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GDE2 expression in oligodendroglia regulates the pace of oligodendrocyte maturation

Bo-Ran Choi, Mateusz Dobrowolski, Shanthini Sockanathan*

The Solomon H. Snyder Department of Neuroscience, Johns Hopkins University School of Medicine, 725 N Wolfe Street, PCTB 1004, Baltimore, MD 21205, Phone: 410-502-3084; Fax 410-614-8432

Abstract

Background: Oligodendrocytes generate specialized lipid-rich sheaths called myelin that wrap axons and facilitate the rapid, saltatory transmission of action potentials. Extrinsic signals and surface-mediated pathways coordinate oligodendrocyte development to ensure appropriate axonal myelination, but the mechanisms involved are not fully understood. Glycerophosphodiester phosphodiesterase 2 (GDE2 or GDPD5) is a six-transmembrane enzyme that regulates the activity of surface glycosylphosphatidylinositol (GPI)-anchored proteins by cleavage of the GPI-anchor. GDE2 is expressed in neurons where it promotes oligodendrocyte maturation through the release of neuronally-derived soluble factors. GDE2 is also expressed in oligodendrocytes but the function of oligodendroglial GDE2 is not known.

Results: Using Cre-lox technology, we generated mice that lack GDE2 expression in oligodendrocytes (*O-Gde2KO*). *O-Gde2KOs* show normal production and proliferation of oligodendrocyte precursor cells. However, oligodendrocyte maturation is accelerated leading to the robust increase of myelin proteins and increased myelination during development. These *in vivo* observations are recapitulated *in vitro* using purified primary oligodendrocytes, supporting cell-autonomous functions for GDE2 in oligodendrocyte maturation.

Conclusions: These studies reveal that oligodendroglial GDE2 expression is required for controlling the pace of oligodendrocyte maturation. Thus, the cell-type specific expression of GDE2 is important for the coordination of oligodendrocyte maturation and axonal myelination during neural development.

Keywords

glia; terminal differentiation; myelination; brain

*Corresponding Author and Lead Contact: ssockan1@jhmi.edu.

Author contributions

B.C and S.S. conceived the project, designed the experiments, interpreted the results, compiled and archived data, and wrote the manuscript. B.C. performed all experiments except for analysis of CCI cells in mature animals, which was carried out by M.D.

Declaration of Interests

The authors declare no competing interests.

Introduction

Oligodendrocytes (OLs) are glial cells that produce myelin, a specialized lipid-rich sheath that wraps axons to facilitate the rapid transmission of electrical signals important for neural circuit function^{1,2}. OLs derive from oligodendrocyte precursor cells (OPCs) that proliferate and migrate to populate the developing nervous system where they differentiate into premyelinating and myelinating OLs³. Because OL production is in part synchronized with neurons and neuronal activity to ensure appropriate axonal myelination, the control of OL maturation is complex^{4,5}. Emergent studies indicate roles for neuronal cues, extrinsic signals and surface membrane proteins in OL differentiation and maturation^{6–10}; however, the mechanisms that regulate the timing of OL maturation and myelination are not fully understood.

OPCs in the brain derive from three waves of OPC production that originate from distinct ventral and dorsal brain areas¹¹. The first wave of OPC generation initiates from the medial ganglionic eminence and the entopeduncular area, and this early population of OPCs is replaced by subsequent waves of OPCs that arise from the caudal ganglionic eminence and from the cortex. Once generated, OPCs proliferate and migrate to populate the nervous system, and on reaching their settling positions, differentiate into premyelinating and myelinating OLs. OPCs exhibit regional diversity in terms of their proliferative and migratory properties, as do OLs with respect to their remyelination capabilities^{12–14}. Interestingly, genetic ablation and transplantation studies indicate that different populations of OPCs are functionally redundant, suggesting that OPCs are plastic and capable of responding to multiple cues that influence their maturation and myelination^{11,15}.

The stages of OPC differentiation and maturation are coordinated with the process of axonal myelination. Accordingly, the mechanisms that control these later aspects of OL development involve communication between neurons and OPCs, as well as cell-autonomous pathways in developing OLs^{16–18}. Both positive and negative regulators of OL differentiation and maturation have been identified in neurons and OLs^{19–22}, suggesting that multiple signaling pathways are integrated to regulate the pace of OL maturation and axonal myelination. In line with this notion, disruptions in OL numbers and myelin production during development are often normalized in juvenile animals suggesting that the tempo of OL differentiation and maturation during development is dynamic and tightly controlled^{23,24}. However, the mechanisms that regulate the pace of OL maturation are not well understood.

Glycerophosphodiester phosphodiesterase 2 (GDE2 or GDPD5) is a six-transmembrane protein that contains an external enzymatic domain that shares homology with bacterial glycerophosphodiester phosphodiesterases (GDPDs)^{25–27}. GDE2 and its two family members, GDE3 and GDE6, are the only known proteins in vertebrates that act on the cell surface to regulate the activity of glycosylphosphatidylinositol (GPI)-anchored proteins by cleavage of the GPI-anchor^{27–30}. GDE2 is primarily expressed in neurons in the developing and adult nervous system, where it plays essential roles in regulating neuronal differentiation and neuronal survival respectively^{26,27,31–33}. Underscoring its role as a regulator of neuronal differentiation, GDE2 can promote the differentiation of neuroblastoma and higher GDE2

expression levels correlates with better outcomes in disease²⁹. A recent study discovered that neuronal GDE2 function contributes to neuron-glia communication pathways that regulate the timing of OL maturation during developmental myelination³⁴. Loss of neuronal GDE2 in the postnatal brain results in delayed OL maturation and myelination. Mechanistically, neuronal GDE2 maintains canonical Wnt signaling in neurons, which is responsible for the release of neuronally-derived soluble factors that promote OL maturation³⁴. Thus, neuronal GDE2 acts non cell-autonomously to positively regulate the pace of OL maturation and myelination during development.

GDE2 is also expressed in a subset of terminally differentiated OLs³⁴, raising the possibility that oligodendroglial GDE2 may play roles in regulating the progress of OL maturation. Here, we examine the requirement of oligodendroglial GDE2 expression in OL development using genetic ablation approaches combined with cell-based models of OL maturation and myelination. In contrast to neuronal GDE2 control of OL development, we find that oligodendroglial GDE2 negatively regulates the pace of OL maturation and myelination. Genetic ablation of GDE2 in oligodendroglia leads to the accelerated production of myelinating OLs and increased myelination during development. This study reveals that the cell-specific expression of GDE2 differentially regulates the timing of OL maturation and myelination and provides new insight into the developmental pathways that ensure appropriate axonal myelination.

Results

***Gde2* expression in oligodendroglia is mainly confined to mature OLs.**

GDE2 protein and transcripts are known to be expressed in neurons and in a subpopulation of Olig2+ oligodendroglia in the postnatal brain³⁴. *Gde2* was found to be expressed in OLs with minimal expression in OPCs³⁴, but the precise temporal expression of *Gde2* in differentiating OLs *in vivo* was not addressed. To gain a more precise understanding of the role of GDE2 in OL development, we examined the temporal expression of *Gde2* in maturing OLs using fluorescent in situ hybridization (FISH). We focused our analysis on the corpus callosum (CC) and the adjacent motor cortex (CTX) on postnatal day (P) 11 (Fig. 1A). Transcripts for Myelin Basic Protein (*Mbp*) are expressed by immature OLs³⁵, while mature OLs express transcripts for Myelin Oligodendrocyte Glycoprotein (*Mog*)³⁶ (Fig. 1A). At this stage in development, the number of *Mbp*+ immature OLs exceeds the number of mature *Mog*+ OLs in the CC and CTX (Fig. 1B). *Gde2* transcripts are detected in a higher proportion of *Mog*+ OLs compared to *Mbp*+ OLs in both CC (55% vs 25%) and CTX (85% vs 25%) (Fig 1C and D). Thus, *Gde2* is primarily expressed in mature OLs. This is in line with published transcriptomic analyses, which show the enrichment of *Gde2* mRNAs in mature OLs compared with earlier stages of oligodendroglial development³⁷.

GDE2 in oligodendroglia does not impact OPC proliferation.

