The mechanisms that regulate the growth of the brain remain unclear. We show that Sonic hedgehog (Shh) is expressed in a layer-specific manner in the perinatal mouse neocortex and tectum, whereas the Gli genes, which are targets and mediators of SHH signaling, are expressed in proliferative zones. In vitro and in vivo assays show that SHH is a mitogen for neocortical and tectal precursors and that it modulates cell proliferation in the dorsal brain. Together with its role in the cerebellum, our findings indicate that SHH signaling unexpectedly controls the development of the three major dorsal brain structures. We also show that a variety of primary human brain tumors and tumor lines consistently express the GLI genes and that cyclopamine, a SHH signaling inhibitor, inhibits the proliferation of tumor cells. Using the in vivo tadpole assay system, we further show that misexpression of GLI1 induces CNS hyperproliferation that depends on the activation of endogenous Gli1 function. SHH-GLI signaling thus modulates normal dorsal brain growth by controlling precursor proliferation, an evolutionarily important and plastic process that is deregulated in brain tumors.

Key words: Mouse, Xenopus, GLI, SHH, Brain, Tumor, Neocortex, Tectum, Growth, CNS
MATERIALS AND METHODS

Animals, human tissue samples and cell lines
Swiss-Webster mouse embryos were staged counting the morning after conception as embryonic day (E) 0.5. Shh homozygote mutant mice were a kind gift from C. Chiang (Chiang et al., 1996). Human tumor samples were derived from the operating room or from the NYU tumor banks. Brain tumor cell lines were obtained from ATCC and grown according to its specifications. GL261 was a kind gift of Dr. D. Zagzag. Frog (Xenopus laevis) embryos were obtained, reared and staged by standard methods. Tadpoles were ~2 days old. All statistical analyses were carried out using the Student’s t test and deviations are shown as s.e.m.

Explants, dissociated cells, cell treatments and chemicals
Neocortical or tectal explants from embryonic day (E) 17.5 to postnatal-day (P) 3 mice were taken from the parietal region, or adjacent to the dorsal midline in the prospective superior and inferior colliculi, respectively. After removal of the meninges, the explants were grown on floating filters in serum-free media (Nothias et al., 1998; Dahmane and Ruiz i Altaba 1999). After 12 hours in culture, SHH was added and incubation continued for a further 48 hours. Explants for RNA preparation were directly collected in Trizol (Gibco-BRL). For dissociated cells, parietal cortical pieces of P3 brains were pooled (~10 explants per experiment) and treated with trypsin for 10 minutes (0.25 mg/ml at room temperature). Tissue was triturated manually in DNase (0.5 mg/ml), and cells were centrifuged, resuspended in supplemented serum-free media and plated at a density of ~400 cells/mm² in poly-L-lysine-coated 16- or 8-well slides. After 12 hours the media were replaced and SHH protein added if required. Cells were cultured for a further 48 hours and processed for immunocytochemistry after fixation in 4% paraformaldehyde for 1 minute. Primary gliomas from the

Fig. 1. Perinatal expression of Glis and Shh in the mouse dorsal brain. (A,D,G) Expression of Gli1 (A), Gli2 (D) and Gli3 (G) in the vz/svz of the cerebral neocortex (Ctx) and striatum (Str) at embryonic day (E) 15.5. The three Gli genes are also co-expressed in the vz of the striatum and olfactory bulb (D and not shown). (B,E,H) Expression of Gli1 (B), Gli2 (E) and Gli3 (H) in the cerebral cortex (Ctx) at E17.5. Gli gene expression is detected near the ventricle (v) with Gli1 also expressed in scattered cells within the cortical plate. (C,F,I) Expression of Gli1 (C), Gli2 (F) and Gli3 (I) in the midbrain at E17.5. Expression of the Gli genes is regionalized in the vz of the tectum (Tct) and tegmentum (Tgt). Expression is also detected in the EGL and Purkinje layer of the cerebellum (Cb). Shh is also detected in the tegmentum as well as in the amygdala (not shown). (J) RT-PCR analyses of Shh expression in the parietal neocortex of E14.5-postnatal day (P)3 mice (right) and of its expression at E17.5 in the neocortex (Nctx), striatum (Str), superior colliculus (SC), inferior colliculus (IC) and cerebellum (Cb). A no RT control is also added (Nctx-RT). Hprt is used to control for RNA levels. (K-M) Shh is expressed in a layer-specific manner in the P2 neocortex (Ctx; K,L) and cingulate cortex (Cc; K), as well as in the tectum (Tct) and cerebellum (Cb), where it is found in the Purkinje layer. Shh is also expressed in the hippocampal dentate gyrus (Dg, also detected by RT-PCR, not shown). Similar expression was detected at P1 and P5. (N,O) Gli1 expression is found in the vz/svz of the cortex and in scattering cells (O) in a P5 mouse brain. Gli1 expression is also prominent in the dentate gyrus (Dg) of the hippocampus (Hipp). Similar expression was detected at P1 and P5. (P) Expression of the oligodendrocyte precursor marker Pdgfrα in scattered cells and in a subset of cells near the ventricle. (Q-S) High magnification of the similar expression patterns of Gli1 (Q), Pch1 (R) and Pdgfrα (S) in scattering cells in the P5 cortex. Arrows point to sites of expression. v, ventricle. All panels show sagittal sections except N and the inset in K, which display coronal sections.
operating room were dissociated with papain and plated in U118 media containing 10% fetal calf serum (FCS) or in DMEM:F12 serum-free media supplemented with BIT-9500 (Stem Cell Technologies) and 20 ng/ml of each of FGF2, EGF and PDGF. After two to three passages, the cells had a homogenous appearance and were then tested. Recombinant N-SHH was a kind gift from Ontogeny and was used at 5 nM. For blocking experiments, anti-SHH mAb 5E1 (Ericson et al., 1996) was used at 20 μg/ml (obtained from the University of Iowa Hybridoma Bank). Cyclopamine (a kind gift from the Poisonous Plant Laboratory or purchased from Toronto Research Chemicals) was used at 0.5-5 mM for 48 hours before assaying. Cell lines were plated at 60% confluency the night before cyclopamine treatment. FK and ddFK (Sigma) were used at 50 μM.

