Mouse Gli1 mutants are viable but have defects in SHH signaling in combination with a Gli2 mutation

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Accepted 1 February; published on WWW 21 March 2000

SUMMARY

The secreted factor Sonic hedgehog (SHH) is both required for and sufficient to induce multiple developmental processes, including ventralization of the CNS, branching morphogenesis of the lungs and anteroposterior patterning of the limbs. Based on analogy to the Drosophila Hh pathway, the multiple GLI transcription factors in vertebrates are likely to both transduce SHH signaling and repress Shh transcription. In order to discriminate between overlapping versus unique requirements for the three Gli genes in mice, we have produced a Gli1 mutant and analyzed the phenotypes of Gli1/Gli2 and Gli1/3 double mutants. Gli3 mutant and Gli2 mutants have polydactyly and dorsal CNS defects associated with ectopic Shh expression, indicating GLI3 plays a role in repressing Shh. In contrast, Gli2 mutants have five digits, but lack a floorplate, indicating that it is required to transduce SHH signaling in some tissues. Remarkably, mice homozygous for a Gli1 mutation that deletes the exons encoding the DNA-binding domain are viable and appear normal. Transgenic mice expressing a GLI1 protein lacking the zinc fingers can not induce SHH targets in the dorsal brain, indicating that the Gli1 allele contains a hypomorphic or null mutation. Interestingly, Gli1dd/dd;Gli2dd/dd, but not Gli1dd/dd;Gli3dd/dd double mutants have a severe phenotype; most Gli1dd/dd;Gli2dd/dd mice die soon after birth and all have multiple defects including a variable loss of ventral spinal cord cells and smaller lungs that are similar to, but less extreme than, Gli2dd/dd mutants. Gli1/Gli2 double homozygous mutants have more extreme CNS and lung defects than Gli1dd/dd;Gli2dd/dd mutants, however, in contrast to Shh mutants, ventrolateral neurons develop in the CNS and the limbs have 5 digits with an extra postaxial nubbin. These studies demonstrate that the zinc-finger DNA-binding domain of GLI1 protein is not required for SHH signaling in mouse. Furthermore, Gli1 and Gli2, but not Gli1 and Gli3, have extensive overlapping functions that are likely downstream of SHH signaling.

Key words: Mouse, Gli1, Sonic Hedgehog, Anteroposterior patterning, Polydactyly, CNS

INTRODUCTION

The developing embryo is dependent on numerous genetic interactions that specify cell fates within tissues and along the body axes. In recent years, a growing number of interesting mouse developmental mutants have been made by gene targeting and the genes responsible for some spontaneous developmental mutants have been cloned (Gossler and Balling, 1992; Melton, 1994; Roths et al., 1999). Phenotypic analysis of many of these mutants has been instrumental in identifying genes required for particular developmental processes. Studies of double mutants have become critical in order to decipher complex genetic pathways and uncover overlapping functions of gene family members. One very interesting genetic pathway conserved across species and required for many patterning processes is the signaling cascade initiated by the Hedgehog (HH) family of secreted factors.

The Drosophila hh gene was the first family member identified, and was shown to be required for many developmental events, including anteroposterior patterning of the body segments and imaginal discs (Basler and Struhl, 1994; Mohler, 1988; Tabata et al., 1992; Tabata and Kornberg, 1994). Patched (Ptc) was identified as a novel transmembrane protein that is a Hh receptor and acts as a constitutive repressor of the Hh pathway in the absence of Hh protein (Ingham et al., 1991; Johnson et al., 1995). Genetic and biochemical studies in Drosophila have shown that cubitus interruptus (ci) encodes a zinc-finger-containing transcription factor that is required for transduction of Hh signaling (Alexandre et al., 1996; Dominguez et al., 1996; Orenic et al., 1990; Schwartz et al.,
genes in SHH signaling, we have produced mice with mutations in Gli1 and Gli2, and identified X^{p} mutants as having a deletion in Gli3 (Hui and Joyner, 1993; Mo et al., 1997). Gli3 mutant mice have many abnormalities including CNS and lung defects and limb polydactyly (Franz, 1994; Grindley et al., 1997; Grove et al., 1998; Hui and Joyner, 1993; Schimmang et al., 1992). Aspects of these phenotypes are similar to SHH gain-of-function effects and, indeed, Shh has been found to be expressed ectopically in the anterior limb buds and dorsal neural tube of Gli3^{−/−} mutants (Büscher et al., 1997; Ruiz i Altaba, 1998), indicating a role for GLI3 in repressing Shh expression. Gli2^{−/−} mutants with a deletion of the exons encoding zinc fingers 3-5 have numerous skeletal defects (Mo et al., 1997) and abnormal lungs (Motoyama et al., 1998). Similar to Shh mutants, Gli2^{−/−} mutants lack a floorplate and adjacent ventral intermediate region (VIR) cells in the spinal cord, providing direct evidence that Gli2 functions downstream of Shh (Ding et al., 1998; Matise et al., 1998). In contrast to Shh mutants, however, Gli2^{−/−} mutants develop motoneurons. Gli2/Gli3 double mutants have skeletal and lung defects that are more extreme than either homozygous phenotype, showing that Gli2 and Gli3 have some overlapping functions (Mo et al., 1997; Motoyama et al., 1998).