To define the contribution of GDE2 expression in OLs to oligodendroglial development, we took advantage of Cre-lox genetics to ablate GDE2 function in oligodendroglia by utilizing mice harboring a conditional allele of *Gde2* (*Gde2lox/-*)³². *Gde2lox/-* mice contain lox-P sites flanking exon 11 that encodes the GDE2 GDPD enzymatic domain. Previous studies

have shown that Cre-dependent excision of exon 11 results in the complete loss of GDE2 protein expression, validating this strategy to be an effective method to ablate cellular function of GDE2 *in vivo*^{32–34}. For this study, we utilized an established inducible mouse line (*PDGFaR-CreER*) where administration of 4 hydroxytamoxifen (4-HT) induces active Cre recombinase expression under the control of Platelet derived growth factor α receptor (PDGFaR) regulatory sequences in OPCs³⁸. Thus, 4-HT treatment of *Gde2lox^{-/-}; PDGFaR-CreER* mice will specifically ablate GDE2 expression in oligodendroglia but will preserve GDE2 function in other cell types (*O-Gde2KO*). *Gde2^{+/-}; PDGFaR-CreER* animals that lack the conditional allele and are similarly injected with 4-HT serve as controls (*Ctrl*). 4-HT was administered once per day intraperitoneally into *Ctrl* and *O-Gde2KO* pups at P1 and P2. To determine the extent of Cre-mediated recombination of the *Gde2lox* allele, we first verified the deletion of the *Gde2* conditional allele using a competitive PCR strategy³². Genomic DNAs from OPCs isolated from *Ctrl* and *O-Gde2KO* P6 cortices were subject to PCR amplification using specific primers that detect the unrecombined *Gde2lox* allele (Lox), the WT *Gde2* allele (WT), and the recombined *Gde2lox* allele (KO) (Fig. 2A). DNAs prepared from separately generated *Gde2lox^{-/-}* and *Gde2^{-/-}* pups were used as positive controls. Different serial dilutions of *Gde2lox^{-/-}* DNA with increasing amount of *Gde2^{-/-}* DNA were prepared so that the total DNA amount was the same across the DNA mixtures (Fig. 2A), and a standard curve of control PCR product that was linear as a function of input DNA was generated^{32,39}. We observed that the amount of Lox PCR product in *O-Gde2KO* OPCs was similar to the amount amplified when a 2:8 ratio of *Gde2lox^{-/-}* and *Gde2^{-/-}* control DNAs was utilized, suggesting that approximately 80% of the *Gde2lox* alleles had undergone recombination in *O-Gde2KO* OPCs (Fig. 2A, Lane B). This analysis suggests that GDE2 expression is efficiently abrogated in *O-Gde2KO* OPCs using the 4-HT administration protocol.

To determine the requirement for GDE2 OL expression in oligodendroglial development, we first characterized the generation and proliferation of OPCs in *O-Gde2KO* mice compared with *Ctrl*. Cells that co-express Olig2 and SOX10 mark oligodendroglia while Olig2+SOX10+ cells that co-express the proliferation marker Ki67 constitute proliferating OPCs (Fig. 2B)^{40,41}. At P7, during the peak period of cortical OPC generation and proliferation, the numbers of Olig2+SOX10+ oligodendroglia and Ki67+Olig2+SOX10+ proliferating OPCs in the CC and CTX were equivalent between *Ctrl* and *O-Gde2KO* animals (Fig. 2C–E). These observations suggest that GDE2 expression in OLs is not required for the generation of oligodendroglia or OPC proliferation and is consistent with the onset of GDE2 expression in maturing OLs.

Oligodendroglial GDE2 prevents precocious OL maturation.

The differentiation of OPCs into mature OLs can be monitored by the temporal expression of specific marker proteins. Premyelinating and myelinating OLs express CC1⁴², while mature OLs express myelin associated proteins that include MBP and MOG^{35,36}. To determine if GDE2 expression in OLs is required for OL maturation, we quantified the number of Olig2+CC1+ cells in *Ctrl* and *O-Gde2KO* at P11, during the onset of OL maturation (Fig. 3A and B). Because studies suggest that OLs show region-specific diversity, we analyzed OL maturation in the white matter and grey matter focusing on the CC and

CTX respectively. Strikingly, O-*Gde2KO* animals showed a 50% increase in Olig2+CC1+ OLs in the CC and a marked increase of Olig2+CC1+ OLs in the CTX compared with *Ctrl* animals with no change in overall numbers of Olig2+ oligodendroglia (Fig. 3A and B). We note that O-*Gde2KO*s exhibit variability in the numbers of Olig2+CC1+ cells in the CTX at this timepoint. While the basis of this is unclear, it is possible that the pace of OL maturation in absence of GDE2 is subject to tight temporal control such that slight differences in age could contribute to differences in OL maturation rate. Nevertheless, these observations suggest that the loss of GDE2 in OLs enhances OL maturation without altering overall numbers of OLs (Fig. 3A and B). We next measured the amounts of MBP and MOG proteins in *Ctrl* and O-*Gde2KO* animals at P14 when myelination is beginning to occur. Western blot analysis of P14 cortical extracts revealed robust increase of MBP and MOG expression in O-*Gde2KO* mutants compared with *Ctrl* (Fig. 3C and D). No obvious changes in the levels of the general oligodendroglia marker Olig2 and the OPC marker PDGF α R were detected, suggesting that overall numbers of oligodendroglia are comparable between genotypes (Fig. 3C and D). Amounts of the neuronal protein Neurofilament Heavy Chain (NFH) were equivalent between *Ctrl* and O-*Gde2KO* confirming that axons are not disrupted in O-*Gde2KO* animals (Fig. 3C). Taken together, these observations suggest that the loss of GDE2 expression in OLs leads to the precocious maturation of OPCs into myelinating OLs.

GDE2 regulates the tempo of OL maturation in vitro.

Our observations thus far identify a cell-autonomous function for GDE2 in regulating OL maturation. To better define the requirement for GDE2 in this process, we immunoaffinity-purified OPCs from WT mice and *Gde2KO* animals that lack GDE2 protein expression (Fig. 4A) and cultured them *in vitro* using defined culture medium. Western blot analysis confirms that GDE2 is expressed in differentiating OLs and not proliferating OPCs, and that *Gde2KO* OLs show complete loss of GDE2 protein (Fig. 4A). WT and *Gde2KO* OPCs were purified from P6 cortices and the same number of OPCs for each condition were cultured in the absence of mitogenic factors such as PDGF α . After 3 days, cultures were fixed and examined for OL maturation based on their morphology and by the expression of MBP (Fig. 4B). We found that the percentage of MBP+Olig2+ OLs was increased by approximately 50% in cultures of *Gde2KO* OLs compared with WT, with no change in the total number of Olig2+ cells between genotypes (Fig. 4B). These observations recapitulate our *in vivo* observations that the loss of GDE2 in OLs accelerates OL maturation and supports the cell-autonomy of GDE2 function in this process.

In addition to increased myelin protein expression, maturing OLs *in vitro* undergo stereotypic morphological changes manifest by changes in the F-actin network that can be visualized by phalloidin staining. Previous studies have defined three stages of OL maturation based on their morphology, MBP expression and phalloidin staining^{34,43} (Fig. 4C). Differentiating Olig2+ OLs *in vitro* initially show arborized morphology with weak MBP expression in and around the cell body with robust phalloidin labeling throughout the cell body and in distal processes (Stage 1, immature). Maturing OLs have increased MBP expression and less strong phalloidin labeling, with some intermittent flattening of the myelin sheath in distal structures (Stage 2, premyelinating). More mature and myelinating OLs show distinct ring-like morphology with strong MBP expression throughout the

membrane sheath and disappearance of the actin cytoskeleton from central processes (Stage 3, myelinating). To better define the requirement for GDE2 in OL maturation, we quantified these three stages of OL maturation in WT and *Gde2KO* OPC cultures. After 3 days in culture we found that *Gde2KO* OLs showed a 2-fold increase in the percentage of OLs at Stage 2 of maturation and a robust 4-fold increase in the percentage of OLs at Stage 3 (Fig. 4C). However, the percentage of Stage 1 OLs was equivalent between WT and *Gde2KO* conditions (Fig. 4C). These observations support our findings that the loss of GDE2 leads to an accelerated pace of OL maturation.

To evaluate if *Gde2KO* OLs are capable of myelinating axons, we utilized an *in vitro* coculture system. In this paradigm, WT cortical neurons were isolated from P0 animals and were cultured for 6 days *in vitro* (DIV). O4+ OPCs purified from P6 WT and *Gde2KO* cortices were then added to the cultured neurons and co-cultured for a further 7 days. Cocultures were subsequently fixed and stained for myelinated axonal segments (Fig. 4D). *Gde2KO* OLs showed a significant increase in the number of MBP+ segments that aligned with NFH+ axons compared to WT OLs (Fig. 4E), consistent with enhanced axonal myelination. Thus, these observations suggest that GDE2 functions cell-autonomously to control the progression of OL maturation and myelination.

