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## Hedgehog signaling mechanism and role in cancer

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### Abstract

Cell-cell communication through evolutionarily conserved signaling pathways governs embryonic development and adult tissue homeostasis. Deregulation of these signaling pathways has been implicated in a wide range of human diseases including cancer. One such pathway is the Hedgehog (Hh) pathway, which was originally discovered in *Drosophila* and later found to play a fundamental role in human development and diseases. Abnormal Hh pathway activation is a major driver of basal cell carcinomas (BCC) and medulloblastoma. Hh exerts its biological influence through a largely conserved signal transduction pathway from the activation of the GPCR family transmembrane protein Smoothened (Smo) to the conversion of latent Zn-finger transcription factors Gli/Ci proteins from their repressor (Gli<sup>R</sup>/Ci<sup>R</sup>) to activator (Gli<sup>A</sup>/Ci<sup>A</sup>) forms. Studies from model organisms and human patients have provided deep insight into the Hh signal transduction mechanisms, revealed roles of Hh signaling in a wide range of human cancers, and suggested multiple strategies for targeting this pathway in cancer treatment.

### Keywords

Hedgehog; Shh; Ptc; Smo; Gli; signaling; phosphorylation; BCC; medulloblastoma; cancer

## 1. Introduction

Initially discovered in *Drosophila*, the Hedgehog (Hh) family of secreted proteins plays critical roles in both embryonic development and adult tissue homeostasis in species ranging from insects to mammals [1–4]. Not surprisingly, deregulation of Hh signaling has been linked to a wide range of human disorders including birth defects such as holoprosencephaly, Gorlin Syndrome, Greig cephalopolysyndactyly, and Pallister-Hall syndrome, and cancer such as basal cell carcinomas and medulloblastoma [2, 5–7].

Members of the Hh family exert their biological influences through a largely conserved pathway to alter the balance between the activator and repressor forms of the Gli family of

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zinc finger transcription factors (Fig. 1) [2, 8, 9]. While *Drosophila* has only one Hh and one Gli protein, Cubitus interruptus (Ci), mammals have three Hh family members: Sonic hedgehog (Shh), Indian hedgehog (Ihh) and Desert hedgehog (Dhh), and three Gli proteins: Gli1, Gli2 and Gli3. In mammals, the Gli repressor (Gli<sup>R</sup>) function is mostly derived from Gli3 whereas the Gli activator (Gli<sup>A</sup>) function is mainly contributed by Gli2. Gli1 is a direct transcriptional target of Hh signaling pathway and acts in a positive feedback to reinforce Gli<sup>A</sup> function.

The Hh signal reception system consists of a twelve-span transmembrane protein Patched (Ptc) that binds directly to Hh and a GPCR family of seven-span transmembrane protein Smoothed (Smo) that transduces the Hh signal across the plasma membrane. Mammals have two Ptc proteins: Ptch1 and Ptch2, with Ptch1 as the major Hh receptor. In the absence of Hh, Ptc blocks Smo signaling activity, allowing the production of Gli<sup>R</sup>/Ci<sup>R</sup> that actively represses a subset of Hh target genes. Binding of Hh to Ptc alleviates its inhibition of Smo, allowing Smo to signal downstream to block Gli<sup>R</sup>/Ci<sup>R</sup> production and promote Gli<sup>A</sup>/Ci<sup>A</sup> formation (Fig. 1A). While the basic framework of Hh signal transduction pathway is similar between *Drosophila* and mammals (Fig. 1B), major differences exist in several regulatory steps. Most notably, vertebrate but not *Drosophila* Hh signal transduction depends on primary cilium, a microtubule-based membrane protrusion found on most mammalian cells including cancer cells [10]. In addition, both Gli-independent noncanonical Hh signaling pathways and Hh/Smo-independent Gli activation pathways exist in mammals [11, 12]. This review focuses on the most recent understanding of the Hh-Gli signaling pathway and its role in tumorigenesis and discuss how this basic knowledge has been translated into strategies for cancer treatment.

## 2. Hh signal transduction

### 2.1. Lipid modification and dispersal of Hh ligand

Hh family members function as morphogens that act over long range with different levels pathway activity specifying distinct developmental outcomes [1]. In Hh-producing cells, full-length Hh undergoes autocleavage to release an N-terminal fragment (HhN) with a cholesterol moiety covalently linked to its C-terminus [13]. HhN is then palmitoylated near its N-terminus by the acyltransferase Skinny Hedgehog (Skn)/Hedgehog acyltransferase (Hhat) (Fig. 1B) [14–17]. While cholesterol modification increases the affinity of Hh for cell membranes and restricts its free dispersal [18, 19], dual lipid modifications facilitate the formation of large multimeric Hh complexes, allowing Hh to move over a long distance [20–26]. Dispatched (Disp), a transmembrane protein structurally related to Ptc [27, 28], is required for the secretion of lipidated Hh to the extracellular space [15, 18, 29–35]. Several Hh carriers have been implicated in long-range Hh signaling, including exosomes [36–38], Lipoprotein particles [39], cytoneme [40, 41], and the Scube family of secreted proteins [33, 42]. A recent study showed that Scube binds lipidated Shh to form a soluble signaling complex and that Hh corepressors CDON/BOC and Gas1 act cooperatively to relay Shh from Scute to Ptc [43]. In addition, many studies have uncovered the role of heparin sulfate proteoglycans (HSPGs) in modulating the release, transport, and reception of Hh [44, 45].