Microinjection, RNAs and antisense oligonucleotides
Injection of synthetic RNAs into frog embryos was performed into one cell at the two-cell stage, targeting the future CNS and epidermis. Frog or human Gli1 RNAs (Lee et al., 1997) were injected at 2 ng/10 nl/embryo. The N-terminal Myc-epitope tag in the frog Gli1 and Gli2 proteins (Lee et al., 1997) was used to monitor protein distribution. Morpholino antisense oligonucleotides were purchased from Gene Tools and used at 0.5 mM. These were frog Gli1, 5’CGGGCGGACAC-TGCGGGAGCCG3’; frog Gli2, 5’GCACAGAAGCGAGGATGCTCATA3’; and frog Shh, 5’GAGATTCGAGTTGGCAACAGCATAC3’. In all cases, the oligonucleotides were designed to be complementary to regions near the initiation ATG codon and are predicted to inhibit translation (Heasman et al., 2000).

RT-PCR and in situ hybridization
In situ hybridization on serial ~20 μm cryostat sections with
digoxigenin-labeled antisense RNA probes and full-length frog, mouse or human Gli1 cDNA clones and histology were as previously described (Dahmane et al., 1997; Lee et al., 1997; Park et al., 2000). Visualization of the low levels of Gli1 and PCH1 expression in CNS tumors and mouse brains older than E17 required long (2 days at room temperature) chromogenic development of the in situ hybridization reactions. Specificity was confirmed using sense RNA probes. RT-PCR of human tumors or cell lines was performed for 27, 32 and 37 cycles to determine the linear amplification range. PCR primers and specific reaction conditions are available upon request. A probe for DRR was made as described (Weiner et al., 2000). A 0.6 kb RT-PCR clone was used as a template for probe production for mouse Pdgfra (platelet-derived growth factor receptor α).

**Immunocytochemistry**

BrdU incorporation in explants and dissociated cells was for 2 hours at 6 μg/ml. Primary tumor cultures were labelled with BrdU for 14 hours. Pregnant mice were injected intraperitoneally with a single dose of 50 μl of 10 mg/ml BrdU and embryos dissected 2 hours afterwards. For tadpoles, one 20 nl injection of 10 mg/ml BrdU into the lumen of the CNS and one into the endoderm were performed 1 hour before fixation. Sections of embryos or explants (14–20 μm) were prepared using a cryostat. Immunocytochemistry with monoclonal anti-BrdU antibody (Becton-Dickinson), monoclonal anti-vimentin antibody (Santa Cruz), monoclonal anti-neuronal tubulin Tuji antibody (Babco), rat monoclonal anti-Nestin antibody (University of Iowa Hybridoma Bank) or O4 monoclonal antibody (Chemicon, also a kind gift of Bob Miller) was performed on frozen sections and cells using fluorescein-conjugated secondary antibodies (Boehringer Mannheim).

**RESULTS**

The Gli genes are expressed in proliferative zones of the brain

First, we sought to clarify the patterns of expression of the Shh and Gli genes (Echelard et al., 1993; Roelink et al., 1994) in the late embryonic and postnatal mouse brain. By E15.5, the three Gli genes are expressed in the ventricular zone (vz) of the future cerebral cortex and tectum (Fig. 1A,D,G and not shown), where they are detected as early as E13.5 (Hui et al., 1994). However, Gli1 was expressed at higher levels in the deeper cortical vz/subventricular zone (svz), Gli2 mostly in vz cells and Gli3 in these two populations (Fig. 1A,D,G). Gli1 and Gli3, but not Gli2, also show a transient graded distribution along the anteroposterior axis (Fig. 1A,D,G). At E17.5, they remain co-expressed in the vz of the cerebral cortex (Fig. 1B,E,H), tectum and tegmentum (Fig. 1C,F,I). Gli expression in the tectum is localized within the vz, suggesting heterogeneity in precursor cells. At this stage, Shh is expressed in the tectum, but is not detectable by in situ hybridization in the tectum or cerebral cortex. However, more sensitive RT-PCR analyses indicated that Shh is indeed found in these regions from E14.5 to P3 (Fig. 1J). The neocortical meninges expressed Gli1 but not Shh (Fig. 2A).