Here we report the generation of mice with a Gli1^{−/−} mutation that deletes the exons encoding the zinc fingers. In contrast to Gli2 or Gli3 mutants, mice homozygous for the Gli1^{−/−} allele appear normal. Since in transgenic mice a mutant Gli1 cDNA lacking the zinc fingers does not induce SHH targets, the Gli1^{−/−} allele contains a loss-of-function mutation. A role for the GLI1 zinc-finger DNA-binding domain and, possibly, the complete GLI1 protein, in SHH signaling was demonstrated by generating Gli1/Gli2 double mutants: all Gli1^{−/−};Gli2^{−/−}^+;Gli2^{−/−}^+ double mutants have multiple defects that are similar to, but milder than, Gli2 mutants and Gli1/Gli2 double homozygous mutants have more extreme defects. In contrast, Gli1^{−/−};Gli3^{−/−}^+ mutants are viable and appear identical to Gli3^{−/−}^+ mutants. Most striking is our finding that mice carrying zinc-finger deletions in both Gli1 or Gli2 retain many processes requiring SHH signaling. Comparison of the Gli1/Gli2 and Shh mutant phenotypes provides an assay for identifying those tissues in which SHH is dependent on normal GL1 and GL2 proteins. These results raise the question of whether GL3 can play a critical role in transducing HH signaling, despite the lack of evidence for overlapping functions between Gli1 and Gli3 in double mutants. Alternatively, other proteins might act downstream of SHH. Recent biochemical studies have indicated that mouse Gli2 and Gli3 have activator and repressor activities, like Ci, whereas GL1 only has activator activity and may not be processed (Dai et al., 1999; Sasaki et al., 1999). Our finding that mouse Gli1^{−/−}^+;Gli2^−/− mutants have normal HH signaling provides the first in vivo evidence that GL1 functions differently from Gli2 and Gli3.

**MATERIALS AND METHODS**

**Generation of Gli1 mutant mice**

RI ES cells (Nagy et al., 1993) were electroporated (Matise et al., 2000) with a targeting construct and following gancyclovir and G418 selection, three targeted colonies were obtained out of approximately
200 colonies screened. The Gli1 mutant allele was identified by Southern blot hybridization using an 800 bp 5¢ external Xhol-EcoRI probe (Fig. 1A) and restriction enzyme digestion of DNA with Xhol-SpeI giving a wild-type 13 kb and mutant 6 kb band (data not shown). Additional restriction enzyme digests were performed to confirm the structure of the mutant allele using two 3¢ probes, a BamHI-EcoRI genomic probe (a) and an external cDNA probe (see Fig. 1A). The targeted cell lines were used to generate chimeras by aggregation with diploid CD1 morulae (Wood et al., 1993) and one cell line was transmitted through the germ line. Chimeras were bred with CD1 outbred mice to obtain heterozygous mutant offspring. Homozygotes were generated by interbreeding heterozygotes, and then breeding homozygotes to either homozygous or heterozygous animals. To routinely genotype Gli1 mutants, Southern blot analysis was performed using a 500 bp 3¢ external Ncol fragment from the 3¢ end of a Gli1 cDNA (Hui et al., 1994) and restriction enzyme digestion of DNA with Xhol giving a wild-type 10.5 kb and mutant 4.5 kb band (Fig. 1B). The Gli2 mutant allele was identified using PCR with Gli2 sense and antisense primers and a primer to the neo (Mo et al., 1997). For genotyping embryos, genomic DNA was isolated from tails or yolk sacs using a PCR Template Purification Kit from Boehringer-Mannheim.

RT-PCR analysis
Poly(A)+ RNA was isolated as below. cDNAs were generated using a reverse transcription kit from BRL (Superscript II). 2 µl of the reverse transcription reaction were used as the template for PCR. The primers used to generate the 5¢ end of mouse Gli1 were: a 5¢ primer based on human GLI1 (CGA CCG AAG GTG CGT CTT GAG) (Kinzler et al., 1988) and a 3¢ primer based on mouse zinc finger 3 sequences (AGC CCT GGA CCC CGC ATC) (Walterhouse et al., 1993). The PCR reaction was carried out as follows: 94°C for 1 minute, 56°C for 1 minute, 72°C for 2 minutes for 35 cycles. For analysis of the Gli1 mutant allele, additional primers were generated flanking the deleted zinc-finger region: a 5¢ sense probe in exon 6 (CAG CAG AGG CCC GGC GCA) and a 3¢ antisense probe in exon 12 (AGC AGC ATG AGC TCT GTC TAC A). PCR products were purified from an agarose gel and cloned using the TA Cloning Kit (Invitrogen). These clones were then sequenced using M13 and T7 primers (ABI Sequencer). The major 5¢ RT-PCR product from normal mRNA was 1.1 kb and sequence analysis confirmed that it contained the predicted cDNA. A minor 1.3 kb product was isolated that contained a 300 bp intron between exons 4 and 5. The two RT-PCR products both contained an additional 5UTR exon (see Fig. 1A) that is not present in the one published human GLI1 cDNA sequence (Walterhouse et al., 1993), although it is present in the human GLI1 genomic locus in a similar position to mouse Gli1 exon 2 (Liu et al., 1998).

Protein expression analysis
A full-length Gli1 cDNA was generated by ligating 5¢ and 3¢ cDNA fragments using the common EcoRI site. It was tagged with FLAG at its N terminus by PCR and then confirmed by sequencing. A Gli1 zinc-finger-deletion vector (Gli1all) was prepared by removing the cDNA fragment between the EcoRI and BamHI sites, which deletes amino acids 272-423 that encodes zinc fingers 2-5 and leaves the reading frame intact. Both FLAG-Gli1 and FLAG-Gli1all were subcloned into the pSRαx vector (Takebe et al., 1988). Transfections of COS7 cells were performed using the Fugene 6 Transfection Reagent (Roche), as recommended by the manufacturer. 48 hours after transfection, cells were lysed. Cleared lysates were then separated on a 6% SDS-polyacrylamide gel. Western blot analysis was performed by using anti-FLAG M1 antibody (Sigma) and developed with ECL reagent (Amersham).