## 2.2. Hh reception: Ptc and Smo

Being the core Hh receptor, Ptc paradoxically functions as an inhibitor of Hh signaling by blocking Smo activation sub-stoichiometrically in the absence of Hh ligand [46]. How Ptc inhibits Smo and how Hh binding alleviates this inhibition have remained mysteries in the field until very recently. Several recent structural and biochemical studies suggest that Ptc functions as a cation-driven sterol transporter and that one Hh ligand binds a Ptc dimer to block the transporter activity of Ptc [47–55]. Cholesterol and its derivatives such as 24, 25-epoxycholesterol have been implicated as endogenous ligands for Smo [56–59]. Binding of these sterols to the extracellular cysteine-rich domain (CRD) and/or seven transmembrane helices of Smo triggers conformational changes in these domains, leading to Smo activation [57, 60–64].

Ptc restricts the accessibility of sterols to Smo and thus inhibits Smo activation in the primary cilium (Fig. 2) [59, 65–67]. A recent study revealed that DHCR7 and CYP7A1, which synthesize cholesterol and oxysterol respectively, are located near the ciliary base to modulate Hh pathway activation, and that their ciliary localization is regulated by Hh [68]. Binding of Hh to Ptc inhibits its sterol transporter activity and promotes its ciliary exit in a manner depending on the Smurf family of E3 ubiquitin ligases, allowing Smo to be activated and accumulated in the primary cilium [65, 66, 69, 70]. In *Drosophila*, Hh induces trafficking of Ptc away and Smo toward the plasma membrane through the Smurf family of E3 ubiquitin ligases [71–74]. Although ciliary trafficking of Smo is also regulated by ubiquitin in mammalian cells, the E3 ligase(s) remains obscured [75]. Hh induces sumoylation of Smo in both *Drosophila* and mammalian cells and at least in *Drosophila*, sumoylation regulates Smo trafficking by antagonizing its ubiquitination through the recruitment of a deubiquitinating enzyme USP8/UBPY [76, 77].

Hh induces phosphorylation of Smo C-terminal intracellular tail (C-tail) by multiple kinases including PKA (*Drosophila* only), CK1 family kinases CK1 $\alpha$  and CK1 $\gamma$ , and Gprk2/GRK2 (Fig. 1B) [78–85]. Phosphorylation of Smo promotes its cell surface/ciliary accumulation and induces conformational change and dimerization of its C-tail that adopts an open and active conformation after Hh stimulation [78, 81, 83, 86]. The mechanism by which phosphorylation promotes Smo ciliary localization remains unknown; in *Drosophila* however, Smo phosphorylation promotes its cell surface accumulation by inhibiting the recruitment of the Smurf family of E3 ubiquitin ligases and a Cul4-DDB1-G $\beta$  E3 ubiquitin ligase complex [74, 87]. Hh signaling also increases the production of phosphatidylinositol 4-phosphate that binds Smo C-tail to promote Smo phosphorylation and cell surface/ciliary localization [88]. A recent study identified a membrane-tethered ubiquitination system consisting of a transmembrane protein MEGF8 and a RING superfamily E3 ligase MGRN1 that regulates mammalian Hh signaling and heart development by catalyzing the ubiquitination and degradation of Smo [89].

## 2.3. Hh signal transduction from Smo to Gli

Smo is a class F GPCR family member and can engage in G $\alpha_i$  activation in both *Drosophila* and mammalian cells [62, 90, 91]. Although G $\alpha_i$  is required for the expression of Hh target gene *decapentaplegic* (*dpp*) in *Drosophila* wing imaginal discs [91], whether G $\alpha_i$  plays a

