HIF1α has also been reported to be crucial for normal brain development [14]. Moreover, HIFs may act cooperatively with other signaling molecules, such as Notch [15] and mammalian target of rapamycin [16, 17], thereby influencing a wide range of processes including tumor malignancy and NPC growth, maintenance and differentiation [11, 18-20].

In this study, we focused on how oxygen tension affects the DNA methylation status of astrocytic genes in mgNPCs. Oxygen levels in the microenvironment around NPCs in the embryonic brain at midgestation were comparable to those seen under hypoxic culture conditions (2-5% O_2). Bisulfite sequencing revealed that these conditions promoted demethylation of the *gfap* promoter. This hypoxia-induced demethylation was mediated by cooperation between HIF1α and the Notch signaling pathway. Furthermore, ectopic expression of a constitutively active form of HIF1α in the embryonic brain induced precocious astrocyte differentiation of NPCs. By contrast, when embryos developed in hyperoxic conditions, astrocyte differentiation of NPCs was suppressed. These findings suggest that oxygen levels in the embryonic brain play a critical role in fine-tuning the timing of NPC fate switching during development.

Materials and Methods

Cell Culture

mgNPCs were prepared from telencephalons of E11.5 embryos and cultured as described previously [5]. E15.5 ventricular zone (VZ) containing NPCs was manually separated from other parts of the brain using a hand-made microknife (Supporting Information Fig. S1). As described previously [5], NPCs were cultured with basic fibroblast growth factor (bFGF; 1×10^6 cells per dish) in poly-L-ornithine/fibronectin-coated 6-cm culture dishes. Hand-made chambers were used to obtain atmospheres of different oxygen levels [21]. Notch signal activation was inhibited with the γ-secretase inhibitor *N*-[*N*-(3,5-difluorophenacetyl-L-alanyl)]-*S*-phenylglycine *t*-butyl ester (DAPT; Calbiochem-MERCK, Darmstadt, Germany, www.merckgroup.com, 10 μM).

Bisulfite Sequencing

Genomic DNA was extracted from NPCs and subjected to bisulfite sequencing as previously described [5]. Specific DNA fragments were amplified by polymerase chain reaction (PCR) using primers described previously [5, 7]. The PCR products were cloned into pT7Blue vector (Novagen, Darmstadt, Germany, www.merckgroup.com/en/index.html), and 10-20 randomly picked clones were sequenced. Each experiment was performed at least tree times.

Lentivirus Production

A mouse *HIF1α*-targeting short hairpin RNA (shRNA) sequence [22] was cloned into pLLX vector [23]. Lentiviruses were pseudotyped with the vesicular somatitis virus–G envelope and concentrated by centrifugation as previously described [24]. *HIF1α* mRNA degradation was confirmed by quantitative PCR (qPCR). All the recombinant DNA experiments in this manuscript followed the guidelines by Ministry of Education, Culture, Sports, Science and Technology of Japan, which conform to the National Institutes of Health Guidelines.

Immunostaining

Cells were fixed with 4% paraformaldehyde and processed for immunostaining as described [5]. The following primary antibodies were used: chick anti-green fluorescent protein (anti-GFP; 1:500, Aves Labs, Tigard, OR, www.aveslab.com), rat anti-hemagglutinating (anti-HA) (1:500, Roche Applied Science, Indianapolis, IN, www.roche-applied-science.com), rat anti-bromodeoxyuridine (1:250, AbD Serotec, Raleigh, NC, www.abdserotec.com) chicken anti-Nestin (1:1000, Aves Labs), mouse anti-Map2ab (1:500, Sigma, St. Louis, MO, www.sigmaaldrich.com), and mouse anti-GFAP (1:500, Sigma). Secondary antibodies were Alexa488-conjugated goat anti-rat IgG (1:500), Alexa488-conjugated goat anti-chick IgY (1:500), Alexa555-conjugated goat anti-rabbit IgG (1:500), Alexa555-conjugated goat anti-rat IgG (1:500), Alexa555-conjugated goat anti-mouse IgG (1:500), or Alexa647-conjugated goat anti-mouse IgG (1:500, Invitrogen, Carlsbad, CA, www.invitrogen.com). Nuclei were stained using bisbenzimide H33258 fluorochrome trihydrochloride (Hoechst; Nacalai Tesque, Kyoto, Japan, www.nacalai.co.jp). All experiments were independently replicated at least three times. A Hypoxyprobe-1 Plus kit (Hypoxyprobe-Millipore, Billerica, MA, www.millipore.com) was used, following the manufacturer's protocol, to determine the hypoxicity of cultured cells and the developing brain. After culturing NPCs for 4 days in 2%, 5%, or 21% O_2, pimonidazole-HCl was added to the culture medium for 1.5 hours and the cells were then fixed. For brain sections, pimonidazole-HCl was injected intraperitoneally into pregnant mice (E15.5). Embryos were fixed 2 hours later with 4% paraformaldehyde and the brains were cryosectioned at 20-μm intervals. Pimonidazole adducts were detected with a fluorescein isothiocyanate–conjugated specific antibody supplied with the kit (1:500). Stained sections were visualized with a confocal microscope (Fluoview FV10i, Olympus, Tokyo, Japan, www.olympus.co.jp) or a fluorescence microscope (Zeiss Axiovert 200M, Zeiss, Jena, Germany, www.zeiss.com).

Animal Procedures and Electroporation

All aspects of animal care and treatment were conducted according to the guidelines of the Experimental Animal Care Committee of Nara Institute of Science and Technology. The surgical procedures performed on pregnant ICR mice and embryo manipulations in utero were conducted as previously described [25]. E11.5 pregnant mice were deeply anesthetized by intraperitoneal injection with sodium pentobarbitone (50 μg/g b.wt.). HA–constitutively active HIF1α (HA-caHIF1α) cDNA was cloned into the EcoRI site of pCAGGS vector. After the uterus was exposed, approximately 1-2 μl of plasmid solution (1 μg/μl in phosphate-buffered saline) was injected into the lateral ventricle of the telencephalon with a glass micropipette. The embryos were held with the tips of a tweezers-type electrode with a diameter of 5 mm (CUY650-P3; Tokiwa Science, Fukuoka, Japan), and five electronic pulses (27V, 50 ms, at intervals of 950 ms) were given to each embryo with an electroporator (CUY21SC; Tokiwa Science). The embryos were reinserted into the abdominal cavity and the abdominal wall was closed with surgical sutures.

