

## Sonic Hedgehog Signaling in the Lung From Development to Disease

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### Abstract

Over the past two decades, the secreted protein sonic hedgehog (SHH) has emerged as a critical morphogen during embryonic lung development, regulating the interaction between epithelial and mesenchymal cell populations in the airway and alveolar compartments. There is increasing evidence that the SHH pathway is active in adult lung diseases such as pulmonary fibrosis, asthma, chronic obstructive pulmonary disease, and lung cancer, which raises two questions: (1) What role does SHH signaling play in these diseases? and (2) Is it a primary driver of the disease or a response (perhaps beneficial) to the primary disturbance? In this review we aim to fill the gap between the well-studied period of embryonic lung development and the adult diseased lung by reviewing the hedgehog (HH) pathway during the postnatal period and in adult uninjured and injured lungs. We elucidate the similarities and differences in the epithelial–mesenchymal interplay during the fibrosis response to injury in lung compared with other

organs and present a critical appraisal of tools and agents available to evaluate HH signaling.

**Keywords:** hedgehog; lung development; lung fibrosis; fibroblast

### Clinical Relevance

New roles for sonic hedgehog signaling, which is essential for embryonic lung development, have emerged during postnatal lung development and in adult lung disease, such as pulmonary fibrosis, chronic obstructive pulmonary disease, and asthma. Our review of the current literature spanning from embryonic period to adulthood highlights the latest findings with particular focus on the regulation of mesenchymal cells due to their importance in the pathogenesis of pulmonary fibrosis and fibrosis of other solid organs.

Developmental signaling pathways orchestrate interactions among endoderm, mesoderm, and ectoderm, resulting in distinct tissue architectures that enable proper organ function and response to injury. Once organ development is completed, many of these pathways are suppressed or restricted to tissue-specific stem cell maintenance. Several pathways regulating embryonic lung development (1) have sparked interest because they are reexpressed in adult disease

states. One such system is the hedgehog (HH) pathway, a signaling cascade that regulates morphogenesis of lung and other organs in a concentration-dependent manner (2). HH signaling also maintains adult stem cells in various fully developed tissues (3–5) and is involved in several cancers (6). In this review we focus on the role of HH signaling in the lung during development and in disease. We do not review the extensive work on the role of HH

in cancer (6). The online supplement contains an appraisal of tools and agents available to evaluate HH signaling.

### The INs and OUTs of the HH Signaling Pathway

The *hh* gene was first described in *Drosophila melanogaster*, where it regulates dorsal–ventral differentiation and segment

(Received in original form March 24, 2014; accepted in final form July 22, 2014)

This work was supported by National Institutes of Health/National Heart, Lung and Blood Institute grants T32-ES7267-20 (W.N.R.) and 5R21-HL104455 (J.S.M.), NRSA Fellowship grant F32-HL120637 from the National Institutes of Health/National Heart, Lung and Blood Institute (M.C.K.), a Grant-in-Aid from the Stony Wold–Herbert Foundation NYC (M.C.K.), an award of the NYU Physician Scientist Training Program (M.C.K.), NCI grant R01CA128158 (A.L.J.), an Irma T. Hirschl Scholar Award from the Irma T. Hirschl/Monique Weill-Caulier Trusts (J.S.M.), and a grant for fibrosis research from the Will Rogers Foundation (M.C.K., J.S.M.).

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This article has an online supplement, which is accessible from this issue's table of contents at [www.atsjournals.org](http://www.atsjournals.org)

Am J Respir Cell Mol Biol Vol 52, Iss 1, pp 1–13, Jan 2015

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Originally Published in Press as DOI: 10.1165/rcmb.2014-0132TR on July 28, 2014

Internet address: [www.atsjournals.org](http://www.atsjournals.org)

polarity (7). Three vertebrate orthologs were identified: sonic (*Shh*), indian (*Ihh*), and desert (*Dhh*) *Hh* (8–12). Sonic HH (SHH), the most broadly expressed HH ligand, influences morphogenesis of many organs (13). The other two *Hh* genes have more restricted developmental roles, *Ihh* in development of bone (14) and *Dhh* in development of the gonads and nerve sheaths (15, 16). The molecular mechanisms underlying HH signaling are complex, and the interested reader is directed to more comprehensive reviews (17, 18). Figure 1 depicts the HH signaling pathway and highlights molecules known to be important in the lung.

Vertebrate HH ligands are processed and secreted in a manner that is not entirely understood. Synthesis of SHH involves posttranslational modification of its 45-kD precursor by autoproteolytic removal of a C-terminal peptide (19) and C-terminal attachment of cholesterol (20, 21), followed by N-terminal addition of palmitate to the remaining 19-kD peptide (22, 23). Lipid-modified SHH monomers localize to sterol-rich microdomains in the outer plasma membrane (24). Due to its lipid modification, SHH is relatively insoluble, and secretion requires dispatched1 (*Disp1*) (25–27). This multipass transmembrane protein contains a sterol-sensitive domain like those in the HH receptors Patched1 (PTCH1) and Patched2 (PTCH2) and directs cellular HH ligand release to the cell membrane (25–28). It may also facilitate long-range transport of SHH through tissue after secretion (29). SHH localizes to apical and basolateral regions (27, 30), but how this affects SHH signaling is uncertain.

Several other mechanisms that facilitate extracellular movement of SHH have been postulated: release of soluble SHH monomers (31), formation of multimers (32), assembly into lipoproteins (33) and exovesicles (34), and cytoneme formation for cell-mediated delivery (35, 36) (Figure 1A, a–d). Controversy remains as to how HH ligands reach their target cells and whether a single mechanism or a combination of processes is involved. SHH dispersion is also controlled by its own pathway components, including PTCH1 (37) and HH inhibitory protein (HHIP) (38). *Ptch1* and *Hhip1* transcription is induced by HH signaling, and the proteins then function in a negative feedback manner by sequestering SHH,

thereby modulating its ability to traverse tissues.

Once HH ligands reach their target cells, several molecules mediate the signaling response. Three core components of the signaling response to HH ligand were identified in *D. melanogaster* (39): the cell surface receptor patched (Ptc), the heptahelical transmembrane protein smoothed (Smo) that transmits the signal into the cell, and the GLI-family transcription factor cubitus interruptus (Ci) that relays the signal to the nucleus. In vertebrates, *ptc* and *ci* are replaced by the *Ptch* family (*Ptch1*, *Ptch2*) and the *Gli* family of zinc-finger DNA-binding proteins (*Gli1*, *Gli2*, *Gli3*) (40–43).