GDE2 regulates developmental OL myelination.

To determine the *in vivo* consequences of disrupted oligodendroglial GDE2 function on the temporal progression of developmental axonal myelination, we examined myelin ultrastructure in P14 animals using transmission electron microscopy (TEM). Focusing on axons in the CC, we found that animals that lacked GDE2 in OLs showed an increase in the number of axons that are myelinated (Fig. 5A and B). Notably, axons that were myelinated showed an increase in the thickness of the myelin sheath, indicated by a decreased g-ratio, which is the ratio of the axonal diameter to the diameter of the myelinated axon (Fig. 5A, C and D; *Ctrl* g-ratio= 0.8501 ± 0.005230; *Gde2KO* g-ratio= 0.8326 ± 0.003728). Axonal caliber is linked to the control of axonal myelination^{18,44,45}. Axonal diameters between O-*Gde2KO* animals and *Ctrl* littermates were comparable, suggesting that the increase in myelin thickness and the increased number of myelinated axons in O-*Gde2KO* animals are not a consequence of alterations in axonal caliber (Fig. 5E). Thus, GDE2 expression in OLs is required for the temporal control of axonal myelination during the peak period of developmental myelination.

OL developmental maturation and myelination deficits are restored in the adult.

The ablation of GDE2 in oligodendroglia leads to advanced OL maturation and myelination during developmental myelination. Previous studies have established that myelination is a tightly regulated process and that multiple pathways are deployed to compensate for irregularities in OL generation and maturation during development. We thus examined if loss of GDE2 function during development leads to persistent changes in premyelinating and mature OL numbers and axonal myelination in adult animals. CC1 expression identifies premyelinating and myelinating OLs while Aspartocylase (ASPA) marks mature, myelinating OLs⁴⁶. At P28, the number of CC1+ and ASPA+ OLs was equivalent between *Ctrl* and O-*Gde2KO* animals (Fig. 6A and B). Thus, the number of premyelinating and

mature OLs in O-*Gde2KO* mice does not exceed *Ctrl* levels and has normalized by the time developmental oligodendrogenesis is complete. We next examined axonal myelination at the ultrastructural level in O-*Gde2KO* animals at 2 months of age when developmental myelination is complete. TEM analysis showed that O-*Gde2KO* animals had equivalent numbers of myelinated axons to *Ctrls*, and that myelin thickness was similar between genotypes (Fig. 6C and D, F and G). No difference in axonal diameters between O-*Gde2KO*s and *Ctrls* was detected (Fig. 6E). Thus, the level and extent of myelination in animals lacking GDE2 expression in OLs are restored by the time developmental myelination is complete.

Discussion

Here we show that GDE2 expression in oligodendroglia is predominantly expressed in mature OLs in the developing nervous system. O-*Gde2KO* mice that lack GDE2 expression in developing OLs show no differences in the generation of OPCs or OPC proliferation compared with WT counterparts. However, the maturation of OLs into myelinating OLs is accelerated, resulting in the earlier onset of axonal myelination and accelerated myelination in O-*Gde2KO* mice during the period of developmental myelination. These *in vivo* studies were recapitulated using primary cultures of purified *Gde2KO*s OPCs that were differentiated to OLs *in vitro*, thus confirming the cell-autonomy of GDE2 function. These observations indicate that GDE2 is a physiological pathway that functions in developing OLs to negatively regulate the pace of OL maturation.

Previous studies have shown that GDE2 is highly expressed in neurons and that during the period of developmental myelination, neuronal GDE2 stimulates the release of soluble factors that promote OL maturation without affecting OPC generation or proliferation^{26,31,34}. While GDE2 function in OLs also does not affect OPC generation and proliferation, the differences in the roles of neuronal and oligodendroglial GDE2 in regulating OL maturation are striking. Neuronal and oligodendroglial GDE2 appear to have opposing functions with neuronal GDE2 promoting OL maturation and oligodendroglial GDE2 slowing the development of OLs into myelinating OLs. Analysis of mice that lack global GDE2 expression (*Gde2KO*) show OL maturation phenotypes that mimic neuronal deletion of GDE2 expression³⁴. This observation suggests that neuronal GDE2 function likely lies upstream of oligodendroglial GDE2 pathways that regulate OL maturation. This is consistent with the temporal profile of GDE2 expression, which initiates in neurons prior to GDE2 expression in premyelinating and myelinating OLs³¹. These collective observations thus suggest a model where neuronal GDE2 promotes the induction of OL maturation, which consequently results in the onset of GDE2 expression in maturing OLs.

Oligodendroglial GDE2 subsequently regulates the pace of OL maturation to ensure the appropriate myelination of axons during the developmental period. We note that the number of mature OLs in O-*Gde2KO* CC and CTX mice stabilizes by P28 and that the myelin ultrastructure of O-*Gde2KO* animals at 2 months is equivalent to controls. Because the CC normally myelinates earlier than the CTX, it is possible that the restoration of myelination in O-*Gde2KO*s occurs earlier in the CC compared with the CTX. These observations suggest that the developmental perturbations in myelination that are elicited by the disruption of GDE2 function in OLs are sensed and ultimately corrected by other regulatory networks.

This is in line with other studies that highlight the complex monitoring and dynamic regulation of OL development and maturation to ensure that axons are appropriately myelinated within the timeframe of developmental myelination^{6,8,47,48}.

The mechanism by which GDE2 oligodendroglial expression controls OL maturation remains to be elucidated. Previous RNAseq studies that compare transcriptional changes in spinal cords from WT and *Gde2KO* animals show that the canonical Wnt signaling pathway is altered in absence of GDE2 function³⁴. Genetic and *in vitro* experiments have determined that activating canonical Wnt signaling in neurons rescues OL maturation deficits elicited by global or neuronal GDE2 ablation, suggesting that neuronal GDE2 preserves canonical Wnt signaling in neurons to promote OL maturation. In contrast, genetic activation of canonical Wnt signaling in OPCs in *Gde2KO* mice leads to a more profound slowing of OL maturation, suggesting that elevated Wnt signaling in OLs negatively regulates the pace of terminal OL differentiation³⁴. Although this latter observation is in line with the proposed roles for oligodendroglial GDE2 in controlling OL maturation, it is unlikely that oligodendroglial GDE2 mediates this function by activating Wnt signaling. This is because reporter mice for canonical Wnt pathway activation reveal that *Gde2KO* animals have dramatically reduced Wnt signaling in neurons and OPCs, but not in OLs during the period of OL maturation. Given that GDE2 is expressed in OLs and not OPCs, these observations suggest that oligodendroglial GDE2 expression likely utilizes mechanisms other than Wnt activation to control the pace of OL maturation. Previous studies have established that GDE2 cleaves the GPI-anchor to release specific GPI-anchored proteins from the cell surface^{27,29}. This suggests that oligodendroglial GDE2 likely regulates OL maturation by regulating the activity of surface GPI-anchored protein substrates and their associated pathways. Several GPI-anchored proteins are expressed in OLs and many of them have known functions in OL development. For example, Contactin (F3) is expressed in migrating, premyelinating and myelinating OLs and is required for OL maturation⁴⁹, myelination and for the formation of paranodal and nodal structures in myelinated nerves^{48,50}, while TAG1 (Contactin2) is expressed in OLs and is involved in juxtaparanodal organization of K⁺ channels⁵¹. Further investigation to determine the role of GPI-anchored proteins and their relationship to oligodendroglial GDE2 control of OL maturation will be of interest to gain further insight into the mechanisms of OL development and myelination.

In summary, our study identifies GDE2 as a physiological pathway that functions in developing OLs to regulate the pace of OL maturation during developmental myelination. In the adult nervous system, resident OPCs differentiate into mature OLs to facilitate axonal myelination in response to multiple events such as experience, injury and disease; importantly, failure of myelination can severely impact neural circuit viability and function⁵². Whether GDE2 expression is reinitiated in differentiating OPCs to promote OL maturation and axonal myelination in the adult nervous system warrants further investigation.

Experimental Procedures

Mice

Gde2^{+/-}, *Gde2*^{flox} mice³² and *PDGFaR-CreER*³⁸ mouse lines were used in this study. Mice were housed and treated according to the approved Institutional Animal Care and Use Committee (IACUC) protocol of the Johns Hopkins Medical Institution. Littermates were utilized as controls, and both male and female animals were used for all analyses.