physiological role in canonical Hh signaling in mammals has remained unclear. In both *Drosophila* and mammals, Smo acts through its C-tail to regulate Gli/Ci. In *Drosophila*, Smo C-tail (SmoC) directly interacts with a multi-protein signaling complex containing Ci, the kinesin-like protein Costal 2 (Cos2) and the Ser/Thr protein kinase Fused (Fu) [92–95], and this interaction depends on the phosphorylation of SmoC by PKA, CK1 and GRK2, which triggers a conformational switch of SmoC to expose a binding pocket for Cos2-Fu [86, 96]. In addition, phosphorylation induces dimerization/oligomerization of SmoC, leading to clustering of the bound Cos2-Fu that triggers trans-autophosphorylation and activation of Fu kinase [96–98]. In the absence of Hh, Cos2-Fu serves as a molecular scaffold to bring Ci in close proximity to its kinases PKA, GSK3 and CK1, leading to efficient phosphorylation of multiple sites in its C-terminal region to generate a degron for the modular E3 ubiquitin ligase containing Slimb/ $\beta$ TRCP [99–104]. SCF<sup>Slimb/ $\beta$ TRCP</sup> catalyzes the ubiquitination of Ci, followed by proteasome-mediated partial degradation to generate a C-terminally truncated Ci<sup>R</sup> (Fig. 1B) [101, 104, 105]. In the presence of Hh, activated Smo attenuates the Cos2-Ci-PKA-CK1 complex formation [103, 106], thus inhibiting Ci phosphorylation, ubiquitination, and proteolytic processing. However, blocking Ci processing is insufficient to convert accumulated full-length Ci (Ci<sup>F</sup>) into Ci<sup>A</sup> because the activity of Ci<sup>F</sup> is blocked by additional mechanisms including cytoplasmic retention by Cos2 and proteolysis-independent inhibition by PKA phosphorylation [107–110]. Furthermore, Ci is inhibited by forming a stoichiometric complex with Sufu [111], which inhibits Ci nuclear localization and blocks the recruitment of Ci coactivator CBP even after Ci enters the nucleus [112, 113]. Previous genetic studies suggest that Fu activates Ci by antagonizing Sufu, leading to the maturation of Ci<sup>F</sup> into a labile Ci<sup>A</sup> [111]. A recent study demonstrated that Fu activated Ci by directly phosphorylating Ci on multiple sites, priming its further phosphorylation by CK1 on adjacent sites, and that these phosphorylation events altered Ci/Sufu interaction (Fig. 1B) [114]. Ci<sup>A</sup> is short-lived and is ubiquitinated and degraded by a modular E3 ubiquitin ligase containing HIB/SPOP, leading to termination of Hh pathway activity (Fig. 1B) [115–117].

Compared to *Drosophila* Hh signal transduction pathway, the immediate signaling events downstream of Smo are poorly understood although phosphorylation of mammalian Smo (mSmo) C-tail by CK1 and GRK2 has been implicated in Shh signal transduction in a manner analogous to *Drosophila* Smo (dSmo) [83, 86, 118]. Nevertheless, the mechanism for Ci<sup>R</sup>/Gli<sup>R</sup> production is conserved between *Drosophila* and mammals and involves the phosphorylation of Gli2 and Gli3 by PKA, GSK3 and CK1, followed by SCF<sup>Slimb/ $\beta$ TRCP</sup>-mediated proteolytic processing [119–121]. A PDD (processing determinant domain) domain located between the Zn-finger DNA binding and Slimb/ $\beta$ -TRCP binding domains of Ci/Gli appears to be critical for proteasome-mediated degradation that selectively removes its C-terminal half [122]. Deletion of this domain from Ci blocks the production of Ci<sup>R</sup> and renders complete degradation of Ci [123]. Gli3 is processed more efficiently than Gli2 into a truncated repressor form probably due to a more potent PDD, and Gli1 lacks a PDD and does not exhibit repressor activity [124]. The generation of Gli<sup>R</sup> requires Sufu as well as Kif7, the mammalian homolog of Cos2, and Sufu recruits GSK3 for efficient Gli3 processing [125–132]. Similar to inhibition of Ci<sup>A</sup> by PKA [107], there is evidence that PKA can inhibit the activity of Gli<sup>A</sup> by directly phosphorylating Gli2 [133, 134].

In addition, association of Sufu with Gli inhibits Gli<sup>A</sup> activity, which is reversed upon Hh stimulation [34, 114, 130, 135, 136]. A recent study revealed that an Itch/ $\beta$ -arrestin2 complex binds Sufu to induce its Lys63-linked polyubiquitylation, which increases its association with Gli3 and converts the full-length Gli3 into a repressor of Hh signaling, and that several Sufu mutants found in medulloblastoma patients are insensitive to Itch [137]. Another study showed that the E3 ubiquitin ligase SCF<sup>Fbx117</sup> binds Sufu and promotes its poly-ubiquitination and degradation, leading to increased Hh pathway activity, and that Fbx117 expression is high in Shh subgroup of medulloblastoma [138]. Sufu also has a positivity role by protecting full-length Gli from SPOP-mediated degradation [129, 139], which explains why loss of Sufu resulted in less dramatic Hh pathway activation phenotypes than loss of Ptc [140, 141].