Reception of the HH signal is mediated by the interaction between the transmembrane proteins PTCH and SMO. In the absence of ligand, PTCH sequesters SMO from the plasma membrane, resulting in HH pathway inhibition. PTCH is inhibited upon binding HH ligand (44), thereby freeing SMO to signal to the GLI transcription factors. The ability of one PTCH molecule to inhibit approximately 50 SMO molecules suggests an indirect interaction involving another signaling molecule (44). Although this putative signaling molecule is unknown, agonistic and antagonistic sterol-like molecules have been identified that bind SMO (45). Oxysterols, for example, are potent activators of HH signaling (46, 47). HH signal transduction is also modulated by several cell surface “co-receptors.” HHIP binds to SHH and IHH (38, 48), thereby decreasing HH pathway activity. Conversely, growth arrest–specific gen1, CAM-regulated by oncogenes (CDO), and brother of CDO promote pathway activity (49–51).

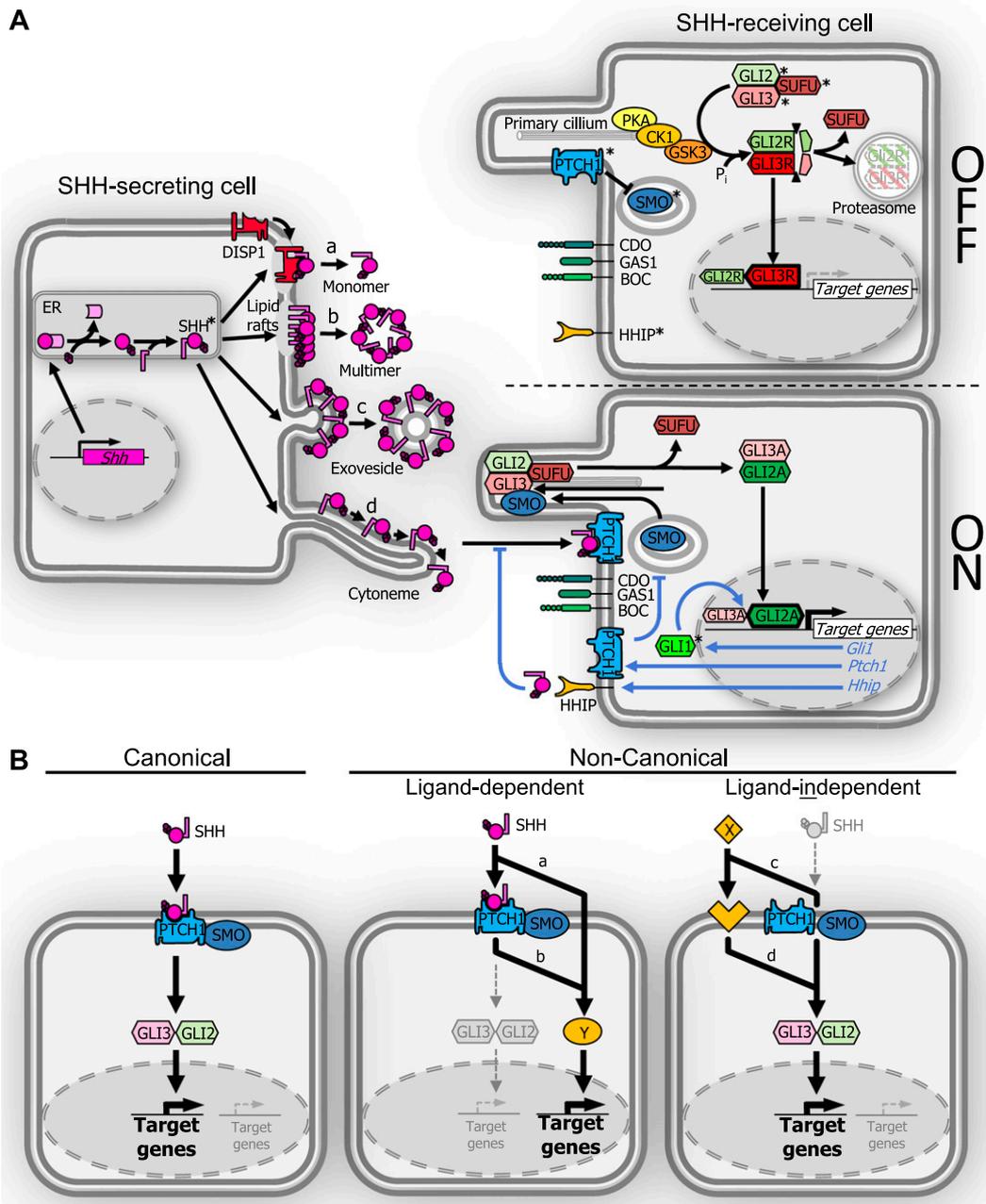
The GLI family of transcription factors relays information to the nucleus about the amount of HH ligand at the cell surface. Similar to Ci in *D. melanogaster*, GLI proteins are posttranslationally altered in response to HH ligand and therefore can act as transcriptional activators or repressors. GLI2 and GLI3 contain an amino-terminal repressor and a carboxy-terminal activator domain (52). GLI1 lacks the repressor domain and thus acts mainly as an activator. *Gli1* is a transcriptional target of HH signaling and reliably reports HH pathway activity (53). GLI2 is the most important pathway activator, whereas GLI3 has primarily repressor function. It is

ultimately the balance between Gli2A and GLI3R accumulation and the resulting target gene transcription in the nucleus that influences the pathway output.

In the absence of HH signals, two processes define the pathway status: (1) GLI2 and GLI3 are modified by PKA/CK1/GSK3-dependent phosphorylation to enter the proteasomal pathway for truncation, resulting (for GLI3) in repressor function as GLI3R (and to a lesser extent GLI2R), and also degradation of both proteins (54–56). (2) Suppressor of Fused (SUFU) inhibits GLI transcriptional activity in the absence of ligand (57). Upon HH pathway activation, GLI2 degradation and repressor formation are reduced, allowing nuclear accumulation of GLI2A (to a lesser extent the same occurs with GLI3A) and induction of target gene transcription. A consensus Gli binding site has been defined (58), and many GLI binding sites have been identified, but only a few genes have been shown to be direct transcriptional targets of GLI transcription factors. Among these confirmed targets are the *Hh* pathway members *Ptch1* and *Gli1* (59, 60), whose proteins provide negative and positive feedback loops to the pathway, respectively. Other tissue-specific direct targets include *FoxA2*, *FoxF1*, *Nkx2.2*, *Myf5*, *Bcl2*, *Nmyc* (6), and *Pdgfra* (61).