Tissue processing and immunohistochemistry

Brain sections were prepared and analyzed for immunohistochemistry as described³⁴. Briefly, mice were anesthetized with a solution of Avertin and butanol in Phosphate Buffered Saline (PBS) at 0.02ml/g body weight and perfused with 0.1M Phosphate Buffer (PB) transcardially followed by fixation in 4% paraformaldehyde in 0.1M PB. Brains were postfixed in fixation solution overnight at 4°C, transferred to 30% sucrose and stored at 4°C for 48 hrs. Tissues were then embedded in O.C.T. Compound (Tissue-Tek 62550–12), and coronally sectioned (50 µm for P7 brain tissues and 35 µm for the rest) with a Thermo Fisher Scientific HM550 cryostat. Immunofluorescence was performed on free-floating sections. Brain sections were boiled in 10 mM sodium citrate with 0.05% Tween-20 before blocking in 1% normal goat serum, 0.3% Triton X-100 in PBS for 2 hours at room temperature. Sections were incubated in primary antibodies overnight at 4°C, washed and incubated in secondary antibodies for 2 hours at room temperature. Tissue sections were mounted onto slides with mounting reagent (Polysciences 18606) and images were acquired using a Zeiss LSM700 confocal microscope with 20x objective. A total of 4–5 sections per mouse and 3–5 mice were quantified per group, with regions of interest (ROI) chosen based on the typical anatomical structures of CC and CTX using DAPI staining (see section on Quantification and Statistical Analyses).

4-HT preparation and administration

4-hydroxytamoxifen (4-HT, sigma H7904) was prepared as described⁵³. Single dose injections of 0.2 mg of 4HT were administered intraperitoneally on two consecutive days at P0 and P1. Pups were sacrificed at P11, P28, and 2 months of age and relevant tissues were collected.

Fluorescent in situ hybridization (FISH)

Brain tissue sections were processed and subjected to FISH as described³⁴. Briefly, 16 µm cryosections were incubated in 3% hydrogen peroxide to block endogenous peroxidase activity, permeabilized with 0.3% Triton X-100 in PBS and acetylated in 0.3% acetic anhydride. For double FISH to visualize *Gde2* transcripts in maturing OLs, tissue sections were hybridized with fluorescein (FITC)-labeled sense and antisense probes that detect *Mbp* or *Mog* transcripts and digoxigenin (DIG)-labeled sense and antisense probes for *Gde2* transcripts overnight at 70°C. Sections were incubated with anti-FITC-horseradish peroxidase (POD), 1:500 (Roche 11426346910) and FITC-labeled fluorescent signals were developed with TSA Plus FITC system (Akoya NEL741001KT) according to the manufacturer's instructions. To develop DIG-labeled *Gde2* transcripts, sections were first

subjected to gradient methanol fixation (30%, 50%, 75%, and 100%) and then incubated in a solution of 3% hydrogen peroxide in methanol for 30 min to inactivate the first POD and then washed in gradient methanol (75%, 50%, 30%) in PBS. To couple FISH with immunohistochemistry, sections were blocked in blocking solution (PerkinElmer FP1020) and incubated with sheep anti-digoxigenin-POD, 1:500 (Roche 11207733910) and rabbit anti-Olig2 (Millipore AB9610) overnight at 4°C. After incubation with secondary antibodies (1 hour, room temperature), fluorescent signals were developed with TSA Plus Cy3 system (Akoya NEL744001KT). Images were acquired on Zeiss LSM800 with 10x and 20x objectives. Oligonucleotide sequences of primers used to generate FISH probes are listed as follows. *Gde2*: Forward: 5' CCTCAAGACCGACCCCTT 3' Reverse: 5' GGGGCATGATCCAGAGTG 3'; *Mbp*: Forward: 5' GAGGCCTGGATGTGATGG 3' Reverse: 5' GGGGAACAAGTCAGGGCT 3'; *Mog*: Forward: 5' CTCCTTCTCCTCCAGTTGTCAT 3' Reverse: 5' CTTCTGCACGAAGTTTTCCTCT 3'.

Transmission Electron Microscopy (TEM)

TEM was performed as described³⁴. Briefly, animals were perfused intracardially with fixative containing 2% paraformaldehyde and 2% glutaraldehyde for 30 min at a rate of 1 ml/min for P14 and 2 ml/min for 2-month old mice. Dissected brains were post-fixed overnight at 4°C, and the CC and adjacent CTX were carefully dissected from 1000µm coronally sectioned brain slices. For TEM imaging of the CC, the sagittal surface near the midline of the CC was further sectioned. All tissues were serially dehydrated, embedded, and sectioned by the JHU SOM Microscope Facility as previously described⁵⁴. Images were acquired with a Hitachi 7600 TEM. Images (under 15000x and 80000x magnification) were obtained from the CC at random with the operator blinded. ImageJ (National Institutes of Health) software was used to measure the number of myelinated axons and g-ratio per surface area (mm²). For g-ratio analysis, the diameters of axons and outer myelinated axons were calculated from the surface area derived from the circumference of each. Selection of myelinated axons was unbiased. Specifically, a grid was first created, and axons located at grid line intersections were selected for g-ratio analysis. The number of myelinated axons was counted from 10 images (under 15000x magnification) per animal and three animals were used per condition.

Cell culture

Mouse primary OPCs were purified from P6 cortices of WT and *Gde2KO* pups using Neural Tissue Dissociation and Isolation kits (Miltenyi Biotec 130–090-312) with magnetic beads (Miltenyi Biotec 130–094-543) to positively select O4+ cells according to the manufacturer's recommendations. Purified OPCs were plated at a density of 3×10^4 cells on glass coverslips coated with poly-D-lysine (0.1 mg/ml in PBS pH 7.4) containing 1% laminin (Sigma-Aldrich L2020). Cells were cultured in DMEM:F12 (Gibco 10565018) with 10 mM HEPES (Gibco 15630080), 2% SM1 supplement, 1% N2B, 0.5% penicillin/streptomycin, 5µg/mL N-Acetyl-Cysteine (Sigma A8199), 5 µM Forskolin (Calbiochem 344270), 10ng/mL CNTF (PeproTech 450–50) for 3 days and then fixed for analysis. For neuron-OL cocultures, cortical neuronal cultures were prepared from P0 WT pups using Neural Tissue Dissociation Kits (Miltenyi Biotec 130–092-628) according to the manufacturer's recommendations. Cortical preparations were plated at a density of 3×10^5

cells on glass coverslips coated with poly-D-lysine (0.1 mg/ml in 0.1 M Trizma buffer pH 8.5) containing 1% laminin (Sigma-Aldrich L2020) and 1% PureCol Type I Bovine Collagen Solution (Advanced Biomatrix 5005-B). Cells were initially cultured in neurobasal medium (Gibco 21103–049) containing 5% fetal horse serum, 1% penicillin/streptomycin (Gibco 15140122), 1% Glutamax-I Gibco 35050061), 1% sodium pyruvate (Gibco 11360070), 30 mM Glucose, and 2% SM1 supplement (STEMCELL Technologies 5711). The next day on DIV1, the medium was replaced with maintenance medium containing Neurobasal medium with 1% penicillin/streptomycin, 1% Glutamax-I, 1% sodium pyruvate, 30 mM Glucose, 2% SM1 supplement, and 1% N2B (STEMCELL Technologies 7156). Cells were treated on DIV2 with AraC (2.5 μ M) for 24 hours to inhibit growth of proliferating cells. Freshly isolated OPCs in coculture media (half DMEM:F12 and half Neural basal media containing 10 mM HEPES (Gibco 15630080), 2% SM1 supplement, 1% N2B, 0.5% penicillin/streptomycin, 5 μ g/mL N-Acetyl-Cysteine (Sigma A8199), 5 μ M Forskolin (Calbiochem 344270), 10ng/mL CNTF (PeproTech 450–50) were added at a density of 30,000 cells on top of DIV6 neurons and cocultured for 7 days.

Immunocytochemistry

Immunocytochemistry was performed as described³⁴. Primary antibodies were used at a dilution of 1:500. Antibodies used in this study are: Rat anti-MBP (Millipore MAB386), rabbit anti-Olig2 (Millipore AB9610), mouse anti-MBP (Covance SMI-99P-100), Rabbit anti-Neurofilament H (Millipore AB1989). After a 1 hour incubation at room temperature with appropriate secondary antibodies, cells were counterstained with DAPI (Invitrogen R37606). Cells were stained with Alexa Fluor 488-phalloidin (Invitrogen A12379) during secondary antibody incubation to visualize F-actin. Cells were mounted on glass slides and imaged on a Zeiss LSM700 confocal microscope with 20x objective or on a Keyence BZ-X710 epifluorescence microscope with 20x objective for tiling (9 \times 9).