Generation of transgenic embryos
The Wnt1-Gli1 and Wnt1-Gli1all transgenes were prepared by blunt end ligation of FLAG-Gli1 and FLAG-Gli1all constructs into the EcoRV site of a modified Wexp3 vector (Epstein et al., 1996), which includes two copies of the chick β-globin insulator (kindly provided by D. Rowitch) and Wnt1 regulatory sequences. Transgenic embryos were generated and collected at E14.5 as described (Hogan et al., 1994). PCR genotyping was performed using two primers specific for the lacZ tag (5¢-CCG AAC CAT CCG CTG TGG TAC and 3¢-CAT CCA CGC GCG CGT ACA TC). Expression of the transgene was monitored by whole-mount RNA in situ hybridization of tails with a lacZ probe.

Northern blot hybridization
Total RNA was isolated from whole 13.5 dpc wild-type (WT) and mutant embryos using Trizol reagent (BRL) and poly(A)+ RNA was purified using magnetic beads (Promega). Approximately 3 µg of RNA was loaded in each lane and run on a formaldehyde gel (Sambrook et al., 1989) and northern blot hybridization was carried out as described (Joyner et al., 1985). Probes used were: the 1.1 kb 5¢ cDNA fragment produced by RT-PCR, a 500 bp Ncol 3¢ DNA fragment, a zinc-finger probe made using PCR from a Gli1 cDNA using a 5¢ primer in zinc finger 2 (ATA CAT GCT GGT GCA CA) and a 3¢ primer downstream of zinc finger 5 (GCA TCG GGA CCA TGC ACT GT), which was subcloned using the TA Cloning Kit (Invitrogen) and a 1 kb fragment of neo.

RNA in situ expression analysis
Whole-mount RNA in situ hybridization was performed as described (Parr et al., 1993) with modifications (Knecht and Harland, 1997). BM Purple was used as a substrate for alkaline-phosphatase-coupled anti-DIG antibodies (Boehringer-Mannheim). Lungs were dissected out and fixed overnight in 4% PFA at 4°C, as previously described (Grindley et al., 1997). Fixed frozen sections were used for section in situ analysis as previously described for 35S-labeled probes (Hui et al., 1994) with modifications as described (Toresson et al., 1999). The following DIG-labelled probes (Boehringer-Mannheim) were previously published: Gli1, Gli2, Gli3 (Hui et al., 1994), Shh (Echelard et al., 1993), Ptc (Goodrich et al., 1996) and Nkx2.1 (Toresson et al., 1999). For immunohistochemistry, embryos were fixed for 1 hour at 4°C and washed in PBS overnight. Frozen sections were prepared and secondary Cy3- and fluorescein-coupled anti-mouse and anti-rabbit antibodies used were as described (Matise et al., 1998). Primary antibodies used were Islet1/2 (Ericson et al., 1992) Nkx2.2 and Hnf3β (Ruiz i Altaba et al., 1995b). Hoechst staining was performed as described (Matise et al., 1999).

Histology
Adult mice were perfused with 10% formalin and then stored in fix. Fixed tissue was paraffin embedded and then stained with Hematoxylin for 5 minutes and Eosin for 2 minutes. Slides were dehydrated in xylene and coverslipped with Permount.

Lung measurement
The individual lobes of E18.5 Gli1and Gli2 mutants were separated and measured in millimeters (Fig. 3A). The variances of Gli1and Gli2 lung measurements were compared to Gli1and Gli2 lungs (WT) using the t-test and a significant difference was observed only in the length of the accessory lobe, suggesting a variability in the mutant phenotype. Using the t-test for unequal variances, the length of the accessory lobe was significantly different from WT (P=0.01). For all other measurements, values were considered equal and the t-test revealed a significant difference in length of the right cranial lobe (P=0.02), the width of the accessory lobe (P=0.013) and the width of the left lobe (P=0.03) in eight embryos. At this stage, the size of the whole embryo did not appear significantly reduced.
RESULTS

Gli1\textsuperscript{zfde}\textsuperscript{zd} mutants are viable and appear normal
In order to address what developmental processes are dependent on Gli1, homologous recombination in embryonic stem cells was used to disrupt Gli1. A gene targeting vector was used to replace exons 9 to 11 that encode part of zinc finger 1, zinc fingers 2-5 and 43 adjacent amino acids with the bacterial neomycin resistance (neo) gene (Fig. 1A and see Materials and Methods). The mutant zinc finger deletion allele (Gli1\textsuperscript{zd}) was transmitted through the germline, heterozygous mice intercrossed and adults of all three genotypes (+/+; +/−; −/−) were detected (Fig. 1B) at the expected Mendelian ratio (20:51:24). Southern blot analysis of DNA from homozygous mutants using a zinc-finger-specific probe confirmed the deletion (Fig. 1C). Gli1\textsuperscript{zd} mutant mice can breed and live past 1 year of age and show no obvious behavioral abnormalities.

The Gli1\textsuperscript{zd} allele expresses an abnormal transcript without a DNA-binding domain that cannot activate SHH targets in the brain.
In order to determine whether the Gli1\textsuperscript{zd} allele transcribes a mRNA that could encode an aberrant GLI1 protein, we characterized the Gli1 mutant transcripts. Northern blot analysis of mRNA from E13.5 WT and Gli1\textsuperscript{zd} homozygous embryos using a Gli1 cDNA probe 3′ to the zinc fingers detected two Gli1 transcripts of approximately 4.0 and 4.4 kb in WT mRNA (Hui et al., 1994; Fig. 1D) and one broad