The primary cilium, a small dynamic tubular structure that transiently forms in interphase and is required for correct cell mitosis (62), is necessary for HH signaling in most cells. Without HH ligand, PTCH1 localizes to the cilium and blocks HH signaling by preventing SMO entry (63). *Hh* ligand binding drives PTCH1 out of the cilium, permitting ciliary SMO accumulation and downstream pathway activation (64). SMO signals to GLI2 and GLI3, allowing their movement through the primary cilium together with microtubular transport proteins (65, 66). In the HH-OFF state, GLI3 undergoes processing to its repressor state GLI3R, which dissociates from SUFU and translocates to the nucleus (67, 68). In the HH-ON state, GLI2 and GLI3 are enriched in the ciliary tip, where their modification facilitates dissociation from SUFU and nuclear accumulation of primarily the activator form GLI2A (66–68).

Three concepts of HH signaling deserve final mention. First, HH ligand gradients, which control anterior–posterior and dorsal–ventral patterning of the embryo



**Figure 1.** Schematic depiction of sonic hedgehog (SHH) synthesis, secretion, and signaling. Pathway molecules with described roles in lung development and/or disease are marked (\*). (A) In the SHH-secreting cell, SHH-precursor protein undergoes autoproteolytic cleavage and C-terminal addition of a cholesterol moiety followed by N-terminal palmitoylation. Lipidated SHH is able to translocate to lipid rafts in the outer cell membrane. Several modes of secretion have been postulated: (a) a monomeric form requiring DISP1, (b) a multimeric form, (c) in exovesicles or lipoproteins, and (d) along tentacle-like cell cytonemes. The HH signal-receiving cell is shown without (OFF) or with (ON) pathway activation. In the OFF-state, Patched1 (PTCH1) receptor sequesters SMO at the base of the primary cilium. In the absence of SMO activation, GLI2/GLI3 are phosphorylated through the PKA/CK1/GSK3 complex, followed by proteolytic cleavage into their repressor forms GLI2R/GLI3R, which dissociate from Suppressor of Fused (SUFU) and either translocate to the nucleus to repress target gene expression (mainly through GLI3R) or undergo proteasomal degradation. SHH binding to PTCH1 (ON-state) removes sequestration of SMO, which then moves into the primary cilium to induce conversion of GLI2/GLI3 to their activator forms Gli2A/Gli3A. Gli2A/Gli3A can then dissociate from SUFU and translocate to the nucleus to activate target gene transcription (mainly through GLI2A). Direct transcriptional targets (*italic blue font and arrows*) can provide either a positive (GLI1) or a negative (PTCH1, HHIP) feedback loop for HH signaling. Further modulation of HH signal transduction is provided by cell surface “co-receptors” CAM-regulated by oncogenes (CDO), brother of CDO (BOC), and growth arrest–specific gen1 (GAS1). (B) Canonical and noncanonical HH signaling. Canonical pathway activation (*left panel*) involves SHH ligand, cell membrane molecules PTCH1/SMO, and GLI transcription factors. In ligand-dependent, noncanonical signaling (*middle panel*), SHH activates target genes using an alternate pathway Y with (a) or without (b) involvement of PTCH1 and/or SMO. In HH ligand-independent, noncanonical signaling (*right panel*), alternate X-ligand-mediated pathways activate GLI-mediated target transcription with (c) or without (d) involvement of PTCH1 and/or SMO.

(9, 69, 70), similarly influence secondary lung bud formation (71). An important mechanism for generating gradients of HH activity is likely the expression of the negative regulators PTCH1 and HHIP, whose genes are direct transcriptional targets of SHH signaling. Second, although many developmental processes involving HH ligands follow canonical pathway activation, there is growing evidence of noncanonical HH signaling during development and in adulthood (for review see Reference 72), where SHH signals to a pathway independent of GLI-mediated transcription (73–75) or GLI function is influenced by another signaling pathway (76–78) (Figure 1B). Finally, PTCH1 can act as a dependence receptor (79, 80). Dependence receptors induce apoptosis in the absence of cognate ligands (81). The fact that primary lung fibroblasts from idiopathic pulmonary fibrosis (IPF) lungs are protected from IFN/TNF/Fas-ligand-induced apoptosis by Shh (82) raises the possibility that fibrosis is maintained by epithelial SHH expression, which prevents PTCH1-mediated mesenchymal cell apoptosis that would otherwise occur.

## HH Signaling in Embryonic Lung Development: What Do We Know?

Embryonic lung development follows the principle of branching morphogenesis. The endodermal cell layer grows into the surrounding splanchnic mesenchyme, generating a branched tubular structure surrounded by mesenchyme-derived structures such as blood vessels, lymphatics, and nerves. Lung formation is divided into five phases (1). The first four phases (embryonic, pseudoglandular, canalicular, and saccular) result in the typical branching structure ending in alveolar sacs with surrounding stromal scaffold and vascular structures. During the final (postnatal) alveolar phase, the terminal sacs give rise to mature alveolar ducts and alveoli. In humans, the last stage spans almost 10 years, whereas in murine lung development it is completed in 4 weeks (83). An elaborate network of growth factors, transcription factors, and extracellular matrix molecules orchestrates embryonic lung growth (1, 84). Localization of *Shh*/SHH expression (Figure 2) and

knockout of Hh pathway molecules (Table 1), among other results, demonstrate that SHH signaling is a crucial aspect of this network.

### HH Pathway Molecule Expression in the Lung: Where and When

*Shh* is expressed in respiratory epithelium throughout embryonic lung development in a complex and changing pattern, starting around embryonic day (E)10 (85–88) (Figure 2). *Shh* expression is high at the tips of the growing bronchial tubules but absent more proximally, suggesting a polarizing role for SHH during branching. This graded SHH expression pattern continues throughout the pseudoglandular and canalicular stages until E16.5 (85). After E16.5, SHH is expressed in proximal and distal airways but only in a subset of the epithelial cells (likely nonciliated) (85). From E17 on, SHH is expressed strongly in the saccular epithelial compartment, only decreasing after birth. Overall expression of *Shh* and *Ptch1* gradually decreases from E15.5 to birth (87). Remarkable similarities were detected when comparing expression of SHH and its pathway molecules in human and murine embryonic lung (89).

*Ptch1* is expressed in the lung mesenchyme around E11.5, highest around the distal tips and lower along the bases of the lung buds (mirroring the *Shh* pattern) (87, 90, 91). *Ptch1* expression remains significant during branching morphogenesis but decreases during late gestation (87). SMO is reportedly expressed in epithelium and mesenchyme between E12.5 and E16.5 (89). *Gli1*, *Gli2*, and *Gli3* are expressed in the mesenchyme during the pseudoglandular stage, and their levels decrease near birth (92). Although all three *Glis* are expressed strongly in distal mesenchyme, *Gli2* is also present in mesenchyme around proximal trachea, and *Gli3* is expressed in intermediate areas between lung buds. *Hhip* is expressed in mesenchyme underlying epithelial regions of high *Shh* expression, starting around E10.5 and overlapping with *Ptch1* and *Gli1* expression (38, 48).