Perinatally, the Gli and Shh genes display largely mutually exclusive expression domains. Shh RNA is found in the Purkinje layer in the cerebellum, and in the superficial layers of the tectum (Fig. 1M) and cerebral cortex (probably layer V; Fig. 1K,L) (Traiffort et al., 1999). Lack of Shh expression in dorsal progenitors would be consistent with its reported absence from late embryonic and postnatal neurospheres (Zhu et al., 1999). Shh and Gli1 were also detected in the dentate gyrus of the hippocampus (Fig. 1K,N).

Gli1, but not Gli2 or Gli3, is also expressed at low levels by single cells scattered throughout the brain (Fig. 1B,O,Q). Given that there is massive gliogenesis in the perinatal cortex, if Gli1+ scattering cells are glial progenitors that respond or have responded to SHH, the pattern of Gli1 expression should be similar to that of its target Pch1 and possibly to that of Pdgfra, a marker of oligodendrocyte progenitors (Goodrich et al., 1996; Pringle and Richardson, 1993). The expression of Gli1 was found in a scattered pattern similar to that of Pch1 and Pdgfra in serial sections (Fig. 1Q–S), although the low levels of their expression, together with the lack of specific antibodies, precluded double-labeling analyses.

**SHH regulates Gli1 expression in neocortical explants**

SHH secreted perinatally from differentiated cells in the cortical plate could affect precursor cells in the vz/svz. To test this possibility, we cultured isolated explants of late embryonic (E17.5) and postnatal (P3) mouse cerebral cortex in vitro (Fig. 2C). SHH treatment dramatically increased Gli1 expression over that seen in untreated sibling explants (Fig. 2A,B). Upregulation was higher at P3 (Fig. 2B). In situ hybridization analyses confirmed this effect (Fig. 2D,E) and localized Gli1 expression mostly to vz cells (Fig. 2E). In response to SHH, the expression of Pch1 showed a small but consistent upregulation, that of Gli2 and Gli3 showed a little variation, and that of endogenous Shh remained unchanged, whereas the expression of Pdgfra in control and SHH-treated samples was uninformative, as its expression was found at high levels in both cases (Fig. 2A,B and not shown).

**SHH is a required mitogen for neocortical and tectal vz cells**

To test whether SHH could act as a mitogen for precursor cells, we cultured P3 neocortical explants for 48 hours and added BrdU to the media 2 hours before fixation. SHH treatment led to an approx. twofold increase in the number of BrdU-positive cells when compared with control untreated explants (Fig. 2F,G,K: control, 105±20 cells/explant section; SHH treated, 226±14 cells/explant section; P<0.005). This increase is similar to that seen in cerebellar precursors after SHH treatment (Dahmane and Ruiz i Altaba, 1999). As with Gli1 expression, the great majority of BrdU-positive cells in SHH-treated explants are in the vz (Fig. 2G).

Treatment of neocortical explants with a blocking anti-SHH antibody, extensively used previously to block SHH function specifically (mAb 5E1) (Ericson et al., 1996; Dahmane and Ruiz i Altaba, 1999; Weschler-Reya and Scott, 1999) produced a twofold decrease in BrdU incorporation after 48 hours in culture when compared with untreated controls (Fig. 2H,F,K: control, 105±20 cells/explant section; mAb 5E1-treated, 45±8 cells/explant section; P<0.005). To corroborate this result, we also attempted to block SHH signaling with cyclopamine and forskolin (FK) and with the inactive derivative 1,9-dideoxyforskolin (ddFK) as control. Cyclopamine treatment inhibits the response to SHH signaling (Incardona et al., 1998; Cooper et al., 1998), by acting on the Patched-Smoothened membrane receptor complex (Taipale et al., 2000). Cyclopamine treatment resulted in a twofold decrease in cell proliferation as measured by BrdU incorporation (Fig. 2K: untreated, 72±5.6 cells/explant section; cyclopamine treated, 38±3.4 cells/explant section; SHH treated, 77±7.4 cells/explant section; SHH+ cyclopamine treated, 30±4.6 cells/explant section).
The brain of Shh mutant late embryos show precursors is in accordance with the localization of BrdU-positive cells. The identity of BrdU-positive cells as Nestin-positive GFAP or the oligodendrocyte marker O4 (Fig. 4C-E) and not rarely did BrdU-positive cells express the astrocyte marker consistent with the proliferation of E13.5 neurospheres after on precursor cells to increase their proliferation, a result (Hockfield and McKay, 1985), this result indicates that SHH acts identities precursors (Lendahl et al., 1990), including radial glia labeling (Fig. 4A,B,E; 88±2.5% BrdU-positive cells per field. Double-labeling analyses showed that BrdU-positive cells with percentage of BrdU-positive cells over total cell number per field in SHH-treated versus control untreated samples (Fig. 3E, first panel: control, 7.1±0.8%; SHH treated, 40±5 cells/explant section; P=0.005). As in the cortex, the increase in the number of BrdU-positive cells was seen near the vz (Fig. 3C,D), and FK, but not ddFK, was also able to inhibit BrdU incorporation by approx. two-fold (Fig. 3E: ddFK treated, 12.8±5.9 cells/explant section; FK treated, 7.3±2.5 cells/explant section; P<0.01).