Exposure to High-Oxygen Atmosphere and Tissue Oxygen Measurement

The animal cage was placed in a hyperoxic oxygen chamber (Terucom, Kanagawa, Japan, www.terucom.co.jp). Oxygen tension was measured using a portable oxygen meter (Terucom) in the same chamber. E11.5 pregnant mice were exposed to 60% O_2 for 2 days, and the oxygen tension was then raised to 80% (the upper nonlethal concentration limit) and maintained at that level until fixation at E17.5.

Local tissue oxygen tension corresponding to each atmospheric oxygen level was measured with an OxyLab pO_2 monitor (Oxford Optronix, Oxford, UK, www.oxford-optronix.com) [26] (Supporting Information Fig. S4Q). The probe was

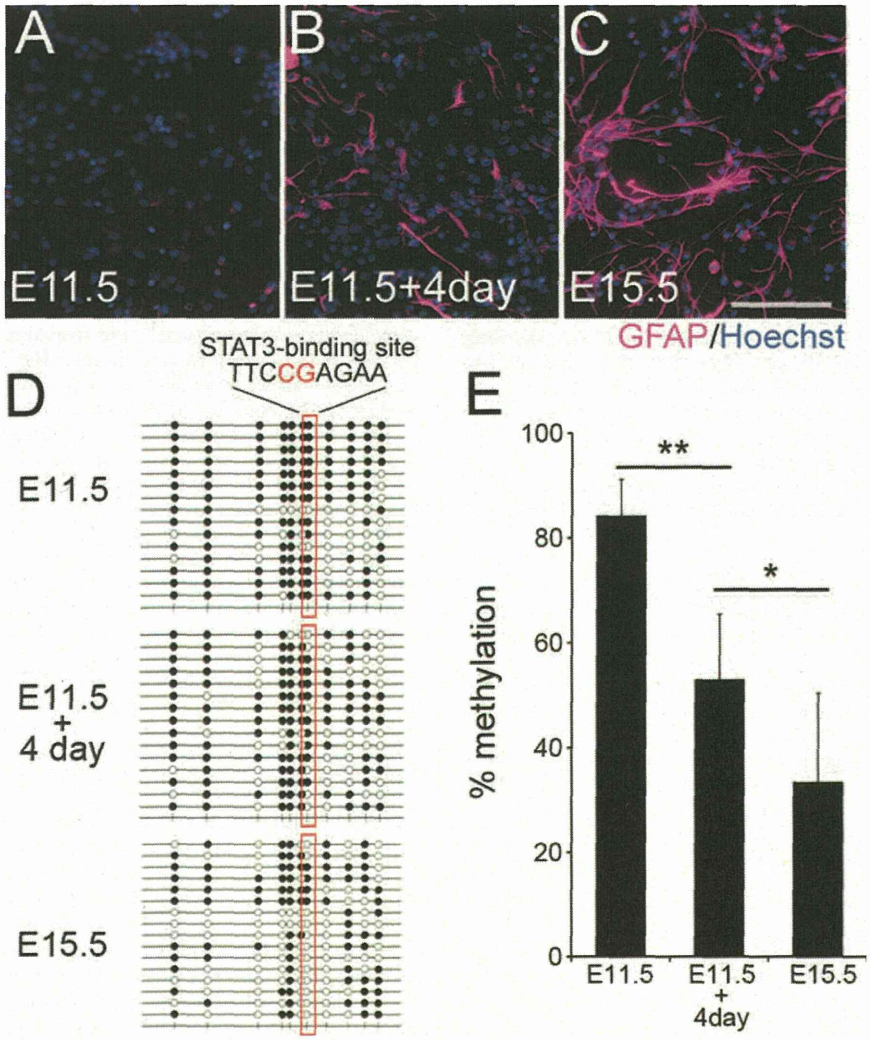

Figure 1. Astrocyte differentiation of midgestational neural precursor cells is retarded in vitro. **(A–C):** Leukemia inhibitory factor (LIF)-induced GFAP-positive astrocyte differentiation in E11.5 (A), in vitro 4-day-cultured E11.5 (B) and E15.5 (C) NPCs. After a 4-day culture in the presence of LIF, the cells were stained with anti-GFAP antibody (magenta) and with Hoechst to identify nuclei (blue). Scale bar = 100 μm. **(D, E):** Genomic DNA was extracted from the cells, and the methylation status of the *gfap* promoter around the STAT3-binding site was examined by bisulfite sequencing. Closed and open circles indicate methylated and unmethylated CpG sites, respectively (D). E11.5 and E15.5 indicate the results obtained for freshly prepared neural precursor cells (NPCs) from E11.5 cortex and E15.5 VZ. The STAT3-binding site is marked by red rectangles. Methylation at the STAT3-binding site in the *gfap* promoter is higher in 4-day in vitro-cultured E11.5 NPCs than in freshly prepared E15.5 NPCs (E). Data are shown as means ± SD ($n = 3$). Statistical significance was evaluated by the Student's t test. *, $p < .05$; **, $p < .01$. Abbreviations: GFAP, glial fibrillary acidic protein; STAT3, signal transducer and activator of transcription.

guided to the E15.5 brain using a 20-gauge needle with a plastic canula (Terumo, Tokyo, Japan, www.terumo.co.jp).