Immunoblotting

Tissue samples were prepared, run on SDS-PAGE gels and transferred to PVDF membranes as described³⁴. Transferred membranes were incubated with primary antibodies overnight at 4°C. Primary antibodies used were as follows: Rabbit anti-Olig2 (1:2,000 Millipore AB9610), Mouse anti-MBP (1:2,000 Covance SMI-99P-100), Mouse anti-MOG (1:3,000 Millipore MAB5680), Rabbit anti-Neurofilament H (1:10,000 Millipore AB1989), Rabbit anti-GDE2 (1:1000), Rabbit anti-PDGF receptor α (1:2,000 Cell Signaling Technology 3174), Mouse anti-Actin (1:10,000 Millipore MAB1501). After 1 hour incubation at room temperature with appropriate HRP-conjugated secondary antibodies, membranes were developed by film or by using a digital imaging system (KwikQuant, Kindle Biosciences).

Quantification and statistical analysis

Quantitative analysis was performed as described³⁴. Briefly, quantification was performed using semi-automated Imaris (Bitplane) from 4–5 sections per animal and 3–5 animals per condition. Images were obtained from the CC and adjacent CTX corresponding to the retrosplenial and motor areas. After 3D image reconstruction, the contour function in Imaris was used to create individual ROIs. Spot and surface rendering functions were used to set parameters for size and fluorescent signal intensity threshold to define an object representing

a nucleus or a cell body. After manual validation, z-stacks were subjected to automated quantification and manually corrected for false-positive and false negative spots and surfaces. Cell numbers were normalized to ROI surface areas. For quantifying the percent of mature OLs expressing *Gde2* transcripts, the numbers of *Gde2*⁺ *Mbp*⁺ cells and *Gde2*⁺*Mog*⁺ cells were divided by the numbers of *Mbp*⁺*Olig2*⁺ cells and *Mog*⁺*Olig2*⁺ cells respectively after normalization to ROI surface areas. For quantifying the number of MBP⁺ OLs at Stage1–3 in culture, 9×9 tiled images with 20x objective (6.22mm² area) were acquired from 2 technical replicates per animal with three biological replicates per experiment. The number of MBP⁺ cells for each stage was divided by the number of *Olig2*⁺ cells in each group and then normalized to control. Plots were generated and statistics were performed using GraphPad Prism 5 software. Mean ± SEM are shown for each plot. Statistical significance was determined by either two-tailed, unpaired Student's t-test, or by 2-way ANOVA and is shown by * p<0.05, ** p<0.01, *** p<0.001.

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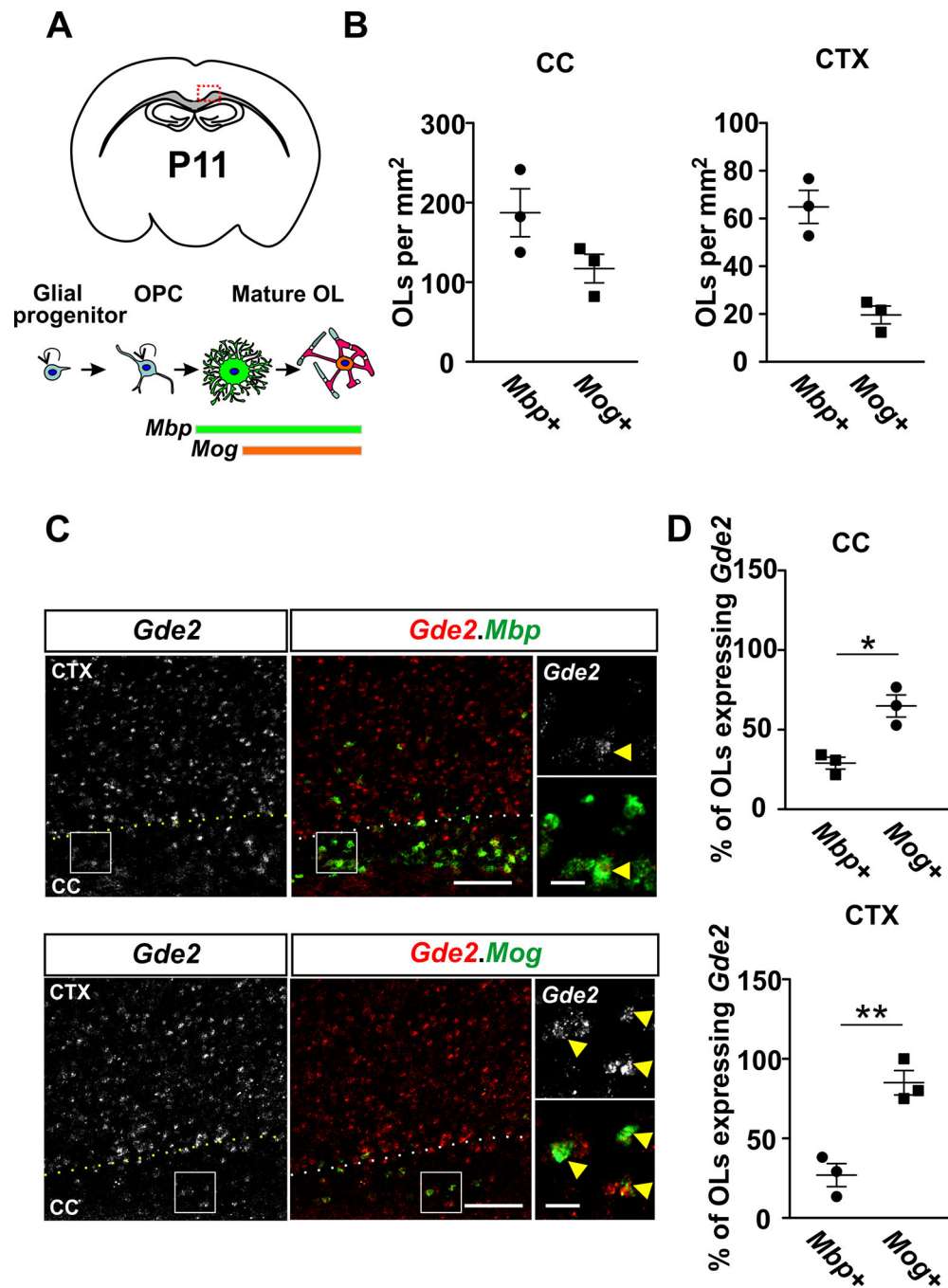


Figure 1. *Gde2* is expressed in maturing OLs in postnatal brain.

(A) Top: Schematic of a coronal brain section; the red box delineates the defined region of interest (ROI) that includes the corpus callosum (CC) and adjacent motor cortex (CTX). Bottom: schematic showing gene expression profiles associated with the progression of OL development. (B) Graphs quantifying the number of *Mbp*⁺ and *Mog*⁺ OLs in the CC and CTX. (C) FISH of *Gde2* mRNA and *Mbp* or *Mog* mRNAs in P11 brain tissue sections. Hatched lines mark the boundary between the CTX and the CC. Boxed areas are shown at higher magnification on the right. Arrows highlight *Mbp*⁺ or *Mog*⁺ OLs that co-express

Gde2 mRNAs. (D) Graphs quantifying the percentage of *Mbp*⁺ and *Mog*⁺ OLs expressing *Gde2* transcripts in CC and CTX. Higher proportions of *Mog*⁺ OLs express *Gde2* transcripts compared to *Mbp*⁺ OLs in CC (**p* = 0.0244) and CTX (***p* = 0.0052). *n* = 3. Scale bar: 100 μm, inset: 20 μm.