![Fig. 1. Generation of Gli1 zinc-finger-deletion mice by homologous recombination. (A) Schematic representation of the normal (top) and targeted (bottom) Gli1 locus highlighting the exons containing the conserved zinc-finger region (black and numbered 1-5ZF) and the exons not present in the human GLI1 cDNA (shaded), one being an alternatively spliced exon with a stop codon (TGA). In the targeting vector (middle), zinc fingers 2-5 were replaced with the neo gene. Probes used for screening and genotyping are indicated under the targeted allele. The position of the primers used to isolate the 5′ Gli1 cDNA are indicated by open arrowheads and the aberrant Gli1 transcript in mutant embryos are indicated by black arrows. (B) Genotyping of Gli1 mutants using Southern blot analysis of XbaI-digested tail DNA from WT, Gli1 heterozygous and homozygous mutant animals using a 3′ cDNA probe b that detects a 10.5 kb WT and 4.5 kb mutant band. (C) A 300 bp zinc-finger probe was used in a Southern blot analysis to confirm the targeted deletion of the zinc-finger-coding exons in tail DNA from homozygous mutants compared to WT DNA digested with BamHI (B), EcoRI (E), and XbaI (X). The arrows indicate the Gli1 bands since the zinc-finger probe also likely binds to other Gli genes. (D) 3 μg of poly(A)+ whole embryo RNA was run on a formaldehyde gel for northern blot analysis. A neo probe does not detect any transcripts in WT RNA, but detects the expected 1.8 kb transcript expressed from the PGK promoter in the neo cassette in Gli1 homozygous RNA. A 3′ cDNA probe, detects 4.4 and 4.0 kb transcripts in WT RNA, and a 3.8 kb transcript in mutant RNA. A 5′ cDNA probe detects only the larger transcript in WT RNA, and smaller aberrant transcripts in mutant RNA.
band that was slightly smaller in mutant mRNA (Fig. 1D). A 5' probe or a zinc-finger probe only detected the 4.4 kb band in WT mRNA (Fig. 1D), suggesting the 4.0 kb transcript has an alternative 5' end. As expected, the mutant ~4 kb band was not detected with the zinc-finger cDNA probe (data not shown) or with a neo probe, but a broad band of approximately 4 kb was detected with the 5' probe (Fig. 1D).

If the Gli1\textsuperscript{zfd} transcript spliced around the neo insertion in the mutant locus from exon 7 to exon 11 this would generate a ~4 kb mRNA encoding an in-frame deletion of 182 amino acids, which would include most of the zinc fingers as well as 43 adjacent amino acids. To determine whether such a transcript was made, RT-PCR was performed with E13.5 Gli1 mutant mRNA using a 5' primer located in exon 6 and a 3' primer in exon 12, 3' of the deleted region (see open arrows in Fig. 1A). Sequence analysis of the ~0.5 kb RT-PCR product showed that a transcript was made that spliced around the neo insert from exon 8 into exon 12 (see Fig. 1A). Thus, the Gli1\textsuperscript{zfd} allele cannot encode for a protein with DNA-binding activity, but could produce a mutant protein lacking amino acids 269-437 that include most of the zinc fingers.

To test whether a GLI1 protein lacking the zinc fingers could activate SHH targets, we produced transgenic embryos that expressed either a 4.0 kb FLAG tagged-Gli1\textsuperscript{zfd} cDNA lacking zinc fingers 2-5 or a full-length FLAG tagged-Gli1 cDNA from a Wnt1 enhancer (Epstein et al., 1999) in the dorsal CNS (see Materials and Methods). Western blot analysis of COS7 cells transfected with expression constructs containing the two cDNAs demonstrated that proteins of the expected sizes are produced by the cDNAs (Fig. 2A). Interestingly, the GLI1 protein did not appear to be processed. Three Wnt1-Gli1 and four Wnt1-Gli1\textsuperscript{zfd} E14.5 transgenic embryos expressing the transgene were generated and analyzed in serial sagittal sections for histological abnormalities and activation of SHH target genes. The neural epithelium in the dorsal midline of the caudal forebrain and rostral midbrain region of Wnt1-Gli1 transgensics was clearly abnormal and had a wavy nature, indicating overproliferation (Fig. 2B). In addition, sections in this region and the mid/hindbrain junction had ectopic patches of HNF3\textbeta (Fig. 2C) and Ptc1-expressing cells (data not shown) similar to En2-Gli1 transgenic embryos (Hynes et al., 1997). In contrast, the Wnt1-Gli1\textsuperscript{zfd} transgenics had a normal morphology and no ectopic gene expression (Fig. 2E), demonstrating that any aberrant Gli1\textsuperscript{zfd} transcript cannot activate SHH targets in vivo.

**Most Gli1\textsuperscript{zfd/zfd};Gli2\textsuperscript{zfd/+} mice die at birth and have multiple defects**

One possible explanation for the lack of defects in Gli1 mutants is that there is a compensation in function by Gli2 and/or Gli3, since there is overlap in their expression domains. Since Gli1 expression is strongest more proximal to Shh than Gli2 or Gli3, we analyzed expression of Gli2 and Gli3 in Gli1\textsuperscript{zfd/zfd} mutants to determine whether their expression was upregulated in the Gli1 domain. The expression patterns of Gli2 (n=8) and Gli3 (n=8) in E9.5 Gli1\textsuperscript{zfd/zfd} mutants, however, appeared normal based on whole-mounts RNA in situ analysis and RNA in situ analysis of sections (data not shown). SHH signaling was also assessed in Gli1\textsuperscript{zfd/zfd} mutants, but expression of Shh (n=8) and the target gene Ptc1 (n=8) also appeared normal (data not shown).