Results

It is well known that lgNPCs but not mgNPCs differentiate into astrocytes in response to stimulation with IL-6 family cytokines [2-5, 7]. When we cultured lgNPCs prepared from the VZ of mouse telencephalon at E15.5 (Supporting Information Fig. S1), we observed their LIF-induced astrocyte differentiation, as judged by the expression of the astrocytic marker GFAP (Fig. 1C, 26.8 ± 6.5%). By contrast, hardly any LIF-treated E11.5 mgNPCs differentiated into astrocytes (Fig. 1A). Interestingly, E11.5 mgNPCs cultured in vitro for 4 days (nominally corresponding to E15.5) did undergo astrocyte differentiation (Fig. 1B, 12.2 ± 1.9%), albeit to a lesser extent than E15.5 lgNPCs.

Since an inverse correlation exists between the potential of NPCs to express *gfap* and the methylation status of the *gfap* promoter, which includes a STAT3-binding site [5, 27], we examined whether the in vitro culture conditions of mgNPCs delayed the demethylation of the promoter compared to its demethylation in vivo. Bisulfite sequencing for the *gfap* promoter of E11.5, E11.5 + 4-day culture in vitro, and E15.5 NPCs revealed that this was indeed the case (Fig. 1D, 1E). These data indicate that the in vitro culture conditions retard the demethylation of the astrocytic gene promoter in NPCs.

In terms of the physical conditions surrounding cells, one of the biggest differences between in vitro and in vivo

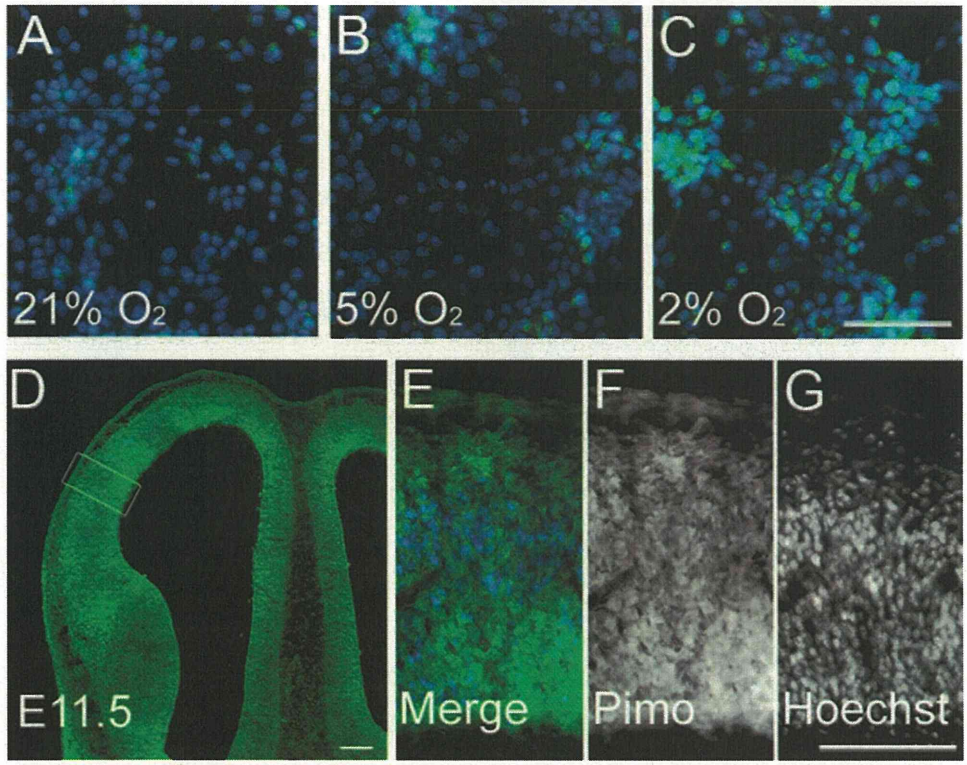

Figure 2. Oxygen levels are low in the embryonic brain. **(A–C):** Neural precursor cells cultured in 21% (A), 5% (B), or 2% O_2 (C) were stained with Hypoxyprobe. Pimonidazole adduct formation under hypoxic conditions (green) was observed clearly in 2% O_2 (C), less markedly in 5% O_2 (B), but not in 21% O_2 (A) (bar = 100 μm). **(D–G):** E11.5 embryonic brain was stained with Hypoxyprobe. Hypoxyprobe (green); Hoechst (blue). The image in (E) is an enlargement of the area in (D) marked by the rectangle. Bar = 100 μm.

environments is oxygen tension. The atmosphere contains 21% O_2 (160 mmHg), whereas interstitial oxygen concentration ranges from 1 to 5% (7-40 mmHg) in mammalian tissues including the embryonic brain [11, 20]. Although hypoxia is generally considered a pathological phenomenon, mammalian embryos develop naturally in a mildly hypoxic environment [28]. To determine the tissue oxygen tension in the embryonic brain, where NPCs reside, we used the chemical reagent pimonidazole. Pimonidazole is reductively activated in hypoxic cells and forms stable adducts with sulfhydryl groups in amino acids, at around or below 10 mmHg, which can be detected with specific antibodies [29, 30]. Pimonidazole adducts were weakly but clearly detected in NPCs cultured in 2% and 5% O_2 conditions, respectively, but not in NPCs cultured in 21% O_2 (Fig. 2A–2C). Pimonidazole adducts were also abundant in midgestational embryonic brain, indicating that oxygen levels there are low, particularly in the NPC-containing VZ (Fig. 2D–2G).

