lyssolecithin-induced lesion, compensation by Dnmt1 might prevent significantly delayed remyelination.

**Discussion**

Here we report that Dnmt1 and Dnmt3a are differentially expressed during remyelination after lyssolecithin-induced demyelination in the adult spinal cord, with Dnmt1 being highly expressed in OPCs at early time points after demyelination (corresponding in this model to the early stages of remyelination) and Dnmt3a being highly expressed in OL at later time points (corresponding...
Figure 3. Ablation of Dnmt3a and both Dnmt1 and Dnmt3a impairs oligodendrocyte differentiation during remyelination. A, Representative OLIG2 and CC1 staining at 14 dpl in tamoxifen-treated Plp\textsuperscript{−/−};Dnmt1\textsuperscript{fl/fl} and Plp\textsuperscript{creER(T)}\textsuperscript{−/−};Dnmt3a\textsuperscript{fl/fl} spinal cords. B, Quantification of OLIG2\textsuperscript{+} and CC1\textsuperscript{+} cell densities and CC1\textsuperscript{+}/OLIG2\textsuperscript{+} cells percentage at 14 dpl (p = 0.7955, p = 0.3573, p = 0.9689). C, Representative OLIG2 and CC1 staining at 14 dpl in tamoxifen-treated Plp\textsuperscript{−/−};Dnmt3a\textsuperscript{fl/fl} and Plp\textsuperscript{creER(T)}\textsuperscript{−/−};Dnmt1\textsuperscript{fl/fl} spinal cords. D, Quantification of OLIG2\textsuperscript{+} and CC1\textsuperscript{+} cell densities and CC1\textsuperscript{+}/OLIG2\textsuperscript{+} cells percentage at 14 dpl (p = 0.7851, p = 0.0550, p = 0.0149). E, Representative OLIG2 and CC1 staining at 14 dpl in tamoxifen-treated Plp\textsuperscript{−/−};Dnmt\textsuperscript{fl/fl};Dnmt3a\textsuperscript{fl/fl} and Plp\textsuperscript{creER(T)}\textsuperscript{−/−};Dnmt\textsuperscript{fl/fl};Dnmt3a\textsuperscript{fl/fl} spinal cords. F, Quantification of OLIG2\textsuperscript{+} and CC1\textsuperscript{+} cell densities and CC1\textsuperscript{+}/OLIG2\textsuperscript{+} cells percentage at 14 dpl (p = 0.1510, p = 0.0357, p = 0.0006). G, Quantification of DNMT1 and DNMT3A expression in CC1\textsuperscript{+} cells at 14 dpl in tamoxifen-treated Plp\textsuperscript{−/−};Dnmt\textsuperscript{fl/fl};Dnmt3a\textsuperscript{fl/fl} and Plp\textsuperscript{creER(T)}\textsuperscript{−/−};Dnmt\textsuperscript{fl/fl};Dnmt3a\textsuperscript{fl/fl};Dnmt\textsuperscript{fl/fl};Dnmt3a\textsuperscript{fl/fl} spinal cords, to detect eventual compensation between DNMTs at the protein level (p = 0.0075, p = 0.0505, p = 0.0074, p = 0.0053, p = 0.0072, p = 0.0012). Scale bar = 20 μm. Data are mean ± SEM. n = 4–6 animals, three sections per animal. *p < 0.05, **p < 0.01, ***p < 0.001 (Student’s t test).
Ablation of Dnmt3a and both Dnmt1 and Dnmt3a impairs methylation levels in oligodendroglial cells during remyelination. 