### Lessons from Functional Inhibition and Overexpression of HH Pathway Molecules

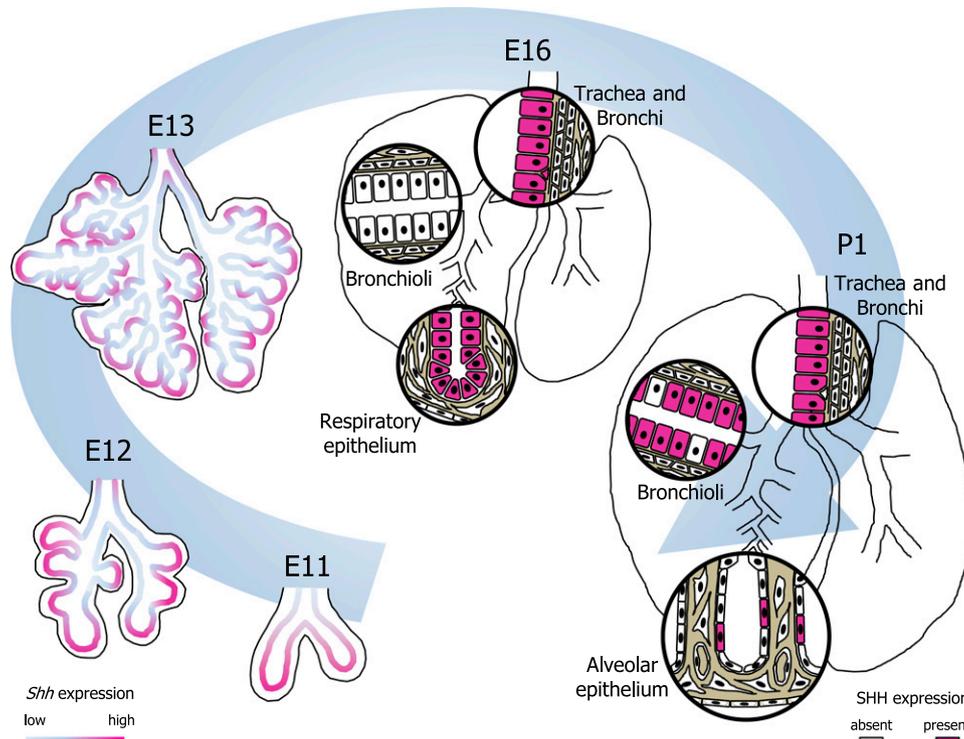
*Shh* is indispensable for embryonic lung formation, regulating branching morphogenesis and mesenchymal proliferation. *Shh*<sup>-/-</sup> mice have single-

lobed hypoplastic lungs with decreased epithelium and mesenchyme, malformations of the trachea, and trachea-esophageal fistulae (93, 94). The preservation of proximal and distal epithelial cell phenotypes and the lack of bronchial smooth muscle cells indicate that SHH influences the mesenchymal scaffold rather than epithelial cell differentiation. This idea is supported by investigations using a doxycycline-inducible *SP-C* promoter-driven *Shh* conditional knockout (CKO) (95). *Shh* CKO before E12.5 causes more severe defects in branching morphogenesis, whereas *Shh* CKO after E12.5 produces mild abrogation of distal bronchial morphogenesis but leaves proximal branching intact. *SPC* promoter-driven SHH overexpression in *Shh*<sup>-/-</sup> mice rescues distal branching but does not affect lung lobulation or the trachea-bronchial cartilage defects (95). The role of *Ptch1* in lung development is obscure due to early lethality of null mutants (53, 96).

The effects of SHH on branching are tightly regulated by its downstream targets PTCH1 and HHIP, which are produced in an overlapping pattern and sequester SHH (38, 95). *Hhip*<sup>-/-</sup> lungs are hypoplastic due to defective formation of the second generation of lung buds. This phenotype is partially rescued by PTCH1 overexpression and involves failure to localize mesenchymal fibroblast growth factor (FGF)10, a target and antagonist of SHH signaling, to areas of new bud formation (38).

SHH also affects proliferation and differentiation of lung mesenchyme. Embryonic *Shh* CKO and SHH overexpression result in respiratory failure at birth but with different phenotypes. *Shh*<sup>-/-</sup> mice have decreased proliferation of mesenchymal cells (94), whereas *SP-C* promoter-driven *Shh* overexpression increases proliferation of lung mesenchyme during late gestation, suggesting that balanced mesenchymal induction by SHH is vital to normal lung formation (87). These observations were accompanied by the expected changes in expression of the SHH transcriptional targets *Ptch1* and *Gli1* in the mesenchyme (87, 93–95). SHH signaling also regulates lung mesenchymal cell lineages, such as the entry of mesothelial cells into the lung mesenchyme (97).

Although no lung abnormalities have been reported in *Ptch1*<sup>+/-</sup> mice (96), the



**Figure 2.** Schematic of SHH-expressing cells in the developing lung from embryonic day (E)11 to postnatal day (P)1. SHH-expressing cells and cell layers are highlighted in *fuchsia*. *Shh* expression is highest at the tips of the primary and secondary lung buds, but also present at lower levels along the developing bronchi. This pattern continues throughout the pseudoglandular stage. Around E16, SHH expression is transiently absent in the distal bronchioli but is vividly present in the respiratory epithelium and along larger bronchi and trachea. Toward P1 the majority of bronchial epithelial cells express SHH, whereas in the saccular-stage alveolar compartment SHH expression is restricted to a subset of epithelial cells.

requirement of the GLI transcription factors during lung development is well documented (Table 1). *Gli2*<sup>-/-</sup> mice have hypoplastic lungs with severe patterning defects, have diminished mesenchyme, and die at birth (91, 98), supporting a role for SHH in facilitating stromal cell expansion by canonical signaling through GLI2. *Gli3*<sup>-/-</sup> mice exhibit decreased lung size and abnormal shape of the lobes (92). In contrast, *Gli1*<sup>-/-</sup> mice have normal lungs and viability, as do *Gli2*<sup>+/-</sup> mice. However, *Gli1*<sup>-/-</sup>;*Gli2*<sup>+/-</sup> compound mutants reveal decreased lung size and death soon after birth, indicating overlapping functions for Gli1 and Gli2 and a supportive role for Gli1 in the developing lung (99). The lungs of *Gli1*<sup>-/-</sup>;*Gli2*<sup>-/-</sup> double mutants have only two lobes and are even smaller than *Gli1*<sup>+/-</sup>;*Gli2*<sup>-/-</sup> and *Gli1*<sup>-/-</sup>;*Gli2*<sup>+/-</sup> lungs (53). The most severe lung defects are seen in *Gli2*<sup>-/-</sup>;*Gli3*<sup>-/-</sup> double mutants, which fail to form trachea, lung, and esophagus (91). Although a single *Gli3* allele in *Gli2*<sup>-/-</sup>;*Gli3*<sup>+/-</sup> mutants partially rescues the distal lung phenotype, proximal lung development is still abnormal, characterized by failure to separate left and right lung and formation of