**SHH is a mitogen for nestin-positive neocortical precursors**

To investigate the identity of BrdU-positive cells seen after SHH treatment, we tested for the mitogenic effects of SHH on dissociated P3 cortical cells. Addition of BrdU for 2 hours after 48 hours in culture showed an approx. twofold increase in the percentage of BrdU-positive cells over total cell number per field in SHH-treated versus control untreated samples (Fig. 3E, first panel: control, 7.1±0.8%; SHH treated, 14.8±0.4%; P<0.005). Double-labeling analyses showed that BrdU-positive cells with nuclear labeling were also nestin-positive cells with cytoplasmic labeling (Fig. 4A,B,E; 88±2.5% BrdU-positive cells per field were also nestin positive in control samples, and 93±3.2% in SHH-treated samples). Because the intermediate filament nestin identities precursors (Lendahl et al., 1990), including radial glia (Hockfield and McKay, 1985), this result indicates that SHH acts on precursor cells to increase their proliferation, a result consistent with the proliferation of E13.5 neurospheres after SHH treatment (Kalyani et al., 1998). By contrast, only very rarely did BrdU-positive cells express the astrocyte marker GFAP or the oligodendrocyte marker O4 (Fig. 4C-E and not shown). The identity of BrdU-positive cells as Nestin-positive precursors is in accordance with the localization of BrdU-positive cells in the vz/svz of explants (Fig. 2F,G).

**The brain of Shh mutant late embryos show decreased proliferation in the vz/svz**

Our experimental in vitro data predicts that lack of SHH in vivo will result in a downregulation of proliferation in the vz/svz of the neocortex. Shh-null mice die at birth and display severe holoprosencephaly (Fig. 5A), resulting in part from the complete lack of ventral CNS structures and the malformation of the face (Chiang et al., 1996). However, dorsal CNS structures are present, as demonstrated by the maintained expression of the Emx1, Otx2 and En2 in the mutant neocortex, diencephalon and tectum, respectively (Chiang et al., 1996). It is thus feasible to ask whether the dorsal-only brain of Shh null mice (Fig. 5L,M) displays normal proliferation prenatally.

Both RT-PCR analyses and in situ hybridization of E18.5 Shh homozygote null embryos revealed that the presumptive cortex expresses the neocortical marker Tbr1 and is present adjacent to the proboscis, which does not express Tbr1 (not shown). To analyze cell proliferation, a pulse of excess BrdU was given to pregnant mothers 2 hours before embryo collection. Within the cortex, cell proliferation was decreased nearly fourfold in mutant versus control embryos (Fig. 5B,C,F,G; 11.2±0.6% BrdU-positive cells in the vz/svz of wild-type embryos versus 3±0.7% BrdU-positive cells in mutant embryos, P<0.001; counting the vz/svz as a width of 10 cell diameters from the ventricle). Nevertheless, nestin-positive vz/svz cells (Fig. 5D,E), Tu1-positive neurons (Fig. 5F,G) and GFAP-positive astrocytes (not shown) could be observed in both wild-type and mutant cortices. More posterior brain regions also showed a marked decrease in proliferation. For example, in the midbrain areas, the malformed tectum showed one-fifth to a half the number of BrdU-positive cells, and E18 mutant mice lacked a recognizable cerebellum, even though the adjacent choroid plexus was clearly present (Fig. 5H,I). Indeed, by E15.5, the cerebellum was already drastically reduced morphologically (Fig. 5L arrow), in line with previous work on the indispensable role of SHH in cerebellar development (Dahmane and Ruiz i Altaba, 1999; Wallace, 1999; Wesczler-Reya and Scott, 1999).