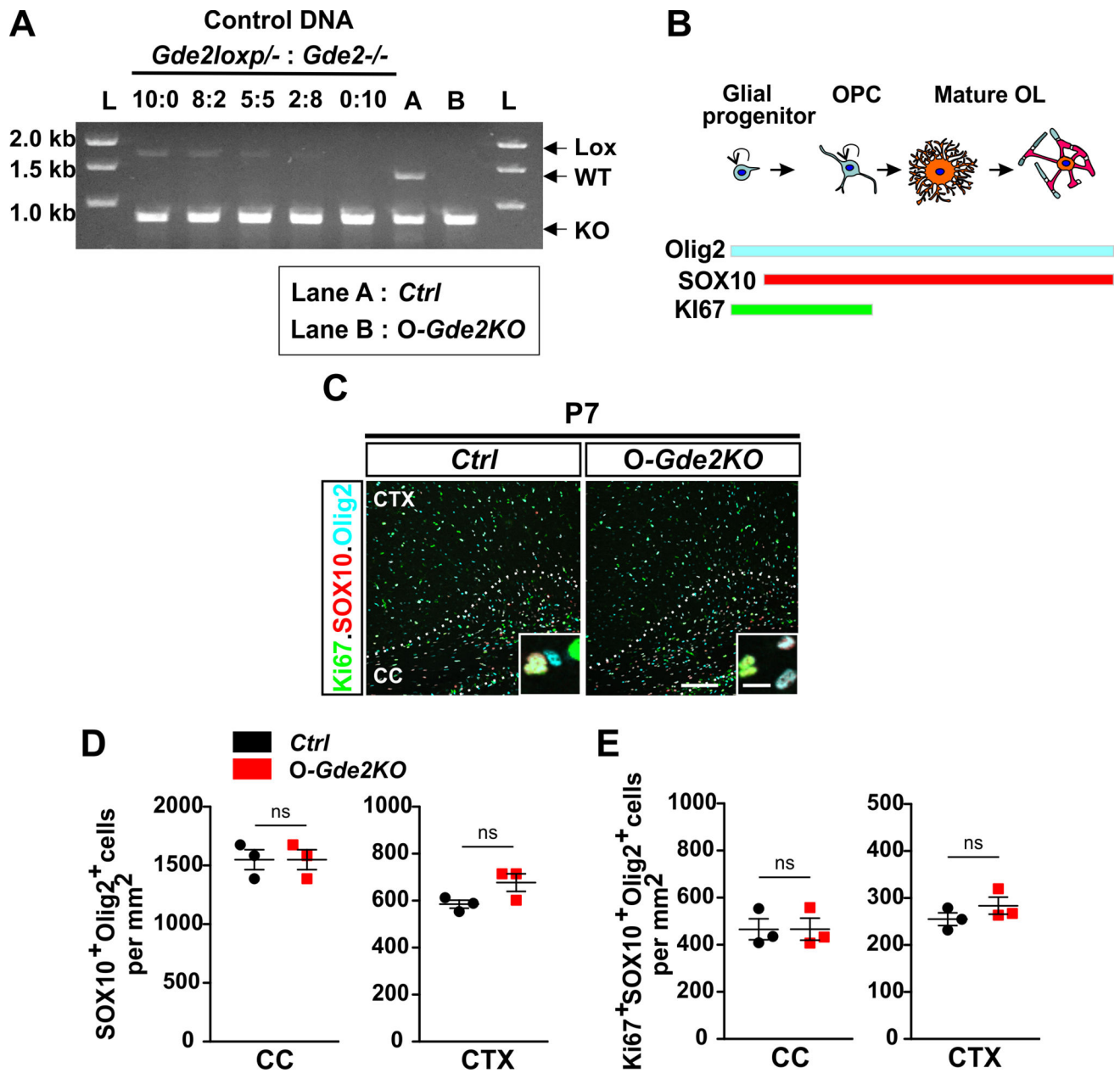


Figure 2. Loss of GDE2 in oligodendroglia does not influence OPC proliferation.

(A) Competitive PCR analysis for *Gde2* from 4-HT injected *Ctrl* and *O-Gde2KO* pups. Control DNA: 5 different ratios of *Gde2lox^{-/-}* and *Gde2^{-/-}* genomic DNAs. *Gde2* PCR primers amplified DNA fragments unique to unrecombined *Gde2lox* (Lox, 1700bp), WT *Gde2* (WT, 1300bp), and recombined *Gde2lox* (KO, 780bp) alleles. *Ctrl* (Lane A) shows presence of WT and KO fragments. *O-Gde2KO* (lane B) shows a similar intensity in the 1700bp fragment to the 2:8 ratio of mixed genomic DNAs. L = DNA ladder. (B) Schematic of marker proteins that distinguish proliferating OPCs. (C) Coronal section of CTX and CC *Ctrl* and *O-Gde2KO* P7 animals. Hatched lines mark the CC. Insets show magnified images of OPCs (Ki67+Sox10+Olig2+). (D) Graphs quantifying the number of oligodendroglia (Sox10+Olig2+) between *Ctrl* and *O-Gde2KO* CC (ns $p = 0.0857$) and CTX (ns $p = 0.1555$).

(E) Graphs quantifying the number of proliferating OPCs (Ki67+Sox10+Olig2+) between *Ctrl* and *O-Gde2KOCC* (ns $p = 0.5147$) and *CTX* (ns $p = 0.2971$). $n = 3$ *Ctrl* (*Gde2*^{+/-}; *PDGFaR-CreER*), 3 *O-Gde2KO* (*Gde2lox*^{-/-}; *PDGFaR-CreER*). Graphs: Mean \pm sem, two-tailed unpaired Students t-test. Scale bar: 100 μ m, inset: 10 μ m.

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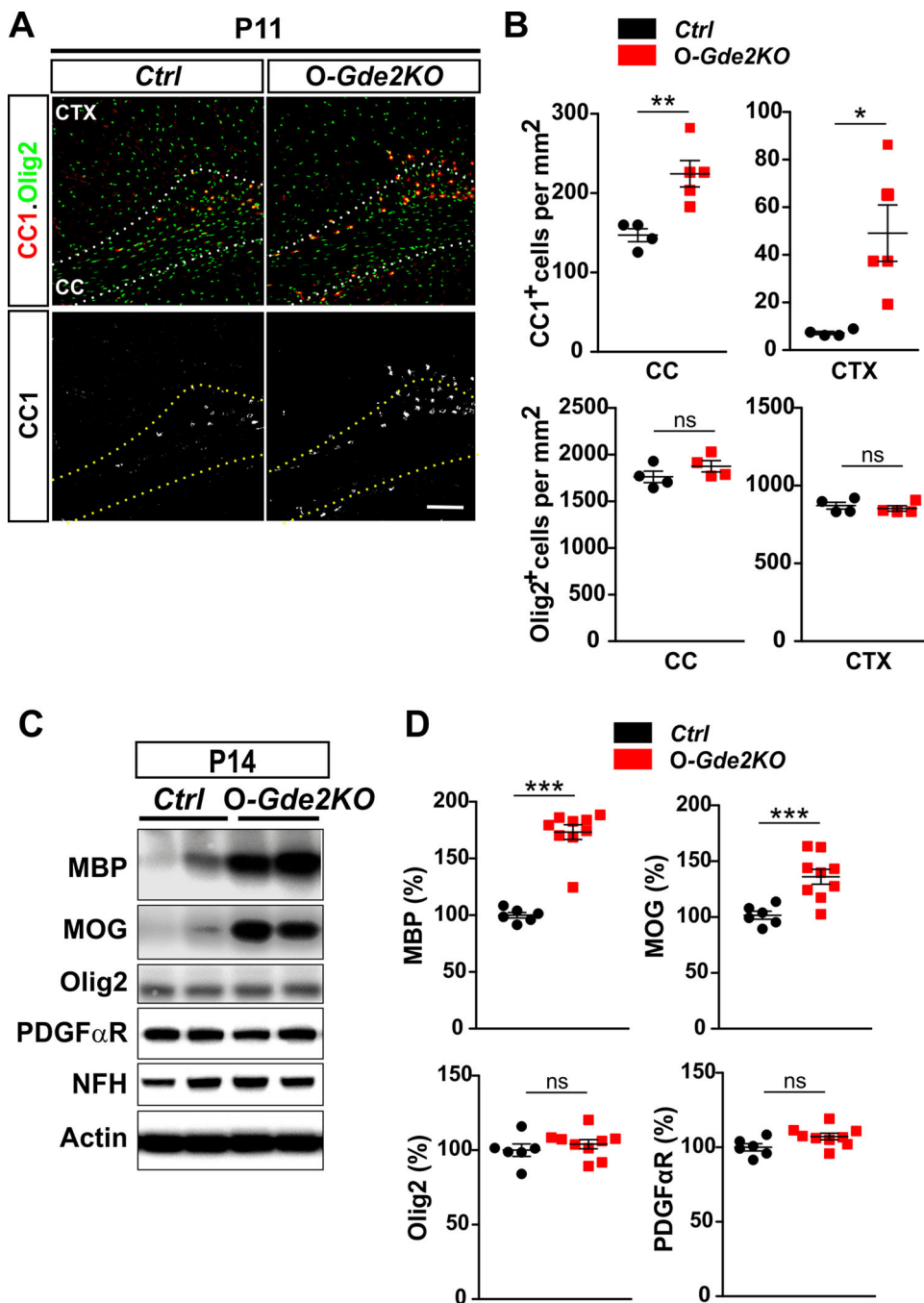


Figure 3. Oligodendroglial GDE2 prevents precocious OL maturation.