A, Representative 5mC and OLIG2 staining at 14 dpl in tamoxifen-treated Pip^+/Dnmt1^{fl/fl} and PipcreER(t)/Dnmt1^{fl/fl} spinal cords (white arrowheads indicate high-5mC/OLIG2+ cells). B, Quantification of low-, medium-, and high-5mC levels in OLIG2+ cells at 14dpl. C, Representative 5mC and OLIG2 staining at 14 dpl in tamoxifen-treated Pip^+/Dnmt1^{fl/fl} and PipcreER(t)/Dnmt3a^{fl/fl} spinal cords (white arrowheads indicate high-5mC/OLIG2+ cells). D, Quantification of low-, medium-, and high-5mC levels in OLIG2+ cells at 14dpl. E, Representative 5mC and OLIG2 staining at 14 dpl in tamoxifen-treated Pip^+/Dnmt1^{fl/fl} and PipcreER(t)/Dnmt1^{fl/fl}, Dnmt3a^{fl/fl} spinal cords (white arrowheads indicate high-5mC/OLIG2+ cells). F, Quantification of low-, medium-, and high-5mC levels in OLIG2+ cells at 14 dpl. Scale bar = 100 μm. Data are mean ± SEM. n = 4–6 animals, three sections per animal. **p < 0.01, ***p < 0.001 (ANOVA).

to the later stages and completion of remyelination. These data validate and extend previous microarray-generated data obtained in laser-capture microdissected tissues from rats with ethidium bromide-induced demyelinating lesions, which revealed initial increased expression of both Dnmt1 and Dnmt3a and their subsequent decrease in expression (Huang et al. 2011). Discordance between the two studies, especially for DNMT3A expression, can be explained by differences in the experimental approach. The Huang et al. (2011) dataset was obtained from whole tissue, which has a mixed composition and percentage of various cell types at different time points, possibly impacting the levels of transcripts. Indeed, Dnmt1 and Dnmt3a are also highly expressed by astrocytes and microglial cells, the latter being massively abundant in the lesion at 5 dpl but less abundant during later stages (Zhang et al. 2014).

Our study reports global hypermethylation in the nuclei of oligodendroglial lineage cells during remyelination, similar to what was described during developmental myelination (Moyon et al. 2016). These data suggested that adult OPC differentiation might recapitulate their developmental differentiation, by activating the same transcriptional pathways and perhaps the same epigenetic modulators (Fancy et al. 2004, 2009; Koenning et al. 2012; Nakatani et al. 2013; Moyon et al. 2015; Zhao et al. 2015).

Indeed, chromatin remodelers (i.e., Chd7 and Brg1) and histone deacetylases have been recently shown to be
essential for OPC myelination as well as remyelination (Shen et al. 2008; He et al. 2016). Using conditional knockout murine strains, we showed that lack of Dnmt3a, and not Dnmt1, in oligodendroglial cells impairs adult OPC differentiation. These data differ from the findings obtained during development, when the ablation of Dnmt1, and not Dnmt3a, resulted in extensive defective myelination of the CNS (Moyon et al.).