In contrast to the decrease in the proliferation of the vz/svz of the brain, other parts of the mutant embryo appeared to proliferate normally or even to overproliferate. For example, basal epidermal cells appeared to have the same amount of BrdU-positive cells in mutants and wild-type littermates (Fig. 5J,K; 34.3±1.3 BrdU-positive cells per field in the basal layer of the epimembranous in mutant embryos versus 36.2±3.1 BrdU-positive cells per field in the basal layer of the interfollicular epidermis of wild-type littermates, P>0.5), even though the mutant skin lacked hair follicles (Fig. 5K) (St-Jacques et al., 1998). The liver, by contrast, appeared to overproliferate, as judged by the number of BrdU- and HNF-3β-labelled cells (not shown).

**GLI gene expression in primary brain tumors and brain tumor cell lines**

Our findings in normal development raise the possibility that inappropriate activation or maintenance of the SHH-GLI pathway could lead to hyperproliferation, the basis of tumorigenesis. To test this idea, we first analyzed sporadic human brain tumors for the consistent expression of the GLI genes. We tested by RT-PCR seven glial tumors and primitive neuroectodermal tumors (PNETs), including those from the cerebellum (medulloblastomas), because the latter have been shown previously to harbor PTCH1 mutations, suggesting the activation of the SHH-GLI pathway (Wolter et al., 1997; Raffel et al., 1997). We found that all the tumors tested expressed GLI1, although at different levels (Fig. 6A). Additional analyses for a total of 22 tumors (Fig. 6B) showed that all samples contained the three GLI transcripts. Expression of PTCH1 followed the expression of GLI1/2, while that of SHH was not consistently detected (Fig. 6B).

In situ hybridization analyses of 22 independent brain tumors showed that GLI1 was expressed in neuronal and in glial tumors, including glioblastoma multiforme and low grade glioma (Fig. 6C,E). GLI1 and PTCH1 mRNAs were detected in the regions containing tumor cells and not in surrounding normal tissues (Fig. 6E,G,F,H).
Analyses of human brain tumor cell lines, including seven glioblastoma (U87MG, U118MG, U138MG, A172, T98G, M059K, M059J), two glioma (Hs683, mouse GL261), one neuroglioma (H4), three astrocytoma (CCF-STTG1, SW1088, SW1783), three medulloblastoma (Daoy, D283, D341) and two neuroblastoma (SK-N-AS, IMR32) lines, showed that all brain tumor cell lines co-expressed GLI1, GLI2 and PTCH1 (Fig. 6I). GLI3 was expressed by all but one (D341) and only a subset (U87MG, U138MG, Daoy, M059K, SW1783) expressed SHH (not shown).

As a control, we also tested a panel of unrelated sporadic human tumors by RT-PCR and found that GLI1 was expressed consistently in prostate carcinomas (9/11 cases) but not in those from the breast (1/7), suggesting that prostate cancer may also result from deregulated SHH-GLI signaling.

**Cyclopamine modulates the proliferation of a subset of brain tumor cells**

Expression of the GLI and PTCH by glioma cells raised the possibility that these harbor mutations that activate the pathway at different levels. Indeed, we expected that only a fraction of these possible mutations would affect the PTCH-SMO receptor complex. To address this possibility we have tested the effects of cyclopamine, a drug that inhibits the function of oncogenic Smoothened forms (Taipale et al., 2000). The glioblastoma/glioma lines U87, U118, U138, M059K, Hs683, C6, GL261, astrocytoma lines, SW1088 and SW1783, and the medulloblastoma line Daoy were tested and four responded to cyclopamine treatment by decreasing BrdU incorporation by ~25-50% (Fig. 6J). These are the glioma lines U87, U118 and U138, and the medulloblastoma line Daoy: untreated U87, 22.5±1.4% BrdU-positive cells/field; 0.5 μM cyclopamine treated, 16.5±0.9% BrdU-positive cells/field, P<0.005; and 5 μM cyclopamine-treated, 13.2±1.2% BrdU-positive cells/field, P<0.001; untreated U118, 12.9±1.3% BrdU-positive cells/field; 0.5 μM cyclopamine treated, 6.7±0.8% BrdU-positive cells/field, P=0.001; and 5 μM cyclopamine treated, 7.1±1.1% BrdU-positive cells/field, P<0.005; untreated U138, 13.3±0.7%
SHH, brain growth and tumorigenesis

BrdU-positive cells/field; 0.5 μM cyclopamine treated, 9.5±0.6% BrdU-positive cells/field, P<0.005; and 5 μM cyclopamine-treated, 7.5±1.2% BrdU-positive cells/field, P=0.001; untreated Daoy, 37.9±2% BrdU-positive cells/field; 0.5 μM cyclopamine treated, 27.7±1.5% BrdU-positive cells/field, P=0.001; and 5 μM cyclopamine-treated, 27.1±1.7% BrdU-positive cells/field, P=0.001. While it is unclear why these four lines respond differently, these results show that their proliferation is modulated by cyclopamine-sensitive targets. Non-responsive cells could have mutations that affect the activation of the pathway downstream of the receptor complex.