The production of Gli<sup>R</sup> depends on the primary cilia (Fig. 2)[10]. Consistent with this, the key cellular components responsible for Gli processing including PKA and proteasome are enriched at the ciliary base [133, 142–144]. In addition, Gpr161, a GPCR receptor coupled to G $\alpha$ s is localized in the primary cilia, which is responsible for the local activation of PKA [145]. As a consequence, in Gpr161 mutant mice, Gli<sup>R</sup> production was blocked, leading to phenotypes indicative of constitutive Hh pathway activation [145]. Hh induces the ciliary exit of Gpr161 through  $\beta$ -arrestin, which is recruitment to Gpr161 after it is phosphorylated by GRK2 [146]. In contrast to Gpr161, another ciliary localized orphan GPCR Gpr175 positively modulates Hh signaling by decreasing cAMP and Gli3 repressor levels via G $\alpha$ i [147], suggesting that multiple ciliary localized GPCRs may regulate local cAMP and PKA activity to govern Gli<sup>R</sup> production.

In response to Hh stimulation, Smo is accumulated along the entire length of primary cilia while the intracellular signaling components including Gli proteins, Sufu, and Kif7 are enriched at the tip of primary cilia where full-length Gli is thought to be converted into Gli<sup>A</sup> and subsequently dissociates from Sufu and translocates to the nucleus (Fig. 2) [65, 127–129, 135, 148–150]. Like Cos2, Kif7 also interacts with Gli and has both positive and negative roles in Hh signaling [126–128]. A recent study suggested that Kif7 binds the plus end of microtubules to organize the formation of cilium tip compartment, thereby indirectly influencing Gli activation [151]. However, the mechanism by which Gli<sup>F</sup> is converted into Gli<sup>A</sup> at the ciliary tip has remained a mystery. In zebrafish, Fu is required for the conversion of Gli<sup>F</sup> into Gli<sup>A</sup> [152]; however, knockout of the Fu homolog Stk36 in mice did not cause any discernible defects Hh signaling during embryonic development [153, 154]. A recent study revealed that another Fu-related kinase Ulk3 acted semi-redundantly with Stk36 to promote Gli activation in cultured cells by directly phosphorylating a conserved site in the N-terminal region of Gli proteins [114]. In addition, phosphorylation of Gli by Ulk3/Stk36 requires Gli ciliary localization, which depends on the PY-NLS/karyopherin-beta2 nuclear import system [155]. It would be important to determine whether Ulk3 is localized to the primary cilia in response to Hh and whether Kif7 is required for the activation of Ulk3.

Additional components acting between Smo and Gli to transduce Hh signal in mammalian cells have been identified. Dlg5 was identified as a Smo interacting protein that localizes to the ciliary base where it is associated with Kif7 [156]. Dlg5 is specifically required for the formation of Gli<sup>A</sup> but not for the inhibition of Gli<sup>R</sup> by Hh; consistent with this,

depletion of Dlg5 did not affect Gpr161 ciliary exit but reduced ciliary tip localization of Kif7 and Gli2 in response to Hh [156]. EVC and EVC2, the products of human disease genes responsible for the Ellis-van Creveld syndrome characterized by impaired Hh signaling in skeletal, cardiac, and orofacial tissues [157, 158], form a complex with Smo in response to Hh [159–161]. Interestingly, EVC2-Smo is localized in the proximal region of primary cilia, which is required for Hh pathway activation [159]. Inactivation of EVC/EVC2 did not affect Smo phosphorylation and ciliary accumulation but impaired Gli ciliary localization and activation, suggesting that EVC/EVC2 acts downstream or in parallel with Smo [159–161]. Protein purification and mass spectrometry identified two ciliary proteins EFCAB7 and IQCE that formed a complex with EVC-EVC2 to regulate Hh signaling by tethering the EVC-EVC2 complex to the base of primary cilia [162]. Centrosome-localized aPKC functions as a positive regulator of Hh signaling by phosphorylating Gli1 to increase its DNA binding activity and association with HDAC1 in basal cell carcinomas (BCCs) [163, 164]. Other kinases, including DYRK1, DYRK2, MAP3K10, Cdc211, Ulk3, S6K1, Plk1, and CK2 have also been identified to influence Gli activity [165–172]. Beside phosphorylation, other PTMs including ubiquitination, sumoylation, acetylation, and methylation also modulate Gli activity and Hh signaling [173–177]. A recent study revealed that a lamina-associated polypeptide 2 (LAP2) nuclear chaperoning system regulates Gli1 movement between the nuclear lamina and nucleoplasm to achieve optimal Gli1 activation in BCCs [178].