(A) Coronal sections of CTX and CC of P11 *Ctrl* and *O-Gde2KO* mice. Hatched lines delineate the CC. (B) Graphs quantifying the number of CC1⁺ and Olig2⁺ cells in CC and CTX in *Ctrl* and *O-Gde2KO* P11 littermates. CC1⁺ OLs are increased in *O-Gde2KO*s in CC (***p* = 0.0087) and CTX (**p* = 0.0242). Olig2⁺ cell numbers are equivalent between *Ctrl* and *O-Gde2KO* in CC (ns *p* = 0.2353) and CTX (ns *p* = 0.5548). *n* = 4 *Ctrl*, 5 *O-Gde2KO*. (C) Western blot of cortical extracts from P14 *Ctrl* and *O-Gde2KO* littermates. Actin is used as a loading control. NFH expression shows equivalent axonal content between the groups. (D)

Graphs quantifying Western blots show increase of MBP (** $p < 0.0001$) and MOG (** $p = 0.0007$) proteins in O-*Gde2KO* cortical extracts compared with *Ctrl*. Levels of Olig2 (ns $p = 0.4388$) and PDGF α R (ns $p = 0.0940$) are unchanged between genotypes. $n = 6$ *Ctrl*, 9 O-*Gde2KO*. All graphs: Mean \pm sem, two-tailed unpaired Students t-test. Scale bar: 100 μ m.

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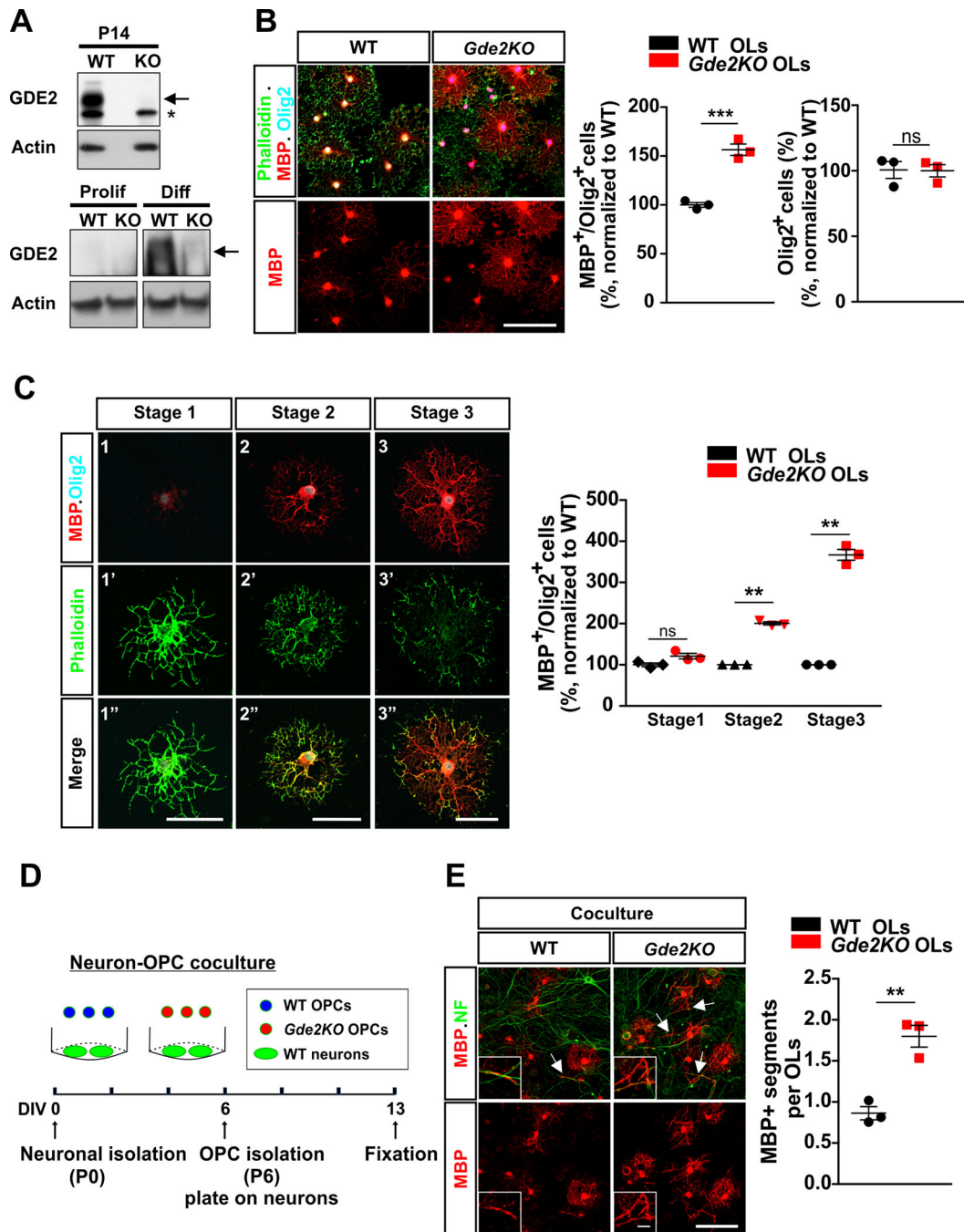


Figure 4. GDE2 regulates the tempo of OL maturation *in vitro*.

(A) Representative Western blot of P14 cortical lysates (Top) and extracts of proliferating OPCs and differentiated OLs (2 DIV) from WT and *Gde2KO*s. Arrow highlights GDE2 protein, * marks nonspecific band. (B). Representative images of WT and *Gde2KO* OLs. Graphs quantifying the percentage of MBP+Olig2+ OLs (***) $p = 0.0008$ and Olig2+ cells (ns) $p = 0.9385$ normalized to WT, $n = 3$ WT, 3 *Gde2KO*. (C) Representative images of 3 stages of OL maturation *in vitro*. Graph quantifying the percentage of MBP+Olig2+ OLs. 2-way ANOVA *** $p < 0.0001$ (Bonferroni correction) ns $p > 0.05$; ** $p < 0.01$; $n = 3$ WT, 3

Gde2KO. (D) Schematic of neuron-OPC co-culture. (E) Representative images of WT and *Gde2KO* OPCs co-cultured with WT neurons. Insets show higher magnification of myelinated axons. Arrows highlight myelinated axons. Graph quantifying the numbers of MBP+ segments (normalized to WT OLs) $**p = 0.0037$, $n = 3$ WT, 3 *Gde2KO*. All graphs: Mean \pm sem. (B, E) two-tailed unpaired Students t-test; Scale bars: (B, E) 100 μm , inset: 10 μm (C) 50 μm .