a tracheobronchial fistula (91). The observations that *Shh*<sup>-/-</sup> lungs show increased Gli3R levels and, strikingly, that GLI3 loss partially rescues the distal lung phenotype with increased mesenchymal cell proliferation in *Shh*<sup>-/-</sup> mice (100) indicate that opposing gradients between SHH and GLI3R contribute to lung development. The fact that the *Gli2*<sup>-/-</sup>;*Gli3*<sup>-/-</sup> lung phenotype is worse than that of the *Shh*<sup>-/-</sup> lung is consistent with the idea that both increased GLI3R and decreased GLI2A contribute to the *Shh* null phenotype. Finally, the adaptor molecule SUFU, involved in GLI protein processing, affects GLI output during lung development, as *Dermo1*<sup>Cre</sup>-dependent CKO of mesenchymal *SuFu* causes hypoplastic lungs with defective distal branching and absence of myofibroblasts (61).

### Morphogens that Are Regulated by HH Signaling

Lung development requires the concerted activity of many morphogens, and the SHH signaling pathway communicates with other key pathways (1). *Shh* CKO affects not only target gene expression of its own pathway

molecules but also affects that of other genes (95). ChIP assays confirmed at least 28 direct GLI1-binding genes in embryonic mouse tissue (59), three of them with important roles in the developing lung.

FGF10 is the only FGF shown to be essential for lung development. *Fgf10*<sup>-/-</sup> mice fail to form lungs distal to the trachea (101, 102). FGF10 is maximally expressed in mesenchyme around the growing lung buds (103), and its expression pattern promotes proximal–distal differentiation during branching (104). *Shh* restricts FGF10 expression to the distal tips of the lung buds and, together with *Hhip*, inhibits FGF10 expression in the interbud regions, allowing localized new bud outgrowth (38, 93). In *Shh*<sup>-/-</sup> lungs, FGF10 expression expands to almost all mesenchyme (93), supporting the model of antagonism between SHH and FGF10.

Bone morphogenetic protein 4, a TGF-β superfamily member, is expressed in proximal mesenchyme and distal epithelium at the tips of the branching lung (105). SHH is able to induce mesenchymal bone morphogenetic protein 4 expression

**Table 1.** Hedgehog Pathway Gene Knockout Lung Phenotypes

Genotype	Lung Phenotype	Comments	Citation
<i>Shh</i> <sup>-/-</sup>	Single-lobe hypoplastic lungs with decreased epithelium/mesenchyme; malformations of the trachea and trachea-esophageal fistula	Lethal at birth	93, 94
<i>Shh</i> <sup>+/-</sup>	No reported abnormalities	Viable	162
<i>Ptch1</i> <sup>-/-</sup>	Lethal before lung development begins	Lethal at E8.5–E9.5	53, 96
<i>Ptch1</i> <sup>+/-</sup>	No reported abnormalities	Viable	96
<i>Gli1</i> <sup>-/-</sup>	Normal appearing	Viable	99
<i>Gli2</i> <sup>-/-</sup>	Hypoplastic lungs with severe patterning defects (single lobe right lung) and diminished epithelium/mesenchyme; mildly hypoplastic trachea and esophagus	Lethal at birth	91
<i>Gli2</i> <sup>+/-</sup>	Normal appearing	Viable	99
<i>Gli3</i> <sup>-/-</sup>	Hypoplastic lungs of decreased size and abnormal shape of the lobes	Lethal around E14.5	92
<i>Gli3</i> <sup>+/-</sup>	Normal appearing	Viable	103
<i>Gli1</i> <sup>-/-</sup> ; <i>Gli2</i> <sup>+/-</sup>	Hypoplastic lungs of decreased size, less severe than <i>Gli1</i> <sup>-/-</sup> ; <i>Gli2</i> <sup>-/-</sup>	50% lethal until P21	99
<i>Gli1</i> <sup>-/-</sup> ; <i>Gli2</i> <sup>-/-</sup>	Severely hypoplastic, two lobes	Lethal at birth	53, 99
<i>Gli2</i> <sup>-/-</sup> ; <i>Gli3</i> <sup>+/-</sup>	Hypoplastic lungs with abnormal proximal lung development with failure to separate left and right lung and formation of a tracheobronchial fistula; distal lung partially formed	Lethal at birth	91
<i>Gli2</i> <sup>-/-</sup> ; <i>Gli3</i> <sup>-/-</sup>	Most severe phenotype; fail to form trachea, lung, and esophagus	Lethal at E10.5; some embryos survive until E13.5	91
<i>Hhip</i> <sup>-/-</sup>	Single-lobe hypoplastic lungs with defective formation of the second generation of lung buds	Lethal at birth	38
<i>Hhip</i> <sup>+/-</sup>	No abnormalities reported	Viable	38
<i>Hhip</i> <sup>-/-</sup> ; <i>Ptch1</i> <sup>+/-</sup>	More severe lung hypoplasia than <i>Hhip</i> <sup>+/-</sup> lungs; mesenchyme thickened	Lethal at birth	38

Definition of abbreviations: E, embryonic day; P, postnatal day.

in early (E11.5) (90, 94) but not late lung development (E18.5) (87).

The forkhead transcription factor FoxF1 is expressed at highest levels in the subepithelial lung mesenchyme between the distal bulbous part of the bud and proximal tubular part (106). Decreased FoxF1 expression in *Shh*<sup>-/-</sup> lungs is rescued by ectopic SHH treatment. *FoxF1*<sup>-/-</sup> lungs share features of *Shh*<sup>-/-</sup> lungs, consistent with other data that FoxF1 is a transcriptional target of HH signaling (107).

### Morphogens that Regulate HH Signaling

The forkhead transcription factors FOXA1 and FOXA2 are expressed in epithelial cells during embryonic lung development (108, 109). Epithelium-specific FoxA1 and FoxA2 deletion causes defects in branching morphogenesis and respiratory epithelial cell maturation (109). *FoxA1*<sup>-/-</sup>; *FoxA2*<sup>-/-</sup> mutants have decreased expression of epithelial *Shh* and mesenchymal *Ptch*

and *Hhip* as well as decreased expression of transcription factors that control pulmonary smooth muscle differentiation. In light of the bronchial wall defects and absence of cells expressing  $\alpha$ -smooth muscle actin in *Shh*<sup>-/-</sup> lungs (95), these findings raise the possibility that epithelial FOXA1 and FOXA2 act upstream of *Shh*, controlling SHH-induced mesenchymal cell expansion and differentiation.