From the above findings, we hypothesized that culturing mgNPCs at a low oxygen level might accelerate their differentiation into astrocytes. To test this idea, mgNPCs were cultured in 2% or 21% O_2 atmospheres for 4 days in the presence of bFGF, and subsequently stimulated with LIF for an additional 4 days. As shown in Figure 3A–3C, a higher proportion of mgNPCs cultured in the presence of LIF under 2% O_2 than under 21% O_2 became GFAP-positive astrocytes. Reflecting the promotion of astrocyte differentiation, NPC (Nestin) and neuron (Map2ab) marker-positive cell numbers were lower under 2% O_2 than under 21% O_2 (Supporting Information Fig. S2A). The proliferation of cells in our normoxic and hypoxic culture was similar as judged by BrdU staining (Supporting Information Fig. S2B). Furthermore, in the 2% O_2 condition, significantly fewer CpG sites in the *gfap* promoter were methylated than in the 21% O_2 condition (Fig. 3D); this was also the case for CpG sites in the promoter of another astrocytic marker, *S100β* (Supporting Information Fig. S3A). Consistent with the lower methylation, *S100β* expression in hypoxic culture in the presence of LIF was higher than that in normoxic condition (Supporting Information Fig. S3B). These results suggest that low oxygen levels facilitate the DNA demethylation of astrocytic genes in mgNPCs.

We have shown previously that Notch signal activation induces the demethylation of astrocytic genes in mgNPCs [7]. Intriguingly, *hairy and enhancer of split 1* (*Hes1*) and *Hes5*, two known targets of Notch signaling, were markedly upregulated in the 2% O_2 culture condition (Fig. 4A), indicating that Notch signaling is more active at lower O_2 levels. Therefore, we examined whether low oxygen levels enhance the astrocyte differentiation of mgNPCs via Notch signal activation. An inhibitor of Notch signal activation, DAPT, was added to the culture medium during the first 4-day expansion phase of mgNPCs with bFGF in the hypoxic condition. The expression of *Hes1* and *Hes5* was dramatically reduced, confirming that hypoxia-induced elevation of Notch signaling was inhibited by DAPT (Supporting Information Fig. S3C). Furthermore, as shown in Figure 4B and 4C, the astrogenic potential of NPCs was almost completely suppressed by DAPT, and the enhanced demethylation of the *gfap* and *S100β* promoters observed in the hypoxic condition was no longer seen after DAPT treatment (Fig. 4D and Supporting Information Fig. S3D).

Activation of the Notch signaling pathway in mgNPCs induces expression of the transcription factor nuclear factor IA (NFIA), which leads to demethylation of astrocyte-specific genes including *gfap* [7]: NFIA binds to astrocytic gene

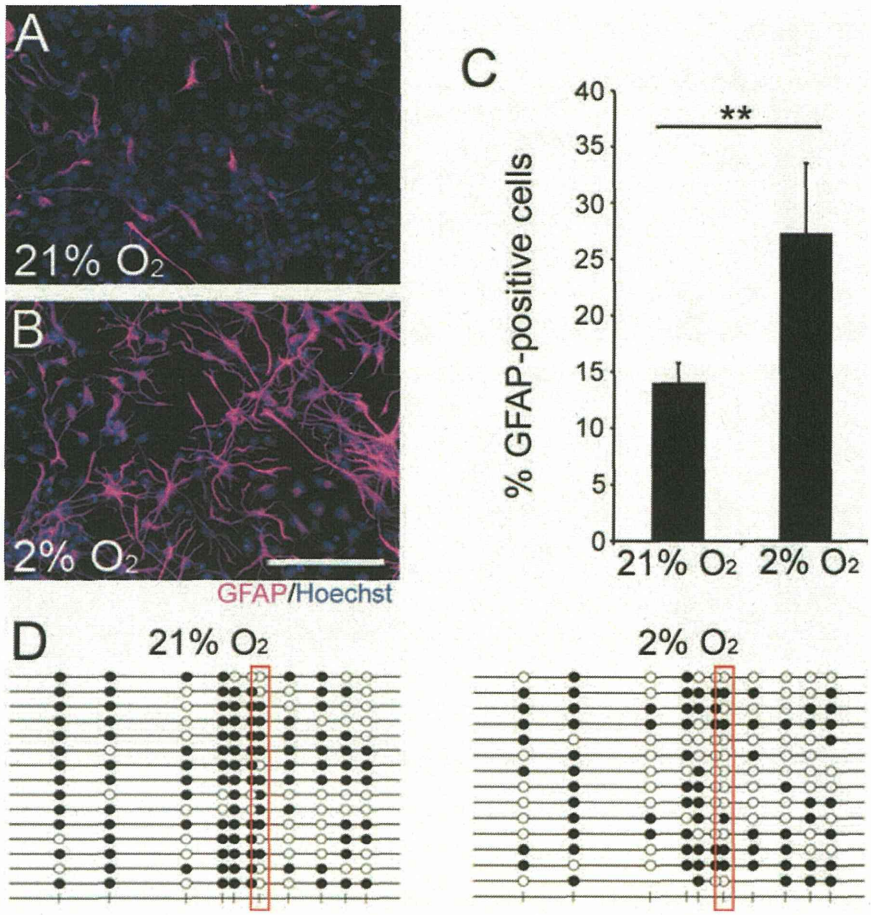

Figure 3. Culturing under 2% O_2 accelerates leukemia inhibitory factor (LIF)-induced astrocyte differentiation of neural precursor cells (NPCs). **(A–C):** E11.5 NPCs were cultured for 4 days under 2% O_2 (A) or 21% O_2 (B), followed by a 4-day LIF stimulation to induce astrocyte differentiation. GFAP (magenta), Hoechst (blue); bar = 100 μm. Proportions of GFAP-positive cells in the total cell populations were quantified (C). Data are shown as means ± SD ($n = 3$). Statistical significance was evaluated by the Student's t test. **, $p < .01$. **(D):** CpG methylation at the signal transducer and activator of transcription 3 (STAT3)-binding site in the *gfap* promoter is lower under 2% O_2 than under 21% O_2 after a 4-day culture of E11.5 NPCs. The STAT3-binding site is indicated by red rectangles. Abbreviation: GFAP, glial fibrillary acidic protein.

promoters and induces dissociation of DNA methyltransferase 1 (DNMT1) from the promoters, resulting in their demethylation. Therefore, we examined the expression of *Nfia* and found that it increased dramatically under the hypoxic condition (Supporting Information Fig. S4A). Moreover, we did not observe astrocyte differentiation of NFIA-deficient NPCs even when cultured with LIF under the hypoxic condition (Supporting Information Fig. S4B). Taken together, these findings suggest that activation of the Notch-NFIA cascade is the mechanism whereby hypoxia induces demethylation of the *gfap* promoter.