To further test possible overlapping functions between Gli1 and Gli2 or Gli3, Gli1\textsuperscript{zfd} homozygotes carrying one mutant allele of Gli2 or 3 were produced. Whereas double Gli1/Gli2 heterozygotes appeared normal, most Gli1\textsuperscript{zfd/zfd};Gli2\textsuperscript{zfd/+} mutants died soon after birth (Table 1) and the rare ones that survived to weaning were smaller than their littermates, had a hopping gait and were unable to right themselves. They were killed at 5-7 weeks of age and gross analysis of tissues following dissection revealed several defects including a smaller lung size than in WT littermates (5/6), undescended testes with incompletely developed external genitalia in males (4/4) and a distended gut (5/5). The cause of death in most mutants is not clear, but might result from the gut defect. In contrast, Gli1\textsuperscript{zfd/zfd};Gli3\textsuperscript{xt/+} double mutants were viable and had the polydactyly phenotype typical of Gli3\textsuperscript{xt/+} mutants. These results demonstrate that a normal GLI1 protein is in fact required for development of many tissues, but that this requirement is only revealed when one allele of Gli2 is also mutant.

To determine whether Gli1/Gli2 double homozygotes had a more severe phenotype than Gli2\textsuperscript{zfd/zfd} mice, we collected litters from double heterozygote intercrosses and genotyped the offspring at three embryonic stages: E12.5, E15.5 and E18.5. Whereas double homozygotes were detected at a Mendelian ratio at E12.5, they had a reduced viability at E18.5 (Table 1). In order to compare the embryonic phenotypes of Gli1/Gli2...
double mutants to Gli2 and Shh mutants, we focused our analysis on the lungs, CNS and limbs where the function of Shh has been characterized in some detail.

**Gli1 and Gli2 have overlapping functions in lung lobe outgrowth.**

Lung development begins at E9.5 as an outpouching of the foregut in an asymmetric pattern that gives rise to four lobes off the right bronchus and one lobe from the left bronchus. All lobes are visible by E11.5 with the accessory lobe being the last lobe to form. Beginning at E11.5, Shh is expressed in the distal epithelium of the developing lung lobes and Gli1, Gli2, and Gli3 are expressed in the surrounding mesenchyme (Bellusci et al., 1997). At birth, Shh null mutants have very small lungs with one lobe and no visible branching of the airways (Litingtung et al., 1998; Pepicelli et al., 1998). At E18.5, Gli1zfd/zfd mutant lungs are much smaller than normal and the three remaining lobes on the right side appear fused (Fig. 3H; data not shown). In Gli1-/-;Gli2++/-- homozygous mutants, the medial lobe does not extend ventrally and all three right lobes are aligned (Fig. 3I). Gli1/Gli2 homozygous mutant mice at E12.5, the two lung lobes are similar in size and appear to be planar (Fig. 3G). Our results suggest that Gli1 and Gli2 have overlapping functions in regulating the proper growth and patterning of lung lobes, but are not required for branching within the lobes.

| Table 1. Most Gli1<sup>zfd/zfd</sup>,Gli2<sup>zfd/zfd</sup> mice do not survive past birth |
|-----------------|-----------------|-----------------|-----------------|-----------------|
|                 | E12.5           | E15.5           | E18.5           | P21             |
| WT              | 12/8.5          | 15/7.3          | 5/5.7           | 7/6.6           | 6.25            |
| Gli1<sup>-/-</sup> | 10/13.1         | 16/13.8         | 9/10.2          | 12/11.3         | 12.5            |
| Gli1<sup>-/-</sup> | 10/7            | 9/5.3           | 6/6.8           | 16/15.1         | 6.25            |
| Gli2<sup>zfd/zfd</sup> | 18/12.3         | 21/22.1         | 5/5.6           | 15/14.1         | 12.5            |
| Gli2<sup>zfd/zfd</sup> | 10/7            | 7/7.4           | 2/2.3           | N/A             | 6.25            |
| Gli1<sup>-/-</sup>/Gli2<sup>zfd/zfd</sup> | 31/21.8         | 22/23.2         | 37/42           | 25/23.6         | 25              |
| Gli1<sup>-/-</sup>/Gli2<sup>zfd/zfd</sup> | 24/16.5         | 6/6.3           | 16/18.2         | 4/3.8           | 12.5            |
| Gli1<sup>-/-</sup>/Gli2<sup>-/-</sup> | 12/8.5          | 8/8.4           | 7/8             | N/A             | 12.5            |
| Gli1<sup>-/-</sup>/Gli2<sup>-/-</sup> | 9/6.3           | 5/5.3           | 2/2.2           | N/A             | 6.25            |
| Total number    | 142             | 96              | 88              | 79              | 100             |
Fig. 3. *Gli1*^zfd/zfd;*Gli2*^zfd/zfd* mice have smaller lung lobes by E18.5. (A) The lung lobes of *Gli1*^zfd/+;*Gli2*^zfd/+ embryos appear WT, whereas *Gli1*^zfd/zfd;*Gli2*^zfd/zfd lung lobes have abnormalities. Lung lobes were measured in length and width as shown by the arrows in the diagram in the top left. The averages of all measurements taken from eight different animals were plotted and standard deviations calculated for the graph (bottom left). The t-test (for either equal or unequal variances) was performed and the stars indicate the lobes that show a significant difference in size compared to WT. (B-D) E18.5 (E-J) E12.5 whole lungs. (B) WT lungs show the appearance of five lung buds and some branching beginning within each lobe. (C) *Gli1*^zfd/zfd;*Gli2*^zfd/zfd* lungs appear smaller and form as two lobes. (D) *Gli2*^zfd/zfd* lungs have an abnormal morphology with a fusion of the right lung lobes and a defect in left lobe outgrowth. (E) At E12.5 WT lungs have five lobes. (F) At E12.5, *Shh*-/- lungs appear to have four tiny lobes, but form sac-like structures without any branching. (G) *Gli1*^zfd/zfd;*Gli2*^zfd/zfd* lungs have a severe phenotype with two very small lobes, but with branching. (H) *Gli1*^zfd/+;*Gli2*^zfd/zfd* lungs also have small buds and are more severely affected than (I) *Gli2*^zfd/zfd* lungs, which are smaller and do not form an accessory lobe. (J) *Gli1*^zfd/zfd;*Gli2*^zfd/+* lungs have a mild phenotype with a slight visible reduction in the accessory lobe at this stage.
loss of the pituitary with 3/6 embryos having no pituitary
tissue (Fig. 5B,H; data not shown). Shh and Nkx2.1
expression appeared normal in the subventricular zone of the
medial ganglionic eminences (Fig. 5A,B; data not shown),
whereas diencephalic expression was abnormal in the more
extreme mutants. Shh was expressed closer to, or in the
ventral midline, in regions above where the pituitary should
form (Fig. 5H) and the Nkx2.1 domain of expression was
smaller and shifted ventrally (Fig. 5E). Animals lacking the
pituitary had more extreme alterations in the gene expression
patterns. The pituitary defect could result from abnormal
ventral hypothalamic development (Takuma et al., 1998),
and/or a loss of SHH signaling in the oral ectoderm.