#### 2.4. Gli action in the nucleus

Numerous studies have revealed the differential employment of Gli<sup>A</sup> and Gli<sup>R</sup> in various contexts during mammalian embryogenesis [2]. While Gli<sup>A</sup> levels are central to cancer formation [173, 179], the involvement of Gli<sup>R</sup> in repressing cancer has been implicated by studies linking primary cilia to Hh pathway-dependent tumorigenesis [180, 181]. Several genome-wide studies on Gli target genes revealed that although many target promoters contain a Gli binding consensus related to the sequence TGGGTGGTC, other target genes may not require this consensus sequence for Gli-dependent transcriptional regulation [182, 183]. Hh signaling promotes tumorigenesis by regulating genes involved in cell growth, proliferation and survival including Myc, CycD1 and D2, and Bcl2 [184]. Several cofactors have been implicated in the transcriptional regulation by Gli proteins, including the SAP18-mSin3 corepressor complex [185], the chromatin remodeling factor Brg [186], NuRD corepressor complex subunit p66b and Myc-binding protein Mycbp [187], the chromatin-associated SAFB-like transcription modulator SLTM [188], the H3K27me<sub>3</sub>-specific demethylases Jmjd3/Kdm6b [189], and BET bromodomain proteins [190]. Although Hh target genes vary depending on developmental contexts, Hh signaling universally activate Ptch1 and Gli1 in all cell types, which function as negative and positive feedback mechanisms, respectively. Therefore, Ptch1 and Gli1 upregulation serves as a signature for mammalian Hh pathway activation.

### 3. Hedgehog signaling in cancer

The Hh pathway has been implicated in the maintenance of stem/progenitor cells in many adult tissues, including the epithelia of many internal organs and brain [4, 191]. Not



surprisingly, abnormal Hh pathway activation in many of these tissues is associated with tumorigenesis. Mutations in Hh pathway components, including *Ptch1*, *Smo*, and *Sufu* leading to constitutive and ligand-independent pathway activation, have been linked to basal cell carcinoma, medulloblastoma, and several other types of cancer (Fig. 3A)[192]. By contrast, ligand-dependent pathway activation has been implicated in a wide variety of cancers including gastrointestinal tumors, prostate and pancreatic cancers (Fig. 3B) [191]. These tumors generally do not harbor Hh pathway mutations and their growth can be effectively suppressed by various pathway inhibitors, such as Hh-neutralizing antibodies or *Smo* antagonists. These findings lead to the model that Hh ligands produced by these tumors and/or their stromal environment act on tumors to maintain stem/progenitor cells in the tumors in an undifferentiated, proliferative state. However, increasing evidence suggests that Hh signaling can also act in a paracrine fashion to promote the tumor microenvironment essential for tumor growth [193]. Thus, Hh signaling activity can influence tumor growth through both cell autonomous (acting on cancer cells) and non-autonomous (acting on stromal cells) mechanisms (Fig. 3B).

### 3.1. Hh signaling in basal cell carcinoma

Basal cell carcinoma (BCC) is the most common skin cancer in western world. Aberrant Hh signaling was initially linked to BCC by the findings that germline mutations in *Ptch1* are the culprits of Gorlin syndrome (also called nevoid BCC syndrome or NBCCS), which is characterized by predisposition of BCCs as well as other cancers [194, 195]. Subsequently, somatic mutations in *Ptch1* and *Smo* were frequently identified in sporadic BCCs [196, 197]. Both germline and somatic mutations in *Sufu* were also identified in BCC albeit at much lower frequency compared to *Ptch1* mutations [197]. The causal relationship of aberrant Hh signaling in BCC was established by studies showing that either loss of *Ptch1* and gain of *Smo* drive BCC in mice [196, 198]. Lineage tracing experiments indicated that oncogenic activation of *Smo* in the interfollicular epidermis stem cells (IFE-SCs) but not hair follicle bulge stem cells induced BCC, identifying the interfollicular stem cells as the origin of BCC in mice [199]. Further study revealed that *Smo* activation in IFE-SCs drove more potent tumor growth than *Smo* activation in progenitor (PCs) cells because SCs have higher capability of symmetric self-renewing divisions and higher P53-dependent resistance to cell death compared with PCs [200].

### 3.2. Hh signaling and Medulloblastoma

Another type of cancer that Hh pathway mutations are frequently identified is medulloblastoma (MB), the most common malignant pediatric brain tumor. A major subtype of MBs (Shh group) is characterized by abnormal Hh pathway activation due to mutations in *Ptch1*, *Smo*, and *Sufu* or amplification of *Gli1*, *Gli2*, and *N-Myc* [201–203]. Studies of *Ptch1* heterozygous Gorlin syndrome patients, as well as analogous mutant mice, have strongly suggested that Hh pathway activation is critical for the transformation of granule cell precursors (GPCs) [204]. Experimental Hh pathway activation either by *Ptch1* deletion or overexpression an oncogenic form of *Smo* in mouse neural stem cells or restricted neural progenitors revealed that medulloblastoma is derived from lineage restricted GPCs [205, 206]. Furthermore, single cell RNA-seq of developing mouse cerebellum showed that childhood SHH-MB transcriptionally mirrors the granule cell lineage, suggesting that

GCPs are also the cell of origin of Shh-MB in humans [207]. Another recent single-cell transcriptome analysis of Shh-MB identified Olig2-expressing glial progenitors as transit-amplifying cells at the tumorigenic onset and showed that Olig2 promotes tumorigenesis by activating oncogenic networks including Hippo-Yap/Taz and Aurora-A/MycN pathways, implying Olig2-driven oncogenic networks as potential therapeutic targets for Shh-MB [208].