Figure 5. Ablation of Dnmt1 and Dnmt3a impairs remyelination in the adult spinal cord. A, Representative semithin sections at 21 dpl in tamoxifen-treated Plp<sup>−/−</sup>;Dnmt<sup>1fl/fl</sup> and Plp<sup>creER (t)</sup>−/−;Dnmt<sup>1fl/fl</sup> spinal cords. B, Relative ranking of remyelination<sup>2</sup> (p = 0.3075). C, Quantification of g-ratios for control and mutants mice, and plot of g-ratios against axonal diameter<sup>7</sup> (p = 0.9426). D, Representative semithin sections at 21 dpl in tamoxifen-treated Plp<sup>−/−</sup>;Dnmt<sup>3afl/fl</sup> and Plp<sup>creER (t)</sup>−/−;Dnmt<sup>3afl/fl</sup> spinal cords. E, Relative ranking of remyelination<sup>4</sup> (p = 0.7144). F, Quantification of g-ratios for control and mutants mice, and plot of g-ratios against axonal diameter<sup>8</sup> (p = 0.1079). G, Representative semithin sections at 21 dpl in tamoxifen-treated Plp<sup>−/−</sup>;Dnmt<sup>1fl/fl</sup>;Dnmt<sup>3afl/fl</sup> and Plp<sup>creER (t)</sup>−/−;Dnmt<sup>1fl/fl</sup>;Dnmt<sup>3afl/fl</sup> spinal cords. H, Relative ranking of remyelination<sup>6</sup> (p = 0.7584). I, Quantification of g-ratios for control and mutants mice, and plot of g-ratios against axonal diameter<sup>9</sup> (p = 0.0005). J, Representative electron microscopic sections at 21 dpl in tamoxifen-treated Plp<sup>−/−</sup>;Dnmt<sup>1fl/fl</sup>;Dnmt<sup>3afl/fl</sup> and Plp<sup>creER (t)</sup>−/−;Dnmt<sup>1fl/fl</sup>;Dnmt<sup>3afl/fl</sup> spinal cords revealing new thin myelin sheaths of remyelination (arrows) and a demyelinated axon (arrowhead). Scale bar = 10 μm. Dots are ranking for each mouse (B, E, H) and g-ratio for each quantified axon (C, F, I). Data are mean ± SEM. n = 3–5 animals, >70 axons per animal. *** p < 0.01 (Mann–Whitney test and Student’s t test).
2016). We also observed that, contrary to developmental data, loss of Dnmt3a was partially compensated for by upregulation of Dnmt1 levels, leading to decreased adult OPC differentiation and remyelination delays in the double conditional knockout mice. It is important to highlight that the Plp-creER(t) line was used to target oligodendroglial lineage in an inducible manner in the adult spinal cord. Although PLP has been shown to be expressed in adult OPCs (Spassky et al. 1998; Ruffini et al. 2004; Lin et al. 2009), our ablation of Dnmt1 and Dnmt3a may have targeted a more mature population, when cells have already exited the cell cycle, and thus when Dnmt1 and Dnmt3a might have a different impact. The remyelination delay observed here is also less drastic than the extensive and global hypomyelination affecting the Olig1cre;Dnmt1fl/fl mutant mice (Moyon et al. 2016). Adult OPCs tend to proliferate less than their neonatal counterparts, suggesting that the absence of Dnmt1 may not as adversely affect their replication, cell division, and survival (Wolsiwjk and Noble, 1989; Wolsiwjk et al. 1991; Shi et al. 1998; Ruffini et al. 2004; Lin et al. 2009; Young et al. 2013; Moyon et al. 2015). Moreover, some epigenetic marks might have been already established and could be irreversibly maintained in adult OPCs, which are emerging from a pool of undifferentiating neonatal OPCs (Zawadzka et al. 2010). Indeed, it has been shown that in cell lines epigenetic markers such as histone methylation, histone deacetylation, and DNA methylation might have specific dynamics, with some being partial committers and others complete commiters, depending on their enzyme recruitment speed and affinity at specific genomic sites (Bintu et al. 2016). For example, the de novo embryonic Dnmt3B is a slow silencer but complete commiter, as its methylated marks could not be easily removed. Thus, it could explain why ablation of Dnmt3a in adult OPCs might have a limited effect and only delay remyelination, as its markers would be maintained long after the enzyme ablation.

Finally, DNA methylation has been shown to be dysregulated in several neurologic pathologies, including amyotrophic lateral sclerosis, schizophrenia, and oligodendroglial pathologies such as MS and gliomas (Chou et al. 2012; Martin and Wong, 2013; Huynh et al. 2014; Hannon et al. 2016; Jaffe et al. 2016). In addition to neuropathy, dementia, and hearing loss, patients with DNA methyltransferase (Dnmt1) mutations present with mild CNS hypomyelination (Klein et al. 2011). Epigenogene-wide methylation study has identified several hypermethylated or hypomethylated loci in MS patient postmortem brain tissues compared with controls (Huynh et al. 2014) and several studies in gliomas have described an extensive global DNA hypomethylation (Watanabe and Maekawa, 2010; Chou et al. 2012) associated with site-specific DNA hypermethylation (Felsberg et al. 2006; Sharma et al. 2010). Further epigenogene-wide studies should be performed on adult OPCs to specifically identify genomic loci that might be hypo- or hypermethylated during their proliferation and their differentiation, in control conditions and after demyelination or in gliomas. We propose that modulating DNA methylation in oligodendroglial cells could efficiently regulate adult OPC proliferation and differentiation capacities. Targeting DNA methylation at specific genomic loci, using engineered zinc fingers or CRISPR-Cas9 methylation modulators, might lead to the development of new therapeutic strategies in gliomas and MS (Chourdhury et al. 2014; Heller et al. 2014; McDonald et al. 2016).

References


March/April 2017, 4(2) e0336-16.2017 eNeuro.org


March/April 2017, 4(2) e0033-16.2017 eNeuro.org