FGF9 is expressed in epithelial and mesenchymal cells during lung development (110). *FGF9*<sup>-/-</sup> lungs have deficient distal branching (less severe than *FGF10*<sup>-/-</sup>) but normal *Shh* expression (111). *In vitro*, FGF9 inhibits mesenchymal cell differentiation without affecting SHH-induced proliferation of mesenchymal cells (90). However, because *FGF9* partially rescues the distal vascular phenotype in *Shh*<sup>-/-</sup> lungs, but not *vice versa*, it is possible that FGF9 modulates SHH signaling *in vivo* during formation of the lung capillary network (112).

WNT5A, one of the ligands of the WNT signaling cascade, is expressed in lung epithelium and mesenchyme during embryonic lung development (113). *Wnt5a*<sup>-/-</sup> lungs show defective distal lung morphogenesis with increased mesenchyme and overexpression of *Shh* and *Ptch1* (113), whereas SP-C promoter-driven epithelial *Wnt5A* overexpression decreases lung mesenchyme and *Shh/Ptch1* expression (114), suggesting a regulatory role for WNT5A in SHH-induced mesenchymal proliferation.

Knockout of transforming growth factor  $\beta$  receptor II, a receptor for TGF- $\beta$  ligands that is involved in epithelial-mesenchymal communication during development, causes cystic lung with defective branching (115). The Hh signaling transcriptional targets *Ptch1* and *Gli1* were increased without altered *Shh* expression, suggesting the possibility of noncanonical pathway regulation.

Eyes absent1 (EYA1) and sine oculis1 (SIX1), two homeobox transcriptions

factors involved in eye development and expressed in lung epithelium and mesenchyme, were also found to affect lung development (116–118). *Six1*<sup>-/-</sup> and *Eya1*<sup>-/-</sup> lungs show a hypoplastic phenotype with branching defects, which is exaggerated in *Six1*<sup>-/-</sup>;*Eya1*<sup>-/-</sup> mutants. Lung mesenchyme is increased, as seen after SHH overexpression (87), and increased SHH signaling is observed. Cyclopamine, a Smo antagonist (details are provided in the online supplement), partially rescues lung structure, confirming the importance of increased SHH signaling in these mutant mice. Similar findings were reported for adrenoceptor *ARα2b*<sup>-/-</sup> mice (119).

From these studies it is clear that (1) during embryonic lung development, expression of SHH and its signaling molecules are highly regulated in location and time and (2) SHH expression exerts its effect on different cellular compartments because it is essential for branching events in the bronchial compartment and is critical to the respiratory epithelial compartment at the canalicular and sacular stages, where it regulates balanced mesenchymal expansion. These studies prompt a fundamental question: Does SHH-mediated regulation of lung mesenchyme play a role after birth and in adult disease?

## HH Signaling during Postnatal Lung Development

Postnatally, mature lung is generated in two phases: an early phase of alveolar septum formation (alveolarization) followed by maturation of alveolar walls and the microvasculature (120). In mice, the second phase commences at about postnatal day (P)10. An important part of septal maturation is a decrease of mesenchymal cells that accompanies the fusion of capillaries as growing, matrix-producing septa transform into mature, thin-walled structures (121, 122). The significance of alveolarization is illustrated by bronchopulmonary dysplasia, which develops in infants secondary to perinatal lung injury and results in abnormal alveolar wall morphology (123, 124). Numerous factors promote or disrupt alveolarization (125, 126), but until recently no role for SHH had been identified.

Murine models established the first evidence of HH signaling in the postnatal lung. Although *Shh* and *Ptch1* expression decreases during late gestation, it is still present at birth (87). At P1, SHH

expression is observed in almost all epithelial cells lining the conducting airways, whereas in the alveolar sacs SHH is restricted to a subgroup of epithelial cells (85). In this study, SHH was detected until P15 but was below the detection threshold at P24. Hyperoxia-induced lung injury, a model of bronchopulmonary dysplasia, causes up-regulation of *Shh* and *Ptch1* in epithelium and mesenchyme, respectively, and thickening of alveolar walls at P7 and P14 (127), raising the possibility that SHH signaling plays a role in postnatal lung pathology.

Using *Gli1*<sup>nlacZ/+</sup> reporter mice (53), we detected HH-responding cells (*Gli1*-positive cells) throughout the postnatal period and into adulthood (128). Two observations are important: (1) *Gli1*-positive cells, mostly fibroblasts, are found in alveolar and peribronchial/perivasculature zones. To further illustrate HH-responding cell location, we used the *Gli1*<sup>creERT2</sup>-*Rosa26*<sup>mT/mG</sup> lineage tracer (129). *Gli1* lineage, labeled at P3, is detectable at P10 in three functionally distinct locations: in and around the peribronchial smooth muscle layer, scattered in alveolar septa, and in mesothelial cells of the visceral pleura (Figure 3). (2) *Gli1*-positive cells (*Gli1*<sup>nlacZ/+</sup> reporter) in the alveolar zones are abundant at P7 in septal walls and tips but are increasingly less numerous at P14 and P21 while remaining constant around airways and vessels. The decreased septal expression coincides with the end of the alveolarization phase. Between P14 and P21, the central region of septa is reduced to a fibrous meshwork interwoven with capillaries, and the number of fibroblasts decreases by 10 to 20% (122). The coincidence of fewer HH-responding cells with the transition to septal maturation suggests a functional connection. Analysis of primary lung fibroblasts from P4 to P12 mice revealed significant *Ptch1* and *Gli1* expression until P8 (130), supporting the presence of HH signaling until the end of alveolarization. In this study, SHH stimulated chemotactic fibroblast migration, presumably an important feature of septal elongation.