HIF1s have been shown to play important roles in cellular adaptation to hypoxia [11, 13, 31]. *HIF1α* and *HIF1β* are expressed in the developing mouse brain [32], and HIF1α protein accumulates to a higher level in hypoxic than in normoxic conditions as a result of increased transcription and protein stabilization [33–35]. Consistent with those observations, we found that both *HIF1α* transcript and nuclear HIF1α protein levels in E11.5 mgNPCs were upregulated under the 2% O_2 culture condition (Supporting Information Fig. S5A, S5B). Expression of the HIF1α target gene *Id1* was also upregulated (Supporting Information Fig. S5C), as was observed in neuroblastoma cells [12].

To determine whether HIF1α contributes to the hypoxia-promoted astrogenic potential of mgNPCs, we suppressed *HIF1α* mRNA using a specific shRNA. mgNPCs were prepared from E11.5 telencephalon and were infected the following day with lentiviruses expressing *HIF1α*-shRNA, cultured under 2% O_2 for 3 days, and then stimulated with LIF for a further 4 days. The level of *HIF1α* mRNA was reduced greatly in cells infected with *HIF1α* shRNA-expressing viruses (Supporting Information Fig. S6A). Moreover, *HIF1α* shRNA expression markedly diminished both the astrogenic potential of mgNPCs and the degree of demethylation in the *gfap* promoter (Fig. 5A–5G, and Supporting Information Fig. S6B).

caHIF1α is a hydroxylation-resistant, constitutively active mutant form of HIF1α in which two amino acids (prolines 402 and 564) are substituted with alanines [36]. One-day in vitro-cultured E11.5 mgNPCs were infected with lentiviruses expressing HA-tagged caHIF1α (HA-caHIF1α) and cultured for a further day, and then subjected to LIF stimulation for 3 days under the normoxic condition. HA-caHIF1α protein was clearly detected in the nucleus (Fig. 5M). In contrast to control virus-infected mgNPCs (Fig. 5H–5K), cells transduced to express HA-caHIF1α became GFAP-positive astrocytes in response to LIF stimulation, even under the 21% O_2 condition

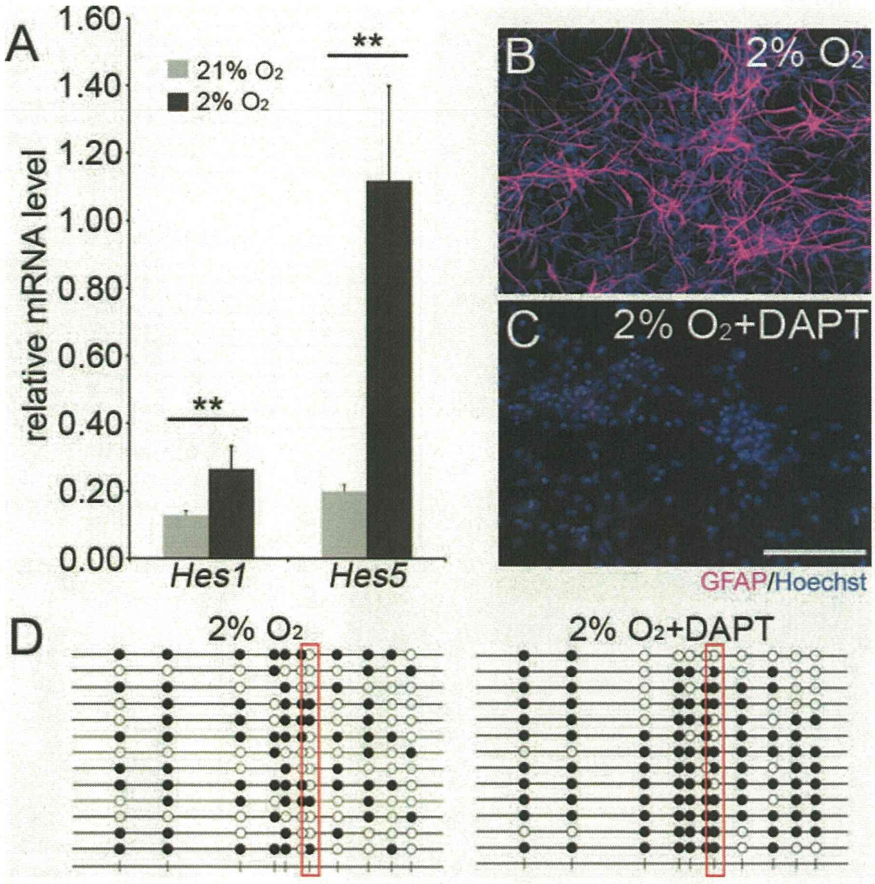

Figure 4. Notch signal activation is required for hypoxia-promoted acquisition of astrogenic potential by neural precursor cells (NPCs). **(A):** Quantitative polymerase chain reaction analysis of the expression of Notch signal target genes. Expression of the representative Notch signal targets *Hes1* and *Hes5* was upregulated in midgestational neural precursor cells cultured for 4 days under 2% O_2. Statistical significance was evaluated by the Student's *t* test. **, $p < .01$. **(B, C):** Hypoxia-induced astrogenic potential of NPCs was blocked by Notch signal inhibition. E11.5 NPCs were cultured for 4 days in the 2% O_2 condition with or without DAPT (10 μM), followed by a 4-day leukemia inhibitory factor stimulation. Bar = 100 μm. **(D):** The methylation status of the *gfap* promoter in E11.5 NPCs cultured with or without DAPT (10 μM) in the 2% O_2 condition was examined by bisulfite sequencing. The signal transducer and activator of transcription 3-binding site is indicated by red rectangles. Abbreviations: DAPT, *N*-[*N*-(3,5-difluorophenacetyl-L-alanyl)]-*S*-phenylglycine *t*-butyl ester); GFAP, glial fibrillary acidic protein.