To determine whether Gli1 contributes to ventral midline
development in the hypothalamus, the brains of
Gli1\(^{zfd/zfd}\);Gli2\(^{zfd/+}\) and Gli1/Gli2 double homozygous
mutants were examined. Marker gene and morphological
analysis of forebrains showed that Gli1\(^{zfd/zfd}\);Gli2\(^{zfd/+}\)
embryos (n=6) were similar to WT, including the presence of
a pituitary (data not shown). In contrast, all Gli1/Gli2 double
homozygous embryos (5/5) lacked a pituitary and had
alterations in Shh and Nkx2.1 expression in the hypothalamus
that appeared more extreme than any of the Gli2 mutants (Fig.
5F,G). Shh and Nkx2.1 expressions were reduced or absent
in the ventral region, although ZLI expression of Shh was
maintained. In the region of the striatum, the medial and
lateral ganglionic eminences expressed Shh and Nkx2.1
appropriately, however, morphologically Gli1/Gli2 double
mutants appeared abnormal in both the dorsal and ventral
regions of the telencephalon, possibly due to the loss of
diencephalic tissue (Fig. 5; data not shown). In addition, the
neural epithelium of all Gli1/Gli2 double mutants appeared
thicker in these regions. In all Gli2 (n=6) and Gli1/Gli2 (n=5)
double mutants examined at E12.5, Gli3 expression appeared
normal except in the ventral diencephalon where it was absent
in Gli1/Gli2 double mutants likely due to loss of ventral
tissue (Fig. 5J-L; data not shown). These results show that
both Gli1 and Gli2 are required for aspects of ventral
forebrain development.

Gli1/Gli2 mutant limbs have five digits and a
postaxial nubbin

Shh mutants have truncated limbs with no anteroposterior
patterning (Chiang et al., 1996). Surprisingly, all four limbs of
the one E18.5 and four E15.5 Gli1\(^{zfd/zfd}\);Gli2\(^{zfd/zfd}\) mutant
embryos examined had five digits, with an extra postaxial
nubbin (Fig. 6). Furthermore, the limbs of E12.5
Gli1\(^{zfd/zfd}\);Gli2\(^{zfd/zfd}\) mutant embryos (n=4) appeared to express
Ptc1 and Gli3 normally (data not shown). In contrast, Shh
mutant limbs expressed Ptc, Gli2 and Gli3 diffusely throughout
the whole limb and Gli1 was downregulated (Zuniga et al.,
1999; data not shown), showing that SHH signaling is
required to maintain their normal expression. These studies
demonstrate that, in contrast to other tissues, the limbs of
Gli1\(^{zfd/zfd}\);Gli2\(^{zfd/zfd}\) mutants do not have defects that are similar
to, and milder than, Shh mutants.
**Fig. 5.** Section RNA in situ analysis shows loss of midline cells in Gli2\(^{zfd/zfd}\) and Gli1/Gli2 double homozygous mutant forebrains at E11.5-E12.5. Nkx2.1 is expressed in the medial ganglionic eminence (MGE), and in the midline in the striatum region of the developing forebrain of WT (A), Gli2\(^{zfd/zfd}\) (B) and Gli1\(^{zfd/zfd}\);Gli2\(^{zfd/zfd}\) (C) embryos. In the rostral diencephalon, Nkx2.1 is expressed in the ventral midline of the diencephalon in WT embryos (D) and Gli2\(^{zfd/zfd}\) (E), although in some embryos there appears to be a ventral shift in the domain of midline expression in mutants. In the severely affected Gli1\(^{zfd/zfd}\);Gli2\(^{zfd/zfd}\) animals (F), Nkx2.1 expression is lost. In WT embryos (G), Shh expression splits in the region of the hypothalamus (caudal diencephalon) and forms two ventrolateral stripes flanking the midline. The pituitary anlage marked by a red arrow is visible at this stage. In the more severely affected Gli2\(^{zfd/zfd}\) embryos (H), Shh is expressed in the midline. In all Gli1\(^{zfd/zfd}\);Gli2\(^{zfd/zfd}\) embryos (I), no pituitary is visible and in the severely affected embryos, Shh expression is lost in the ventral midline but is maintained in the ZLI. Gli3 is expressed in the dorsal regions of the caudal diencephalon and in the telencephalic vesicles in WT embryos (J) and in a similar pattern in Gli2\(^{zfd/zfd}\) (K) and Gli1\(^{zfd/zfd}\);Gli2\(^{zfd/zfd}\) (L) mutants. Also note the thickened neural epithelium in the Gli1/Gli2 double mutants.