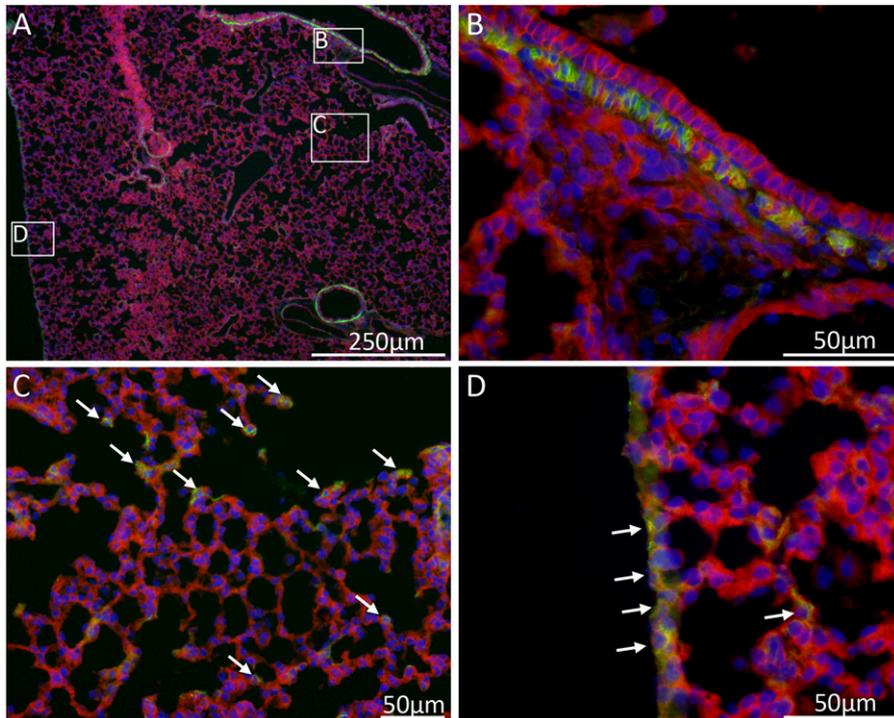
A role for postnatal HH signaling has recently been confirmed. When HH signaling is reduced *in vivo* beginning at P3, before its normal decline around P8, enlarged airspaces develop, without a decreased number of septal tips or grossly abnormal elastin formation, suggesting

accelerated lung maturation due to premature reduction of mesenchyme (128). Conversely, treatment with a SMO agonist from P1 to P7 causes “lung hyperplasia” with preserved epithelial differentiation at P9 and P21 (131), hinting that enhancing HH signaling affects lung maturation by preventing fibroblast loss.

## HH Signaling in Pulmonary Fibrosis

Given the mitogenic effect of SHH on mesenchyme during development, it is intriguing that increased HH signaling is associated with fibrosis in lung (Table 2) and other organs (132–134). IPF is a progressive fibrosing interstitial pneumonia of unknown etiology, characterized by fibroblastic foci and deposition of extracellular matrix leading to destruction of alveolar structures (135, 136). The current paradigm of IPF pathogenesis is that epithelial injury leads to aberrant epithelial–mesenchymal communication in a manner that prevents epithelial repair, promotes expansion and activation of mesenchymal cells, and stimulates angiogenesis (136, 137). In human IPF lungs, microarray data showed increased expression of several developmental pathway genes, including *PTCH1* (138). SHH expression is high in epithelial cells lining fibrotic areas in samples of IPF and other interstitial pneumonias but is undetectable in normal lung (139–141). Abnormal expression of *PTCH1*, *SMO*, and *GLI1* was also found in IPF lungs (82, 142). The localization of *PTCH1* and *GLI1*, which are expressed only in mesenchymal cells during development, to epithelial and mesenchymal cells in fibrotic lungs suggests that the strict separation of SHH-expressing and SHH-responsive cells is lost during the fibrotic process. However, these opposing observations of the expression pattern during development and in disease also raise the more general issue of technical difficulties in analyzing tissues that contain different cell types and gene expression levels.

Experimental lung fibrosis models also show abnormalities in the HH pathway. FITC-induced lung fibrosis (143) results in SHH overexpression in airway and alveolar epithelial cells (140, 144). Endotracheal bleomycin administration, the most studied animal fibrosis model (145), results in up-regulated expression of *Shh* and *Gli1* in fibrotic lesions (146). In *Gli1*<sup>nlacZ/+</sup> mice,



**Figure 3.** Hh-responding cells in different functional areas of the lung. *Gli1*-expressing cells were marked at P3 with a single dose of tamoxifen using the *Gli1<sup>creERT2</sup>-Rosa26<sup>mT/mG</sup>* lineage tracer mouse. Immunofluorescence images of lung sections at P12 illustrate that cells in the *Gli1*-lineage (green) are present in three locations: in the peribronchial smooth muscle layer (B), scattered in the alveolar septal walls (C, arrows), and in many mesothelial cells of the visceral pleura (D, arrows). Unmarked cells appear red. DAPI-stained cell nuclei appear blue.

the number of *Gli1*-positive cells, which are mostly fibroblasts and myofibroblasts, is increased in fibrotic lesions when compared with uninjured lung (128). Numbers of *Gli1*-positive cells in morphologically normal lung are also increased, indicating either *de novo* activation of a resident pool of potentially HH-responsive cells and/or production of additional HH-responding cells (e.g., by local fibroblast proliferation).

Inhibition of HH signaling at the level of SHH or SMO in the bleomycin model fails to prevent fibrosis (128, 146). Enhancement of HH signaling by *Shh* overexpression during the fibrotic phase worsens lung fibrosis (128), pointing toward a potential role for HH signaling in controlling fibroblast expansion and/or survival. *In vitro* data support this hypothesis: in primary lung fibroblasts, SHH up-regulates *Ptch1* and *Gli1* expression, increases proliferation, and protects from TNF- $\alpha$ /IFN- $\gamma$ /FasL-induced apoptosis (82). We also reported increased survival of SHH-stimulated primary lung fibroblasts *in vitro* (128). These findings suggest that HH signaling may sustain

fibrosis and prevent resolution. GANT61, an inhibitor of GLI2/3, decreases fibrosis (146). Although caution is warranted because of possible off-target effects and unknown effects on GLI3R, this result raises the possibility of ligand-independent HH pathway activation in fibrosis.

The hypothesis that epithelium-derived SHH drives the mesenchymal cell response in fibrotic lung is supported by evidence from other organs. Skin lesions of patients with systemic sclerosis reveal SHH overexpression and abnormal HH signaling (132). SHH stimulation of human primary skin fibroblasts induces a myofibroblastic phenotype and increases collagen expression. Dermal *Shh* overexpression and bleomycin treatment cause skin fibrosis in mice, and the latter is blocked by the SMO inhibitor LDE223 and Smo siRNA. *Ptch1*<sup>+/-</sup> mice, which likely have elevated HH signaling, are more susceptible to bleomycin-induced skin fibrosis (132, 147). In the liver, chronic cholestasis and nonalcoholic steatohepatitis are characterized by enhanced HH signaling, which promotes activation of hepatic stellate cells to

a myofibroblastic phenotype (133, 148). In the kidney, ureteral obstruction-induced fibrosis is accompanied by myofibroblast transformation of fibroblasts with active HH signaling and is blocked in *Gli1*<sup>-/-</sup> mice and by SMO antagonists (134, 149).