Cyclopamine was also tested in three primary cortical gliomas that were dissociated and cultured in vitro. Dividing cells from all three tumors expressed vimentin (not shown), which marks neural precursors in culture (Palmer et al., 1999) among other cell types. These cells also expressed GLI1 and GLI2 but not Shh. Treatment with 5 μM cyclopamine resulted in the inhibition of BrdU incorporation in one of them by ~60% (untreated tumor 3, 11.4±1.5% BrdU-positive cells/field; cyclopamine treated, 3.6±0.5% BrdU-positive cells/field, P<0.001), while the other two were unresponsive (untreated tumor 4, 4.5±0.5% BrdU-positive cells/field; treated, 4.6±0.5% BrdU-positive cells/field, P=0.9; and untreated tumor 5, 2.4±0.7% BrdU-positive cells/field; treated, 3.2±0.3% BrdU-positive cells/field, P=0.3).

Deregulated GLI1 function is sufficient to induce hyperproliferation of CNS cells with precursor character

The results with brain tumors and cell lines suggest that the deregulated SHH-GLI pathway may be involved in abnormal
proliferation. To directly test this idea, we have misexpressed Gli1 in the CNS of the developing frog embryo. Tadpoles expressing Gli1 after unilateral injections developed ipsilateral neural tube hyperplasias (Fig. 7A; 24/36 embryos), first detected at tailbud stages, that expressed the β-gal lineage tracer (Fig. 7C; 15/15 embryos). Most hyperplasias appeared in the hindbrain and spinal cord, consistent with the more frequent distribution of the injected materials in these areas, and showed an increase in the number of BrdU-positive cells (more than fivefold: 19±1 BrdU-positive cells on average per control neural tube side in three sections counted of independent control embryos and 91±5.6 BrdU-positive cells per injected neural tube side in three sections of independent Gli1-injected tadpoles; P<0.005) when compared with the normal, uninjected contralateral side where BrdU-positive cells were confined to the vz zone (Fig. 7D). As expected, abnormal tissue contained HNF-3β-positive floor plate cells and neurons (Fig. 7B and not shown) (Lee et al., 1997; Ruiz i Altaba, 1998) but a large proportion of the hyperplastic masses had an undifferentiated appearance. In cases where the injected Gli1 mRNA localized to the epidermis, the resulting skin hyperplasias or BCC-like tumors (Dahmane et al., 1997) also showed a marked increase in the number of BrdU-positive cells (not shown) over that seen in the normal, contralateral epidermis. Gli2 or Gli3 did not have these effects because they induced ectopic mesoderm earlier (Brewster et al., 2000).

The expression of Gli1 in glial tumors, together with the involvement of the SHH-GLI pathway in the development of glial lineages (Pringle et al., 1996; Poncet et al., 1996; Orentas et al., 1999; Nery et al., 2001), raised the possibility that Gli1-glial lineages (Pringle et al., 1996; Poncet et al., 1996; Orentas et al., 1999) involved in the development of the SHH-GLI pathway in the CNS leads to hyperproliferation of precursor cells and suggests its involvement in the initiation and maintenance of brain tumorigenesis.

Sources of SHH and effects in the dorsal brain

Shh is the only Hh family member reported to be normally expressed in the mammalian CNS (Echelard et al., 1993; Traiffort et al., 1999), raising the question of the localization of its sources that affect dorsal brain development. SHH is abundantly expressed in ventral brain regions throughout embryogenesis and is required for ventral development (Chiang et al., 1996). By contrast, early dorsal neural tube development requires the absence of SHH as dorsal cells, including those in the prospective cerebral cortex and thalamus, can be ventralized by SHH (Roelink et al., 1994; Ericson et al., 1995; Kohtz et al., 1998; Watanabe and Nakamura, 2000; Agarwala et al., 2001). However, forebrain competence for ventralization is lost by ~E11.5 in mice: SHH does not repress the cortical markers Emx1 or Tbr1 in E17.5 explants (not shown) as it does in similar ~E10-11.5 explants (Khotz et al., 1998). After this early period, there is a change in the response to SHH. We show that Shh is expressed dorsally and that it is an endogenous late embryonic and postnatal mitogen modulating dorsal brain growth. From E14.5 to E17.5, we cannot localize the expression of Shh by in situ hybridization in the dorsal brain. As Shh may be expressed by layer V cortical neurons (Fig. 1) (Traifort et al., 1999) and these are born at ~E13-E14, it is possible that their precursors already express Shh in the vz, where they may affect neighboring cells. It is also possible, however, that as in the cerebellum (Dahmane and Ruiz i Altaba, 1999), Shh is expressed transiently by precursor cells, which later become dependent on SHH secreted from mature neurons at a distance.

SHH could also have survival functions, although TUNEL assays in our cortical explants did not show obvious differences between treated and untreated samples (not shown). Moreover, this effect is first detected at fivefold higher concentrations than those used here (Miao et al., 1997; Oppenheim et al., 1999).