**Fig. 6.** Gli1/Gli2 homozygous mutant late embryonic limbs have a postaxial nubbin. At E15.5, the five digits of the forelimb are clearly visible in normal (A) and Gli2 mutant embryos (B), but Gli1\(^{zfd/zfd}\);Gli2\(^{zfd/zfd}\) limbs (C) have a small posterior outgrowth (red arrow) as well as 5 digits. At E18.5 in ventral view the limbs of Gli1\(^{zfd/zfd}\);Gli2\(^{zfd/zfd}\) (F) mutants have a clear postaxial nubbin (red arrow), whereas WT (D) and Gli2 mutant (E) limbs do not.
DISCUSSION

We took a genetic approach to address the different requirements for the three Gli genes in developmental processes regulated by HH signaling in mammals. We demonstrate that the DNA-binding domain of GLI1 protein is not required for HH signaling, because mice homozygous for a Gli1zfd mutation that deletes the zinc-finger encoding exons are viable and appear normal. A requirement for two normal Gli1 alleles was found, however, in mice with one mutant Gli2 allele that also deletes zinc-finger-encoding exons. Most Gli1zfd/Gli2zfd;Gli2zfd/+ mutants die at birth and all have defects in a number of processes including floorplate development, notochord regression and lung lobe formation. Furthermore, mice with homozygous mutations in both Gli1 and Gli2 have more severe defects than Gli2 homozygotes and have a mild limb polydactyly. Strikingly, in Gli1/Gli2 double homozygous mutants aspects of many of the developmental defects seen in Shh mutants are normal, including formation of motoneurons, branching within the lung lobes and development of five digits in the limbs. These mutant studies raise the interesting possibility that GLI3 can play an essential role downstream of HH signaling and/or that there are transcription factors other than full-length GLI proteins that act downstream of HH signaling. Since, Gli1zfd;Gli3zfd+ double mutants appear identical to Gli3zfd+ mutants, whereas Gli2zfd/Gli3zfd- mutants are more severely defective, Gli3 must primarily have overlapping functions with Gli2 and not Gli1. The extent to which the overlapping functions include activation of HH targets in addition to repression of Shh targets, remains to be determined. Our studies have also revealed that two different signaling mechanisms function downstream of HH. Based on a comparison of the phenotypes of Shh and Gli1/Gli2 double mutants, one mechanism is active in tissues such as the ventral CNS and is dependent on full-length GLI1 and GLI2 proteins, whereas the other functions in organs like the limbs and does not require the proteins, despite SHH-dependent Gli1 and Gli2 expression in both tissues.

Gli1 and Gli2 have different extents of overlapping function in each tissue

Interestingly, distinct tissues have different requirements for the number of normal Gli1 or Gli2 alleles. For example, the ventral spinal cord of most Gli1zfd/Gli2zfd;Gli2zfd+ mutants appears normal and Gli1zfd/Gli2zfd;Gli2zfd+ mutants have defects that are similar to Gli2zfd+ mutants at E10.5. In contrast, the lung phenotypes are graded in severity as Gli1 and Gli2 alleles are deleted, except that Gli1zfd+ mutants appear normal. The lack of regression of the notochord, which could be the result of a defect in somite patterning, appears to be the most sensitive phenotype, since all Gli1zfd/Gli2zfd+ mice have a similar phenotype to Gli2zfd+ mutants. These results could be taken to indicate that each tissue is sensitive to a certain dose of GLI1 plus GLI2 proteins. In every tissue, however, Gli2 seems to be the main limiting factor. Since the GLI protein levels can not be measured, this apparent difference based on genetic studies could reflect a difference in gene expression, rather than in protein functions.

It is interesting that some tissues, such as the limbs, of Gli1zfd/Gli2zfd+;Gli2zfd+ mutants show no signs of loss of SHH signaling. In fact, in contrast to Shh mutants that lack digits, Gli1zfd/Gli2zfd+;Gli2zfd+ mutants have a postaxial nubbin in all limbs. The basis of this phenotype is not clear, although it could reflect tissue overgrowth rather than altered patterning. Whether this is due to altered SHH signaling is not clear. The finding that some tissues do not require full-length GLI1 and GLI2 proteins for SHH signaling, whereas others do, provides evidence that two different molecular mechanisms can function downstream of SHH in different tissues. The basis of these mechanisms does not seem to involve differences in regulation of Gli expression in the different tissues since, in both the neural tube and limbs of Shh mutants, Gli2 and Gli3 are expressed throughout the tissue and Gli1 is lost (H. L. P. and A. L. J., unpublished observations).

Molecular basis for the distinct phenotypes of the three Gli mutants

Previous studies showed that Gli1zfd+ and Gli2zfd+ mutants have distinct defects and we show here that Gli1zfd+ mutants are apparently normal. Double mutant studies provided evidence that Gli2 and Gli3 have overlapping requirements in many developmental processes. Our present studies show that Gli1 primarily has overlapping requirements with Gli2, and not Gli3. The apparent unique requirements for each of the Gli genes could be due to differences in gene expression patterns and/or biochemical properties of the three GLI proteins.

Recent biochemical studies and tissue culture transfection assays indicate that each GLI protein has a unique set of functions. Mouse GLI3 has been shown to have weak activator activity in tissue culture cells, as well as possessing an N-terminal repressor domain (Dai et al., 1999; Sasaki et al., 1999), Consistent with having a repressor activity, it appears that GLI3 can be processed similar to Ci in a SHH-dependent manner (Dai et al., 1999). Mouse GLI2 has similar activator and repressor domains and forms of GLI2 and GLI3 that contain an internal deletion in the N terminus can activate floorplate genes in the dorsal CNS of mice (Sasaki et al., 1999). In contrast, mouse GLI1 only appears to have an activation domain that does not depend on CBP binding and may not be processed (Dai et al., 1999; Fig. 2). Furthermore, a recent comparison of human GLI1 and GLI3 functions in transgenic flies has shown they have different functions (Mering and Basler, 1999) and protein studies indicate that the frog GLI proteins have different functions and may be cleaved (Ruiz i Altaba, 1999). Finally, in vertebrates, unlikeCi in fly, GLI1 mRNA expression is upregulated by SHH signaling and GLI3 is repressed (Belluscio et al., 1997; Hynes and Porter, 1995; Lee et al., 1997; Platt et al., 1997).