(Fig. 5L–5O). HA-caHIF1α expression also augmented Notch signal activation in these cells (Fig. 5P). Furthermore, HA-caHIF1α-induced astrocyte differentiation and Notch signal activation were both abolished by DAPT treatment (Fig. 5P and Supporting Information Fig. S6C–S6J). Consistent with the results of these in vitro experiments, ectopic expression of HA-caHIF1α in E11.5 brains led to precocious GFAP expression in NPCs (Supporting Information Fig. S6K–S6P). These experiments suggest that HIF1α promotes the astrogenic potential of mgNPCs by enhancing Notch signal activation, probably because hypoxia-stabilized HIF1α can form a complex with the Notch intracellular domain (NICD) to effectively induce the expression of Notch-target genes [15].

Given that the 21% O_2 condition delayed the acquisition of astrocyte differentiation ability by NPCs in vitro, we next asked whether a hyperoxic environment has a similar effect on NPCs in vivo. To address this, pregnant mice were housed in a normoxic or hyperoxic chamber for 6 days (E11.5 to E17.5). To confirm that the embryonic brain was indeed under hyperoxia, we measured the local brain oxygen tension at E15.5 using an oxygen electrode. When the pregnant mice were in the normoxic (21% O_2) and hyperoxic (80% O_2) conditions, the oxygen tensions were 5.24 and 112.9 mmHg, respectively (Supporting Information Fig. S6Q), indicating that local brain oxygen tension was increased as a result of the atmospheric oxygen levels surrounding the pregnant mother mouse. After 6 days of hyperoxic housing, embryonic brains were then subjected to immunostaining and Western blotting. Interestingly, as shown in Figure 5Q–5S, exposure to high oxygen markedly decreased GFAP expression in the brains of embryos of mice housed in the hyperoxic condition.

These results suggest that a hypoxic environment is important for the proper timing of astrocyte differentiation during embryonic development.

Discussion

HIF1α is known to be an important factor in the response of various types of cells to hypoxic stress such as ischemia [11, 13] and to play a critical role in normal brain development [14]. In the present study, we have shown that astrocytic genes are progressively demethylated in the mildly hypoxic environment of the developing brain (Figs. 1–3). We further