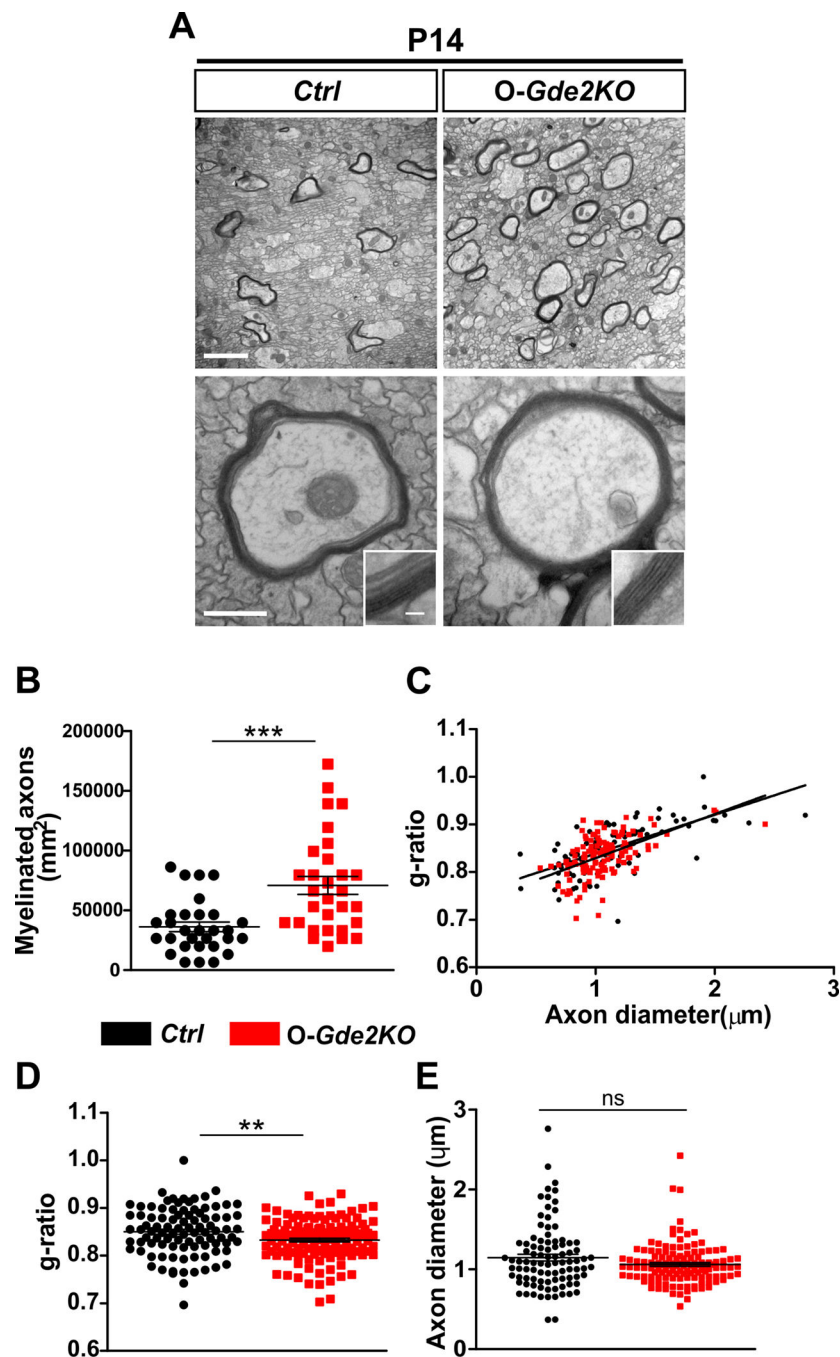


Figure 5. GDE2 ablation in oligodendroglia results in increased myelination.

(A) TEM of P14 CC of *Ctrl* and *O-Gde2KO*s. Insets show higher magnification images of the myelin sheath. (B-E) Graphs show an increase in myelinated axons (B, *** $p < 0.0001$; points refer to individual regions of interest [ROI] from 3 *Ctrl* and 3 *O-Gde2KO*s), and decrease in g-ratios (C, D ** $p = 0.0056$; points refer to individual myelinated axons; 3 *Ctrl* and 3 *O-Gde2KO*s) in *O-Gde2KO* compared with *Ctrl* but no change in axon diameters (E, ns $p = 0.0624$; points refer to individual axons, 3 *Ctrl* and 3 *O-Gde2KO*s). All graphs: Mean

± sem, two-tailed unpaired Students t-test. Scale bars: (A) 2 μm (top), 500 nm (bottom), inset 50 nm.

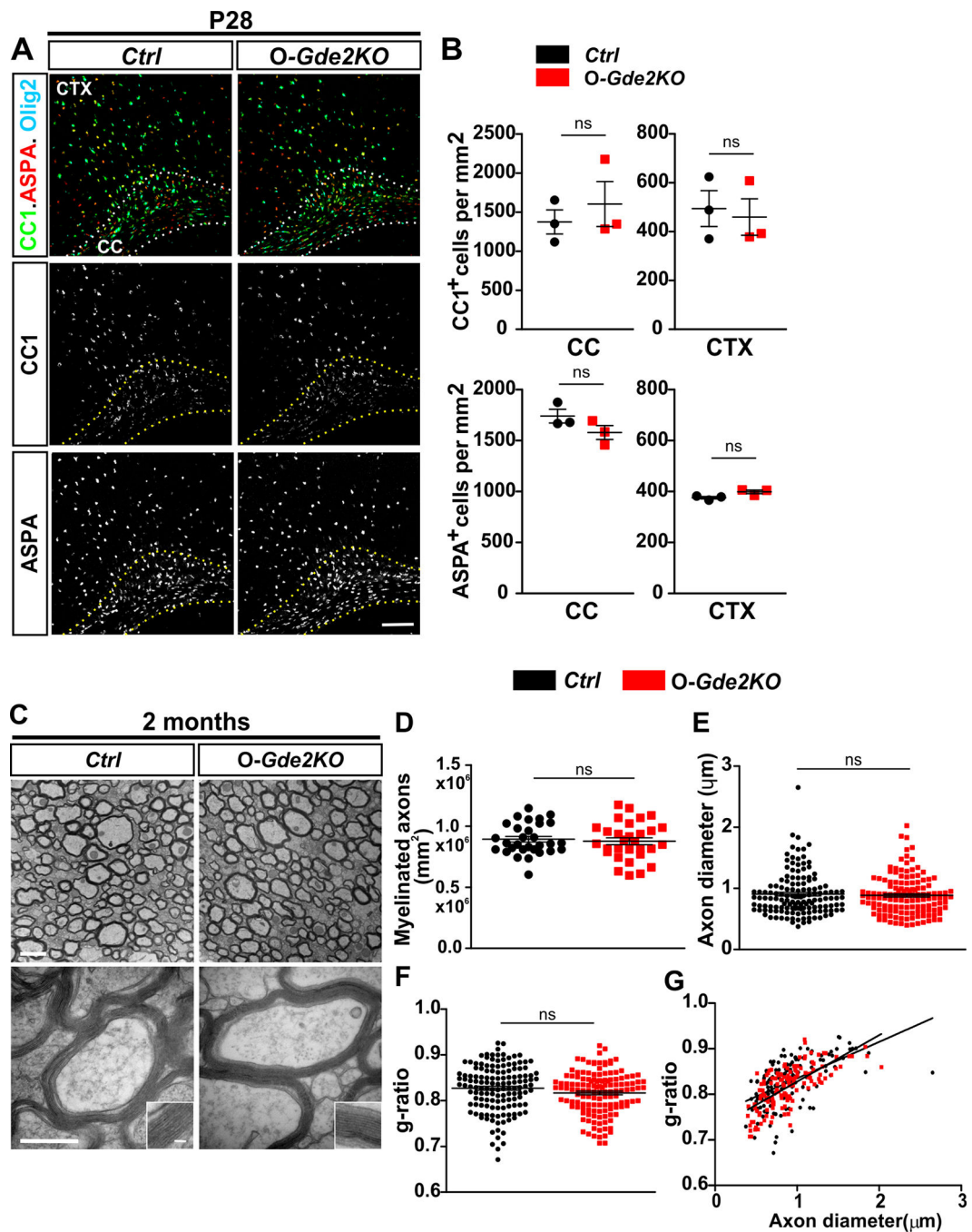


Figure 6. *O-Gde2KO* OL maturation and myelination deficits are restored in the adult. (A) Coronal sections of mouse CTX and CC from *Ctrl* and *O-Gde2KO* P28 animals. Hatched lines delineate the CC. (B) Graphs quantifying the number of mature OLs (CC1⁺ and ASPA⁺) show no difference in CC1⁺ OLs between *Ctrl* and *O-Gde2KO* CC (ns = 0.5217) and CTX (ns = 0.7564) and no change in ASPA⁺ OLs in CC (ns = 0.1922) and CTX (ns = 0.0721) at P28. n = 3 *Ctrl*, 3 *O-Gde2KO*. (C) TEM of the CC of 2-month *Ctrl* and *O-Gde2KO* animals. Insets show higher magnification of the myelin sheath. (D-G) Graphs show comparable numbers of myelinated axons (D, ns P=0.6555; points refer to individual

ROI from 3 *Ctrl* and 3 *O-Gde2KO*s), g-ratios (F, G, ns $p = 0.0728$; points refer to individual myelinated axons; 3 *Ctrl* and 3 *O-Gde2KO*s), and axon diameters (E, ns $p = 0.6076$; points refer to individual axons, 3 *Ctrl* and 3 *O-Gde2KO*s) between genotypes. All graphs: Mean \pm sem, two-tailed unpaired Students t-test. Scale bars: (A) 100 μm (C) 1 μm (top), 500 nm (bottom), inset 50 nm.