### HH Signaling in COPD and Asthma

Obstructive airway diseases such as COPD and asthma are also associated with altered HH signaling (Table 2). Both diseases manifest peribronchial fibrosis as a result of chronic inflammation and tissue remodeling (150, 151), processes that involve fibroblast expansion and matrix deposition, similar to lung fibrosis. Gene-wide association studies linked a locus near *HHIP* on 4q31 to decreased lung function and COPD-related phenotypes (152, 153). A SNP in this region is located in a potential enhancer region of the *HHIP* promoter and thus could alter *HHIP* gene expression. *HHIP* protein is reduced in COPD lungs, implying a role for HH signaling (153). Because *HHIP* is a direct transcriptional target of Hh signaling, this observation could indicate decreased Hh pathway activation in COPD; however, because *HHIP* is a negative feedback molecule in the HH pathway, a direct effect of low *HHIP* levels would be enhanced HH signaling.

Another gene-wide association study revealed linkages of the *HHIP* and *PTCH1* regions to decreased lung function and asthma-related phenotypes (154); however, it is unclear how HH signaling might contribute to asthma pathophysiology. One possibility is that HH signals from airway epithelial cells are received by CD4 T cells, which play an important role in airway inflammation and require HH signaling for normal differentiation in the thymus (155, 156). Although SHH expressed by airway epithelium promotes TH2 differentiation of CD4 T cells, thereby exacerbating the allergic response in a dust mite-induced asthma model, CD4-specific gene deletion of *Ptch1* did not alter allergic response in an ovalbumin-induced asthma model, raising the question of noncanonical HH pathway activation in CD4 T cells. It must also be noted that lymphocytes do not have primary cilia, but alternate modes of HH signaling may exist (157). Another possibility is that epithelial SHH signals to peribronchial stromal cells, including fibroblasts and

**Table 2.** Evidence for Sonic Hedgehog Signaling in Human Lung Disease

Disease	Method	Findings	Citation
Parenchymal lung diseases			
IPF	Microarray	<i>PTCH1</i> gene expression altered in IPF lungs	138
	ISH	<i>SHH</i> highly expressed in epithelium of fibrotic areas	139, 142
	qRT-PCR	<i>SHH</i> , <i>PTCH1</i> , and <i>GLI1</i> up-regulated in IPF lungs	82
	IHC	<i>SHH</i> expressed in hyperplastic alveolar type II cells in fibrotic areas	140, 141
NSIP	IHC	<i>PTCH1</i> , <i>SMO</i> , and <i>GLI1</i> expressed in fibroblastic foci of IPF lungs	82
	ELISA	<i>SHH</i> elevated in BALF from IPF lungs	142
	ISH	<i>SHH</i> weakly expressed in epithelium, but higher than in normal lung	139
COP	IHC	<i>SHH</i> expressed in epithelial cells of thickened alveolar walls	140, 141
	IHC	<i>SHH</i> expressed in buds of organizing exudate	141
Airway diseases			
COPD	GWAS	SNPs in region close <i>HHIP</i> gene on 4q31 linked to decreased lung function (FEV <sub>1</sub> /FVC ratio) and COPD-related phenotypes	152, 153
	qRT-PCR	<i>HHIP</i> decreased in COPD lungs	153
	WB	<i>HHIP</i> decreased in COPD lungs	153
Asthma	GWAS	SNPs in regions of <i>HHIP</i> on 4q31 and the <i>PTCH1</i> gene on 9q22-31 linked to decreased lung function (FEV <sub>1</sub> /FVC ratio) and asthma-related phenotypes	154

*Definition of abbreviations:* BALF, bronchoalveolar lavage fluid; COP, cryptogenic organizing pneumonia; COPD, chronic obstructive pulmonary disease; GWAS, gene-wide association study; IHC, immunohistochemistry; IPF, idiopathic pulmonary fibrosis; ISH, *in situ* hybridization; NSIP, nonspecific interstitial pneumonia; qRT-PCR, quantitative reverse transcription polymerase chain reaction; SNP, single-nucleotide polymorphism; WB, Western blot.

pericytes, with subsequent implications for tissue remodeling. At least in adult uninjured murine lung, the vast majority of HH-responding cells are located in the interstitial spaces around airways and vessels (128). Given the use of inhaled glucocorticoids in asthma and COPD, it is thought provoking that several clinically used glucocorticoid derivatives, such as budesonide, can modulate SMO localization and HH pathway activity, thereby increasing sensitivity to HH ligand input (158).

## Conclusions and Future Directions

In this review we highlight the general principles of HH signaling and apply the knowledge available from embryonic lung development to review the latest insights into the functions of HH signaling during postnatal lung development and in adult disease, both occurring during time periods when HH signaling changes. One newly emerging concept of HH signaling is that it influences the alveolar phase during

postnatal lung development and, by extension, adult lung morphology and function. A second concept in need of further testing involves regulation of the stromal compartment in fibrotic lung diseases.

An element connecting the embryonic period, postnatal lung development, and adult fibrotic diseases appears to be a fibroblast population capable of responding to HH signals. Up- or down-regulation of HH might push HH-responsive fibroblasts down different paths. An appropriately timed reduction in HH signaling might be necessary to decrease the number of fibroblasts and thereby allow a physiologic process such as alveolar wall thinning and maturation to occur. In contrast, the continuation and/or enhancement of HH signaling in response to epithelial cell injury might sustain or expand fibroblasts in areas of tissue remodeling, such as fibroblastic lesions in IPF, thereby preventing fibrosis resolution.

The lung and other organs manifest mesenchymal HH pathway activation during fibrosis, and in some examples experimental HH inhibition is antifibrotic, suggesting a more

general mechanism involving HH pathway activation. To what extent HH signaling contributes to lung fibrosis is a critical question because HH pathway inhibitors are becoming available for clinical use. The ability of tumor-derived HH to cause a stromal response supporting tumor growth further substantiates the importance of the HH pathway in regulating pathological mesenchymal cell behavior (159–161). The physiologic role of HH signaling in uninjured adult lung, if there is one, remains unclear. However, the presence of HH-responding cells in the perimeter of the bronchovascular bundles indicates there could be a pool of mesenchymal cells that have progenitor characteristics and that normally replenish the lung stroma but expand abnormally during lung disease and injury repair. ■

**Author disclosures** are available with the text of this article at [www.atsjournals.org](http://www.atsjournals.org).

**Acknowledgments:** The authors thank Edward Laufer from Columbia University for providing the lungs of the *Gli1<sup>creERT2</sup>-Rosa26<sup>mt/mG</sup>* lineage tracer mouse and William Rom for his ongoing generous support of our work.

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