**DISCUSSION**

The results presented here demonstrate that the SHH-GLI pathway has a general role in controlling progenitor cell number in the developing dorsal brain, and contrast with its earlier role in ventral neural tube patterning. The approx. twofold changes in proliferation we detect in neocortical and tectal precursor after manipulating SHH signaling are similar to those we detected in the cerebellum (Dahmane and Ruiz i Altaba, 1999), indicating that SHH signaling modulates the normal growth of the three major dorsal brain regions that are layered and evolutionarily plastic. Additionally, our findings demonstrate that deregulation of SHH-GLI signaling in the CNS leads to hyperproliferation of precursor cells and suggests its involvement in the initiation and maintenance of brain tumorigenesis.
Fig. 6. GLI gene expression in human brain tumors, cell lines and effects of cyclopamine. (A,B) RT-PCR analyses of independent brain tumor samples. Note the varying levels of GLI1 and GLI2 expression and its general correlation with the levels of PTCH1. HFB, human fetal brain RNA, used here as control; PNETs, primitive neuroectodermal tumors. Varying levels of two GLI2 bands in B represent previously described differentially spliced forms (arrows) (Tanimura et al., 1998). Levels of expression are interpreted in relation to that of discoidin domain receptor 1 (DDRI) mRNA, used to measure the relative amount of tumor in a given sample (Weiner et al., 2000), assuming homogenous expression per tumor cell.

Expression of the housekeeping gene GAPDH served as positive control to quantify the total amount of mRNA. A total of 22 DDR1-positive primary tumors were tested by RT-PCR. Of these, nine glioblastoma multiformes from the frontal, parietal or temporal lobes expressed GLI1 (9/9), GLI2 (7/9), GLI3 (9/9), PTCH1 (7/9) and SHH (7/9). Co-expression of GLI1 and SHH could suggest that the origin of these gliomas is the GLI1- and SHH-positive SVZ of the lateral ventricle (N. D., D. Lim, A. Alvarez-Buylla, A. R. A., unpublished); one gliosarcoma from the temporal lobe and one anaplastic oligodendroglioma from the parietal lobe expressed all these genes; one low grade glioma from the insula expressed GLI1, GLI3, PTCH1 but not GLI2 or SHH; four PNETs from the posterior fossa expressed GLI1, GLI3 and PTCH1; one PNET from the thalamus expressed all of these genes; and six PNETs from the cerebellum expressed all genes except SHH. Ages of the individuals with gliomas ranged from 20 to 74 years and those with PNETs from 2 to 38 years. There was no correlation of gene expression with gender. (C-H) In situ hybridization of cortical glioma (C-F) and cerebellar PNET (G,H) tumor sections showing the expression of GLI1 (C,E,G) coincident with that of PTCH1 (F,H). Sense GLI1 RNA probes did not show specific hybridization (D; six tumors tested). The localization of regions with tumor was determined by the high levels of DDR1 expression and the histopathological examination of Hematoxylin- and Eosin-stained sections (not shown). Matched slides of the same tumor are C,D, E,F and G,H. GBM, glioblastoma multiforme; LGA, low grade astrocytoma. A total of 22 DDR1-positive tumors were tested by in situ hybridization. Of these, seven GBMs from the temporal and parietal lobes expressed GLI1 (7/7) and PTCH1 (6/7); one oligodendroastrocytoma from the temporal lobe and one oligodendroglioma from the frontal lobe expressed both genes; two low grade gliomas from the cerebellum and centrum ovale expressed GLI1 (2/2) and PTCH1 (1/2); five juvenile pilocytic astrocytomas from the cerebellum, thalamus and hypothalamus expressed GLI1 (4/5) and PTCH1 (2/5); one anaplastic oligodendroglioma from the frontal lobe expressed both genes; two anaplastic astrocytomas from the frontal lobe expressed GLI1 (2/2) and PTCH1 (1/2); and three PNETs from the cerebellum, posterior fossa and occipital lobe expressed both genes. The age of individuals with glial tumors ranged from 6 to 60 years and those with PNETs from 3 to 17 years. There was no correlation of gene expression with gender. As controls, one ependymoma from the fourth ventricle and one hemangioma from the cerebellum did not express GLI1 or PTCH1.

Our results differ from those obtained in postnatal mice after SHH misexpression in the early forebrain using recombinant viruses, in which infected cells only become oligodendrocytes (Nery et al., 2001). This difference, however, may result from the fact that retroviral infections were performed at ~E9.5, when SHH induces oligodendrocyte differentiation in early forebrain cells (Zhu et al., 1999) but does not yet act as a dorsal mitogen. Later on, SHH continues to induce oligodendrocytes in the ventral forebrain (Tekki-Kessaris et al., 2001). In addition to being a mitogen for precursors, our results therefore raise the possibility that endogenous SHH is involved in late embryonic and postnatal dorsal oligodendrogenesis.