Although Sufu mutations are found in human MBs, loss of Sufu is insufficient to induce MBs in mice [209]. However, a recent study showed that deletion of SPOP together with Sufu in mice resulted in MB formation in a manner depending on Gli2 [139]. Further analysis revealed that the bHLH transcription factor Atoh1, which is a target gene of Gli2, cooperates with Gli2 to activate core Shh MB signature genes [139]. Germline mutations in *Gpr161* as well as *GNAS*, which encodes G $\alpha$ s, have been identified in infant-onset Shh-MB [210, 211]. Deletion of *Gpr161* or *GNAS* in mice is sufficient to induce Shh-MB, highlighting the importance of the cAMP-PKA axis in restricting Shh-MB [212, 213]. A recent large-scale cancer genomic study identified frequent somatic mutations in the splicing factor U1 snRNA that resulted in inactivation of *Ptch1* or activation of *Gli2* and *CyclinD2* in about 50% of SHHMB [214]. Another recent study identified loss-of-function mutations in the elongation factor ELP-1 leading to translation deregulation in 14% pediatric Shh-MB patients, suggesting that disruption of mRNA translation and protein homeostasis is a novel pathological mechanism for Shh-MB [215].

### 3.3. Hh signaling in other cancers

Beside BCC and MB, Hh pathway mutations have also been identified, albeit at much lower frequency, in several other cancers including rhabdomyosarcoma [216, 217], the most common pediatric soft tissue sarcoma, esophageal squamous cell carcinoma [218], and meningioma [219]. Furthermore, abnormal Hh pathway activation in the absence of pathway mutations has been implicated in a wide range of human malignancies including but not limited to lung cancer [220–222], prostate cancer [223–225], pancreatic [226–228], colon cancer [229], bladder cancer [230, 231], esophageal cancer [226, 232, 233], gastric cancer [226, 234, 235], liver cancer [236–238], melanomas [239, 240], gliomas [241–243], breast cancer [244–247], ovarian cancer [248], and hematological malignancies [249–251]. In most cases, elevated Hh ligand expression has been observed and transgenic expression of Hh in mice is sufficient to promote tumorigenesis [233, 252]; therefore, these cancers are classified as “ligand-dependent” group (Fig. 3B). Initial studies suggest Hh acts in an autocrine fashion to promote the growth of tumors in the ligand-dependent group [220, 226]; however, several later studies using xenograft models revealed that tumor cells did not activate Hh pathway but rather stromal cells that surround the tumor cells responded to Hh and that deletion of Smo in the stromal microenvironment inhibited tumor growth, suggesting that tumor-derived Hh acts on tumor microenvironment to promote tumor growth in a paracrine fashion [193, 253, 254].

An early study suggested that Hh-Gli signaling acts in human colon cancer cells to promote their growth, recurrence, metastasis and stem cell survival and expansion [229]. Later studies using mouse models of intestinal tumors revealed context dependent role of Hh



signaling in stroma cells [255, 256]. In a mouse model of colitis-associated colon cancer, stroma-specific Hh activation markedly reduced the tumor growth and blocked progression of advanced neoplasms partly via the modulation of BMP signaling whereas attenuation of Hh signaling accelerated tumorigenesis [256]. By contrast, Hh pathway activation by Sufu reduction in gut mesenchyme promoted intestinal tumorigenesis in *APC<sup>Min/-</sup>* mice in part by modulating the expression of niche signals such as Wnts whereas reduction of Hh pathway activity by removing one copy of *Gli2* suppressed the tumorigenesis [257]. Hence, stromal Hh signaling can either restrain or promote intestinal tumorigenesis depending on the context. Similarly, evidence for both autocrine and paracrine mechanisms for lung cancer and prostate cancer exists [193, 222, 224, 258, 259], suggesting that the mode of Hh action may vary depending on cancer subtypes and/or stages.

Tumor suppressor function of paracrine Hh signaling has also been observed in other cancers including bladder and pancreatic cancers. Shh-expressed basal cells are thought to be the cell of origin from which bladder cancer is derived [260]. Despite its initial presence in the cancer cell of origin, Shh expression is invariably lost during progression to invasive urothelial carcinoma, implying that Hh signaling could be incompatible with cancer progression [261]. In mouse models of bladder cancer, deletion of *Smo* from stroma dramatically accelerated cancer progression and reduced survival time due to reduced stromal expression of BMPs, which are urothelial differentiation factors, suggesting that Hh signaling restrains bladder cancer progression by stimulating stromal production of differentiation factors [261]. Whether Hh plays a similar role in human bladder cancer awaits to be determined.