Based on the different in vitro functions of the GLI proteins, it has been suggested that GLI2 and GLI3 are the GLI proteins that respond to, and are activated by, SHH signaling, whereas Gli1 is a transcriptional target of activated GLI2 and GLI3 (Dai et al., 1999; Sasaki et al., 1999). Our mutant studies, which show that mice expressing at most a GLI1 protein lacking a terminal repressor domain and/or biochemical properties of the three GLI proteins.
GLI1 and GLI2 in Sonic Hedgehog Signaling

Our studies demonstrate that zinc-finger-containing GLI1 and GLI2 proteins are required downstream of SHH in only some cell types, since our Gli1/Gli2 double homozygous mutants have a considerably milder phenotype than Shh mutants in all tissues. It is unlikely any remaining aberrant GLI1 protein can induce motor neurons and other tissues in Gli1/Gli2 double mutants, as we have shown that GLI1 protein lacking zinc fingers cannot activate SHH targets in the dorsal brain. Although Gli3 does not appear to be upregulated in cells adjacent to sources of SHH in Gli1/Gli2 double mutants, it is possible that very low levels of Gli3 can activate appropriate targets in response to SHH when Gli1 and Gli2 are mutant. Since Ptc expression is reduced in Gli2 mutants, this provides a second mechanism for inhibiting proteolysis of Gli3. In a similar way, Gli2 might act upstream of Shh in some tissues in addition to acting downstream. The limb phenotypes of Gli2/Gli3 double mutants are consistent with GLI2 functioning upstream of Shh, since Gli2/Gli3 double heterozygous and homozygous/heterozygous mutants have a more extreme polydactyly than either Gli3 mutant alone.

The finding that lung lobes are lost, in both Gli1/Gli2 and Gli2/Gli3 double mutant combinations, could be taken as evidence that all the genes act in the same manner in the Shh pathway. However, one striking finding that is not consistent with Gli2 and Gli3 functioning only downstream of SHH signaling in the lung is that Gli2/Gli3 double homozygous mutants do not form lungs at all (Motoyama et al., 1998). This is a more extreme phenotype than in Shh mutants and might be due to a role of Gli2/Gli3 in repressing SHH targets in some cells in the lungs. If Gli1 is only an activator, and since the phenotype of Gli1/3 mutants suggests little functional overlap between the two genes, Gli3 normally might not be required as an activator in many cells since Gli2 is present. Alternatively, Gli1 and Gli3 may have little overlap in expression and Gli3 might only share activator functions with Gli2 (see Fig. 7). The contributions of the two competing functions of Gli1 and Gli3 in various tissues remain to be determined.

Another possible explanation for why the Gli1/Gli2 mutant phenotypes are milder than Shh is that there are two separate pathways downstream of SHH, only one of which is GLI protein-dependent. This hypothesis is supported by two studies that analyzed the regulatory sequences of Hh-responsive genes. In vertebrates, the CoupTFII gene is expressed in motoneurons and the gene can be induced by SHH. Sequences sufficient for SHH-dependent CoupTFII expression were identified, but they were found not to contain consensus GLI-binding sites (Krishnan et al., 1997). Similarly, regulatory sequences in the Drosophila HH target gene wg were identified that do not depend on Ci function (Lessing and Nusse, 1998). A recent analysis of expression of SHH targets in the chicken Talpid3 mutant also suggests a bifurcation in the SHH signaling pathway (Lewis et al., 1999). Given our results, it is of interest to determine whether in cancers induced by inappropriate SHH signaling any of the GLI proteins are required for activation of genes involved in the tumor phenotype.

Finally, an additional explanation for the presence of tissues such as motoneurons in Gli1/Gli2 mutants, but not in Shh mutants, is that in such tissues the primary function of SHH is to prevent repressor forms of GLI2 and GLI3 proteins from forming, rather than to induce GLI transcriptional activators. For example, in the developing spinal cord Hnf3β expression in the floorplate would be dependent on GLI-binding sites and an activator form of GLI protein. In Shh mutants, a repressor form of GLI2 would be present and inhibit Hnf3β transcription whereas, in Gli2 mutants, no GLI2 protein would be produced and the low level of GLI1 present would not be sufficient to induce Hnf3β. Motoneuron genes, on the contrary, would not be dependent on GLI proteins for activation. In Shh mutants, however, a repressor form of GLI2 would be present and inhibit motoneuron gene expression, whereas in Gli2 mutants such a repressor would not be present and additional transcription factors would be able to activate transcription. Studies of GLI protein processing in vivo and Shh/Gli2 double mutants are required to distinguish between the various possibilities.

We especially thank Jessica Treisman for suggesting a negative regulatory hypothesis for SHH signaling and for stimulating discussions. We also thank Samuel Park for assisting with statistical analysis, Bob Holmgren for providing the Gli1 genomic clone and Doug Epstein for comments on the manuscript. This work was supported by a grant to A. L. J. from NICHD. C. c. H. is a Research Scientist of the National Cancer Institute of Canada. A. L. J. is an Investigator of the Howard Hughes Medical Institute.

**Fig. 7.** Model. The overlapping area between Gli2 and Gli3 indicates the redundancy between GLI repressor activity in tissues such as the limbs, the dorsal CNS and possibly the lungs. This diagram also demonstrates the overlapping activator functions of GLI1 and GLI2 in the lungs, ventral CNS, notochord regression and pituitary development. It is still unclear whether there is overlap in activator properties of GLI2 and GLI3 and, in addition, there appears to be little, if any, overlap in Gli1 and Gli3 function at all.
not most ventral neurons in the mouse central nervous system. Development 125, 2759-2770.