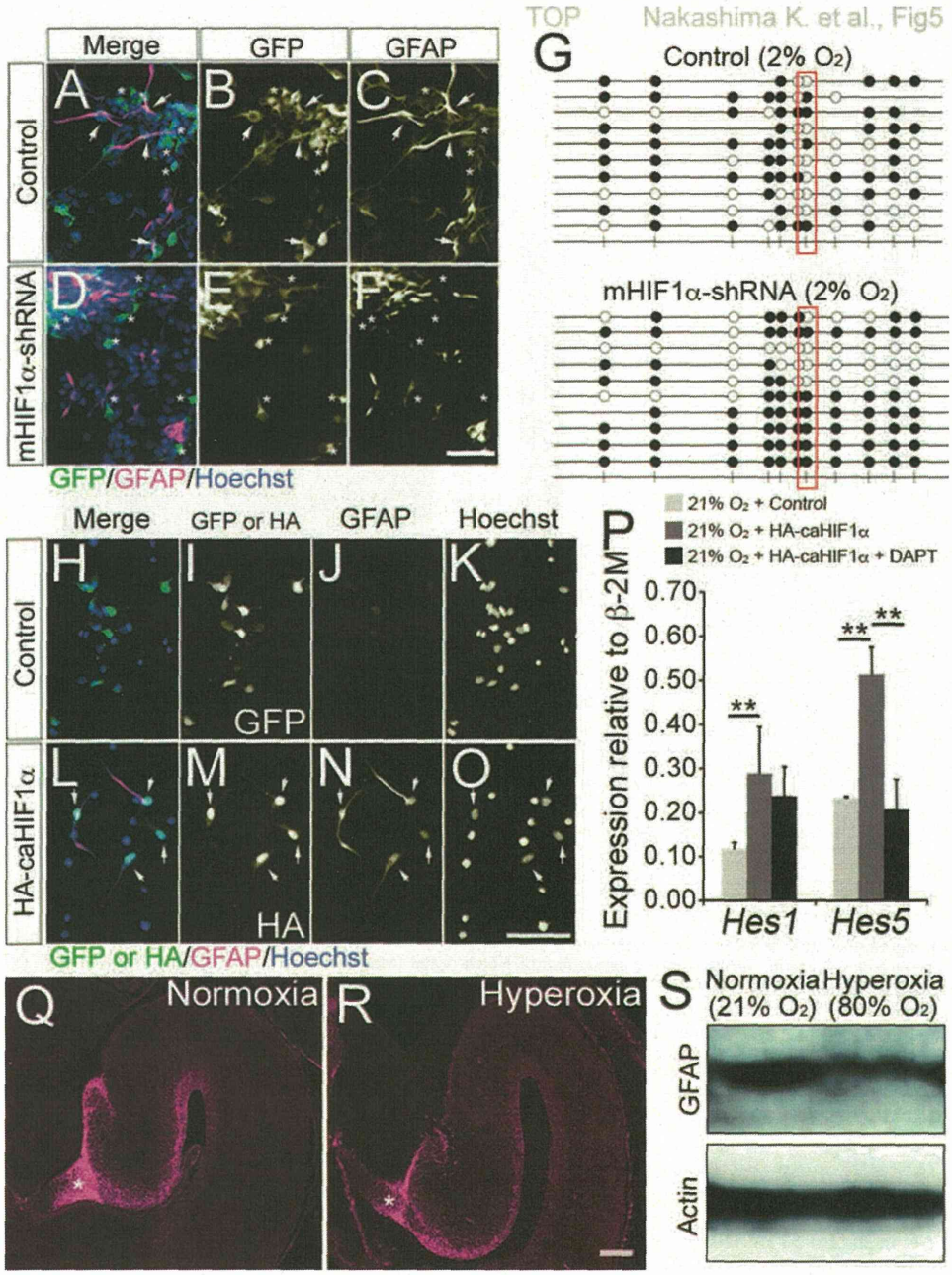

Figure 5. Astrogenic potential of neural precursor cells (NPCs) is regulated by HIF1α and oxygen levels. **(A–F):** E11.5 NPCs were infected with lentiviruses encoding GFP alone or GFP together with mHIF1α-shRNA, and cultured under 2% O_2 for 3 days followed by a 4-day leukemia inhibitory factor (LIF) stimulation. Virus-infected cells were identified by their GFP expression (green) and analyzed for GFAP expression (magenta) by immunocytochemistry. Hoechst, blue. GFP and GFAP double-positive cells (arrows) were observed in control virus-infected cells (A–C), whereas most of the mHIF1α-shRNA-expressing virus-infected cells were positive for GFP only (asterisks) (D–F). Bar = 50 μm. **(G):** The methylation status of the *gfap* promoter in 3-day-cultured virus-infected cells was examined by bisulfite sequencing. Demethylation in mHIF1α-shRNA-expressing virus-infected cells was inhibited. The signal transducer and activator of transcription 3-binding site is indicated by red rectangles. **(H–O):** Hydroxylation-mediated degradation-resistant constitutively active HIF1α (HA-caHIF1α) was introduced into E11.5 NPC by lentivirus infection, and the cells were cultured for 1 day followed by a 3-day LIF stimulation under 21% O_2. Precocious GFAP expression was observed in HA-caHIF1α-expressing virus-infected cells (arrows), even under 21% O_2 (L–O). Bar = 50 μm. **(P):** E11.5 NPCs were infected with control or HA-caHIF1α-expressing lentiviruses on the day after preparation and cultured in the presence of LIF for 3 days with or without DAPT under 21% O_2, and their RNAs were then subjected to quantitative polymerase chain reaction. *Hes1* and *Hes5* expression was normalized to that of β-2M. The expression of both of these genes was upregulated by HA-caHIF1α expression, and this effect was abolished by DAPT treatment. Statistical significance was evaluated by the Student's *t* test. **, $p < .01$. **(Q, R):** GFAP expression in E17.5 brain was reduced when pregnant mice were housed in a hyperoxic atmosphere (80% O_2) from E11.5 to E17.5. Brain sections are stained with anti-GFAP antibody (magenta). Hippocampal regions are shown as representatives. Asterisks, fimbria. Bar = 100 μm. **(S):** Whole brains of embryos from pregnant mice housed in normoxic (21% O_2) and hyperoxic (80% O_2) atmospheres were lysed and subjected to immunoblot to detect GFAP and β-actin (as loading control) expression. Abbreviations: β-2M, β-2 microglobulin; caHIF1α, constitutively active HIF1α; DAPT, *N*-[*N*-(3,5-difluorophenacetyl-L-alanyl)]-*S*-phenylglycine *t*-butyl ester); GFAP, glial fibrillary acidic protein; GFP, green fluorescent protein; HA, hemagglutinating; mHIF1α, mouse HIF1α; shRNA, short hairpin RNA.

suggest that this demethylation process is executed by a collaboration between HIF1α and Notch signal activation (Figs. 4, 5), probably through the formation of a complex between HIF1α and NICD, to effectively induce the expression of Notch-target genes [15]. The augmentation of Notch signal activation under hypoxia led to higher expression of *Nfia* (Supporting Information Fig. S4A), which has been shown to induce dissociation of DNMT1 from astrocytic gene promoters, resulting in demethylation of the promoters [7]. It has been suggested that HIFs act cooperatively with other signaling molecules, thereby influencing a wide range of biological processes including NPC maintenance and differentiation [11, 18-20]. Nevertheless, we report for the first time, to the best of our knowledge, that oxygen levels not only modify the behavior of transcription factors but also affect the epigenetic status of genes. The promotion of astrocytic gene demethylation by the hypoxic condition contributes to specifying the appropriate timing of the neural-to-glial cell fate switch of NPCs, by ensuring a proper balance between neurons and astrocytes that are generated during brain development.

We also found in this study that oxygen tension affects the DNA methylation status of astrocytic genes in mgNPCs via HIF-Notch signaling. Strikingly, hypoxia, HIF1α, Notch signaling and DNA methylation are all known to participate in the onset and/or progression of glioblastoma [12, 13, 15, 37], the most common and malignant type of brain tumor. Thus, a deeper understanding of glial cell-generating mechanisms, including astrocyte differentiation, may be of therapeutic interest.

As has been shown in a previous study [5] and the present work, DNA demethylation in the astrocytic gene promoters of NPCs is crucial for astrocyte differentiation, and the efficacy of astrocyte differentiation of NPCs is influenced by oxygen levels in the brain throughout development. Premature infants in neonatal intensive care units (NICUs) are often incubated under hyperoxic conditions to support their immature respiration. Oxygen concentration is strictly controlled in NICUs, since it has been shown that excess oxygen administration causes retinopathy of prematurity [38]. Furthermore, a few studies report other risks of hyperoxia to the central nervous system of extremely premature infants, including defects in mental and psychomotor development [39, 40]. The present study suggests that such effects may be attributable to an imbalance in NPC differentiation caused by a high level of oxygen in the incubator, and identifying their underlying mechanism in future work could provide new approaches for clinical applications that address developmental abnormalities in the nervous system, particularly in the context of neonatal intensive care.

Conclusion

We showed that local oxygen concentration can affect the fate of NPCs through an epigenetic mechanism. Unraveling how actual microenvironmental oxygen levels in the embryo influence epigenetic gene regulation in NPCs will provide new aspects for the study of NPC regulation.