Pancreatic ductal adenocarcinoma (PDA) is associated with upregulation of Shh and preclinical studies suggest that pharmacologic blockade of Hh signaling with *Smo* antagonists or Shh ligand-blocking antibody can reduce the growth and distant metastases of human pancreatic cancer xenografts [193, 226, 262, 263]. Activation of *Gli2* can cooperate with Ras signaling to drive the formation of pancreatic intraepithelial neoplasia, the earliest stages of human PDA tumorigenesis [228]. In addition, elevated *Gli2* is observed in basal-like PDA cell lines and human specimens and correlates with poor prognosis, and *Gli2*-mediated basal-like subtype switching can rescue PDA cell viability after KRAS ablation [264]. However, deletion of *Smo* in the pancreatic epithelium does not affect PDA pathogenesis in a genetically engineered mouse model of pancreatic cancer [265]. Nevertheless, *Gli1*, which is regulated by TGF $\beta$  and KRAS, is required both for survival and for the KRAS-mediated transformed phenotype of cultured PDA cancer cells [265]. Furthermore, *Smo*-independent elevation of *Gli1* and *Gli2* has been shown to drive chemotherapy resistance in PDA through upregulating *Sox2* [266], suggesting that non-canonical and *Smo*-independent activation of *Gli* in cancer cells is essential for PDA progression and drug resistance. Modulation of Hh signaling in stroma revealed that stromal response to Hedgehog signaling restrains rather than promoting pancreatic cancer progression [267]. Consistent with this finding, high SHH levels correlate with the well-differentiated classical subtype of PDA and longer disease-free survival of PDA patients [264]. These findings may explain why clinical trial using *Smo* inhibitor to treat pancreatic cancer patient failed [268].

## 4. Targeting Hh pathway for cancer treatment

The importance of Hh signaling in a wide range of human cancers has stimulated great interest in targeting this pathway for cancer therapy. Unbiased screens using various pathway readouts as well as rational designs based on the understanding of the Hh signaling mechanism have yielded a garden-variety of pathway antagonists that block Hh signal transduction at different steps (Fig. 4), including Hh acyltransferase inhibitors [269], small molecule Hh inhibitors [270–272], Smo inhibitors [273–277], and Gli inhibitors [278–280]. Multiple pathway inhibitors have entered clinical trials for many solid tumors and blood cancers and several Smo inhibitors have been approved by FDA for the treatment of advanced and metastatic BCC [281].

### 4.1. Multiple strategies for Hh pathway inhibition

Being a GPCR family protein, Smo is the most prominent and druggable target in the Hh pathway. The first identified Smo antagonist is cyclopamine, a plant-derived steroidal alkaloid that inhibits Hh signaling by binding to Smo [273, 274]. Since its discovery, cyclopamine has been employed as a main Hh pathway blocker by numerous studies to test the requirement of Hh signaling for cancer cell growth. Nevertheless, treating cells with high dose of cyclopamine can lead to cytotoxicity that could compromise the interpretation of the results. Later, more potent and specific Smo inhibitors have been developed and entered clinic trials, which include GDC-0449/Vismodegib [282], LDE225/Sonidegib [283], IPI-926/Saridegib [284], itraconazole [285], and PF-04449913/Glasdegib [286]. However, cancer cells treated with Smo inhibitors can quickly develop resistance. In addition, tumors bearing constitutive Hh pathway activity independent of Smo are insensitive to Smo inhibitors, making it necessary to develop alternative approaches to block the Hh pathway downstream of Smo.

Cell-based screens identified several compounds such as GANT61 and HP-1 as well as natural products including Arcyriaflavin C, Physalin F and Glabrescione B that selectively inhibit Gli-dependent transcription [278–280, 287]. In addition, Arsenic trioxide (ATO) can reduce the stability and ciliary accumulation of GLI2 and bind Gli1 to inhibit its transcription activity [288, 289]. A recent screen for small molecules that inhibit endogenous Gli activity in *Sufu*<sup>-/-</sup> MEFs identified a family of bicyclic imidazolium derivatives that can inhibit Gli-dependent transcription without affecting its ciliary trafficking or proteolytic processing [290].

Targeting the mechanisms that regulate Gli can also inhibit Gli-dependent transcription and tumorigenesis. For example, modulating the cAMP-PKA axis by rolipram, which elevates cAMP levels by selectively inhibiting phosphodiesterase-4 (PDE-4), inhibited Gli activity in granule neuron precursors [212]. Inhibitors of Gli activation kinases including aPKC and Ulk3 can attenuate Gli transcriptional activity and inhibit tumor growth [163, 291]. As CK1 acts downstream of PKA to phosphorylate Gli and promote its instability, pyrvinium, an FDA-approved anti-pinworm compound that is a potent CK1 agonist, can inhibit Hh pathway activity downstream of Smo and Sufu [292]. A phosphoproteomics study identified CK2 as critical for the stabilization and transcriptional activity of Gli2 in granule neuron precursors and demonstrated that CK2 inhibitors such as CX-4945 can decrease the viability