Our results also differ from those obtained after misexpression of SHH in the dorsal spinal cord, in which the SHH-induced an approx. twofold increase in the proliferation of early precursors ceases before E18 (Rowitch et al., 1999). Thus, the differential growth of the dorsal regions of the brain and spinal cord could be related to the inability of the latter to proliferate in response to SHH.
SHH signaling, growth modulation and morphological plasticity

The SHH-GLI pathway may not only modulate growth, and thus size, but also the shape of the brain. This idea derives from the proposal that differential use/localization of SHH would be responsible for the size and foliation patterns of the cerebellar cortex (Dahmane and Ruiz i Altaba, 1999) and from results in the ventral midbrain (Agarwala et al., 2001). Our experimental findings and the differential expression of Gli genes in the neocortex and tectum now allow us to extend this proposal to the two other major dorsal brain structures. It remains possible that SHH also regulates hippocampal cell proliferation. Indeed, changes in the spatial and/or temporal regulation of the SHH-GLI pathway within the dorsal brain could underlie the differential growth of the neocortex, tectum and cerebellum during evolution, as the sizes and shapes of these three structures vary enormously in phylogeny. A doubling of cortical cell proliferation could account for the development of the large primate neocortex (Rakic, 2000).

The late layer-specific expression of Shh in the dorsal brain (Fig. 1) suggests that it regulates Gli1+ precursor proliferation in germinative zones. There appears to be, therefore, a common mechanism by which SHH secreted from early differentiated neurons in the neocortex, tectum and cerebellum regulates precursor proliferation and, thus, the number, of later-born cells. This system would allow the independent growth of each dorsal structure during evolution by changing the region-specific action of SHH or its response. In this sense, the action of additional signals, such as BMPs and PACAP (Li et al., 1998; Zhu et al., 2001), could affect growth by antagonizing the proliferative effects of SHH.

The robust induction of Gli1 by SHH may pinpoint its primacy in the mediation of SHH signals (Lee et al., 1997; Hynes et al., 1997). However, because Gli1 null mice appear normal (Park et al., 2000), Gli2/3 could compensate for the loss of Gli1. Consistent with this, all Gli proteins have neurogenic activity (Brewster et al., 1998), and Gli3 mutant mice have smaller and disorganized cortices (Franz, 1994; Theil et al., 1999; Toole et al., 2000). Nevertheless, in the dorsal brain, as in the early embryonic neural tube (Ruiz i Altaba, 1998; Litingtung and Chiang, 2000), an antagonism between Gli3 and SHH/Gli1 may be crucial for normal development.

Hyperplasia, brain tumorigenesis and deregulation of the SHH-GLI pathway

In addition to sporadic BCCs and PNETs (Dahmane et al., 1997; Raffel, 1997; Xie et al., 1998; Reifenberger et al., 1998), we have found that two new types of sporadic human tumors, glial brain tumors and prostate carcinomas, consistently express the Gli1 genes. This expression may reflect their site of origin or the types
of cells affected. For example, in the GLI1-positive follicle or basal layer of the skin, maintained or ectopic GLI1 function could give rise to a BCC; in the GLI1-positive prostate (Podlacek et al., 1999), to carcinoma development; in the GLI1-positive cerebellum, to a medulloblastoma; in the GLI1-positive svz of the perinatal neocortex or striatum; and in adult regions where GLI1-positive precursors reside (such as the adult striatal svz (N. D., D. Lim, A. Alvarez-Buylla and A. R. A., unpublished) (Traiffort et al., 1999; Doetsch et al., 1999)), to a glioma.

Beyond being a marker of the origin of tumors, GLI expression is likely to reflect a participation of deregulated SHH-GLI signaling in tumorigenesis: GLI proteins may control precursor proliferation in many organs including the prostate and brain and their deregulation could lead to tumor formation. Support for this idea in brain tumors derives from the ability of cyclopamine to inhibit the proliferation of several human glioma cells, suggesting that these harbor mutations in the SMO-PTCH receptor (Taipale et al., 2000), that provoke constitutive signaling. Further support derives from our finding that the targeted, transient, somatic misexpression of GLI1 is sufficient to initiate a hyperplastic program in tadpoles, which could also occur in transgenic mice (Hynes et al., 1997; Park et al., 2000), that is dependent on endogenous GLI1 function. Moreover, mutations in PTCH1 and SMO have been detected in non-medulloblastoma PNETs (Vorechovsky et al., 1997; Wolter et al., 1997; Reifenberger et al., 1998) but not yet in gliomas. Nevertheless, why individuals with Gorlin syndrome heterozygous for PTCH1 develop some but not all tumor types associated with SHH-GLI signaling remains unclear. Interestingly, the consistent expression of the GLI genes in nearly all human primary brain tumors tested, as well as in all tested tumor cell lines, together with the action of cyclopamine, raises the possibility that SHH-GLI signaling also involved in tumor maintenance. If so, the viability of many human tumors in the brain and other organs could be based on persistent GLI function, thus providing an avenue for rational therapies.

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