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Disclosure of Potential Conflicts of Interest

The authors indicate no potential conflicts of interest.

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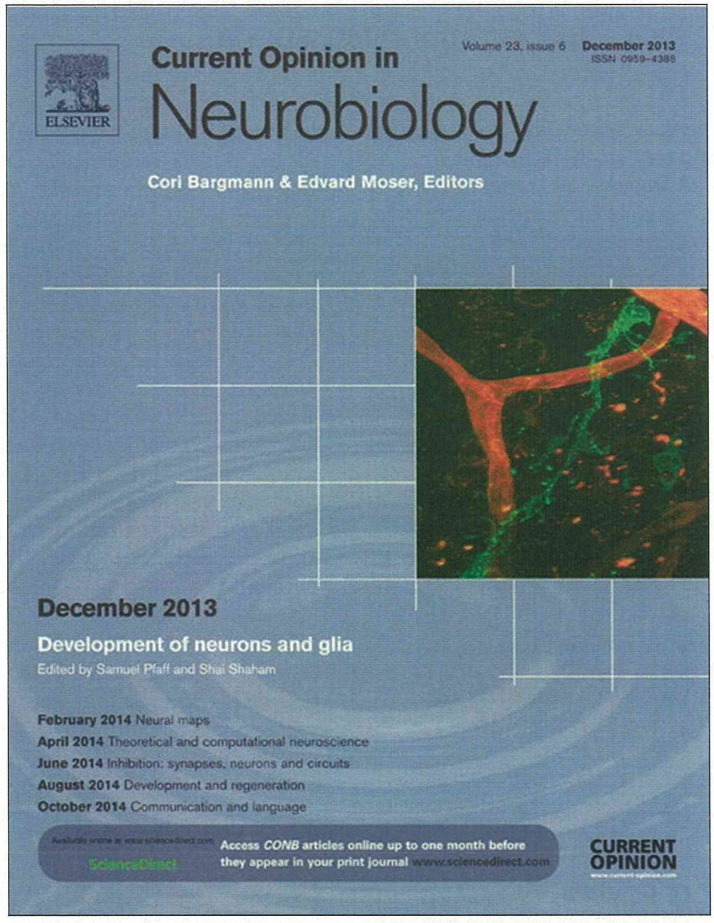

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Current Opinion in Neurobiology

Mechanisms of astrocytogenesis in the mammalian brain

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In the mammalian central nervous system, astrocytes are the most abundant cell type and play crucial roles in brain development and function. Astrocytes are known to be produced from multipotent neural stem cells (NSCs) at the late gestational stage during brain development, and accumulating evidence indicates that this stage-dependent generation of astrocytes from NSCs is achieved by systematic cooperation between environmental cues and cell-intrinsic programs. Exemplifying the former is cytokine signaling through the gp130-Janus kinase/signal transducer and activator of transcription 3 pathway, and exemplifying the latter is epigenetic modification of astrocyte-specific genes. Here, we introduce recent advances in our understanding of the mechanisms that coordinate astrocytogenesis from NSCs by modulating signaling pathways and epigenetic programs, with a particular focus on the developing mammalian forebrain.

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Introduction

Nearly 50% of the cells in the adult human brain are glial cells, among which astrocytes are the most abundant cell type and are ubiquitous throughout the brain and spinal cord [1]. Astrocytes play a variety of crucial roles in brain development and function, such as structural support, maintenance of water balance and ion distribution, and construction of the blood–brain barrier to control the passage of substances from the blood into the brain. During mammalian development, astrocytes are generated from neural stem cells (NSCs) located in the ventricular zone and subventricular zone in the gliogenic phase of late gestation [2]. NSCs, known as neuroepithelial cells in early-gestational to mid-gestational stages, divide both symmetrically, to increase their own numbers, and asymmetrically, to generate early neurons (Figure 1). As development proceeds, the morphology of NSCs changes: the cells display extended radial processes to the pial surface from their somata, which reside in the ventricular zone [3], and become known as radial glial cells (Figure 1). These NSCs generate more neurons but now also have the potential to differentiate into astrocytes. At the late embryonic and early postnatal stages, most NSCs begin to detach from the apical side and migrate into the cortex, where they differentiate into astrocytes [4,5] (Figure 1), although a recent report demonstrates that the majority of astrocytes in the postnatal cortex arise from the local proliferation, during the early postnatal period, of cells that have already differentiated [6•].

In this review, we focus on recent molecular insights into astrocytogenesis from NSCs in the developing mouse brain. It is well established that there are two important components in astrocytogenesis during mammalian brain development. One is the epigenetic derepression of astrocytic gene transcription, a prerequisite for the progressive acquisition of astrocyte differentiation potential by NSCs; the other is the activation of cytokine signaling through the gp130-Janus kinase/signal transducer and activator of transcription 3 (JAK–STAT3) pathway to induce astrocytic gene transcription. Accumulating evidence indicates that various factors contribute to astrocyte production from NSCs by regulating these two processes. In this review, we survey reports investigating astrocytogenesis from NSCs in the mammalian central nervous system, with a special emphasis on the developing forebrain.

Regulators modulating the signaling pathway of astrocyte-inducing cytokines

The JAK–STAT3 pathway is activated by members of the interleukin (IL)-6 family of cytokines, including leukemia inhibitory factor (LIF), ciliary neurotrophic factor, and cardiotrophin-1 (CT-1), through homodimerization or heterodimerization of the common signal transducer gp130 either with itself or with another receptor component such as LIFRβ [7]. Activated STAT3 then induces astrocyte differentiation by activating astrocytic genes such as glial fibrillary acidic protein (*gfap*) [8,9] (Figure 2). In a convergent pathway, the action of another group of cytokines, the bone morphogenetic proteins (BMPs), is mediated by heterotetrameric serine/threonine kinase receptors and their downstream transcription factors Smad1, 5, or 8. After being phosphorylated, these