of primary Shh-type MB patient cells in culture and block the growth of smo inhibitor-resistant MB tumors in mice [171]. A gain-of-function screen identified Bcl-2 family proteins as inhibitors of Sufu [293]. Bcl-2 proteins directly bind Sufu to disrupt its inhibition of Gli activity essential for tumor growth and small molecule BH3-mimetics can inhibit Gli by interfering with Bcl-2/Sufu interaction [293]. Another study found that BET domain proteins such as BRD4 bind *Gli1* and *Gli2* gene promoters to promote their transcription and that a small molecule inhibitor of BRD family proteins JQ1 can inhibit Hh-driven tumors including BCC and MB even when these tumors harbor genetic lesions rendering them resistant to Smo inhibitors [190]. Finally, ciliary localization and activation of Gli proteins are regulated by the PY-NLS/Karyopherin- $\beta$ 2 (Kap $\beta$ 2) nuclear import machinery and inhibition of Kap $\beta$ 2 by a small peptide M9M can attenuate Gli activation [155, 294, 295].

#### 4.2. Hh pathway inhibitors in the clinics

Hh pathway inhibitors including multiple Smo antagonists such as vismodegib, sonidegib, and glasdegib have entered clinical trials for BCCs and basal cell nevus syndrome [296–299], pediatric and adult MBs [300–302], other solid cancers including small cell lung cancers [303, 304], pancreatic cancers [305–307], ovarian cancer [308], prostate cancer [309, 310], and colorectal cancer [311], as well as hematological malignancies such as acute myeloid leukemia (AML) [312–317]. The Gli inhibitor arsenic trioxide (ATO) is currently in clinical trials for treatment of Smo inhibitor-resistant BCC as well as other cancers including glioma and neuroblastoma [318]. The Smo inhibitors vismodegib and sonidegib have been approved by FDA for the treatment of locally advanced BCC in 2012 and 2015, respectively, with vismodegib also approved for metastatic BCC [281, 319]. In 2018, FDA approved glasdegib in combination with low dose cytarabine (LDAC) for the treatment of newly diagnosed AML or high-grade myelodysplastic syndrome in elderly patients or patients not suitable for intensive chemotherapy [320]. However, Hh pathway inhibitors have limited single agent activity in unselected patients with other types of cancers in early phase clinical trials [318].

#### 4.3. Mechanisms of therapeutic resistance

Despite the high potency of Smo inhibitors in preventing BCC and MB progression in animal models and human patients, acquired drug resistance rapidly emerged, which limits long-term efficacy [321, 322]. Both genetic alterations in Smo and compensatory mechanisms downstream of Smo can contribute to the resistance to Smo inhibition. Genomic analyses of resistant tumors identified point mutations in Smo drug-binding pocket or Smo-activating mutations that account for ~ 50% of the resistant BCCs [321, 323, 324]. Genomic loss of Sufu and amplification of Gli2 or the Hh target gene Cyclin D1 have also been observed in the resistant cancer cells [324–326]. Noncanonical mechanisms that activate Gli through PI3K, aPKC, and the SRF-MLK complex have also been shown to contribute to resistance to Hh pathway inhibitors, suggesting that targeting the corresponding noncanonical pathways could be strategies to overcome cancer resistance to Smo inhibitors [163, 325, 327]. A recent study found that JNK/AP-1 and TGF $\beta$ /Smad3 pathways cooperatively activate the nuclear myocardin-related transcription factor (nMRTF),

which binds SRF and acts as a coactivator for Gli1 in resistant BCCs [328], suggesting that a combinatory treatment with Smo and AP-1 inhibitors could be beneficial.

In addition to genetic and epigenetic alternations leading to persistent Gli activation that allows tumors to evade Smo inhibition, lineage plasticity and cell fate switch also contribute to drug resistance and tumor reoccurrence. In several BCC patients treated with vismodegib, invasive squamous cell carcinoma emerged from BCC [329, 330], and in one case, the recurrent lymph-node squamous cell carcinoma harbored new mutations in genes that are commonly mutated in cutaneous squamous cell carcinoma including Notch1/2 and KMT2C/MLL3, indicating that these mutations may drive BCC to SCC switch and resistance to vismodegib treatment [330]. Other studies revealed that SCCs derived from BCCs in patients treated with vismodegib activated the RAS/MAPK pathway and that loss of primary cilia appeared to be responsible for the switch from Hh to RAS/MAPK pathway in resistant tumors [331, 332]. Two recent studies using mouse models of BCC showed that Smo inhibition drove tumor evolution from Hh-dependent to Wnt-dependent tumors, suggesting that dual pathway inhibition of Hh and Wnt signaling could be a clinically relevant strategy for overcoming tumor relapse in BCC [333, 334].

Finally, Hh pathway components have been implicated in chemotherapy resistance of cancer. For example, one study suggested that high levels of Ptc in cancer cells may contribute to chemotherapy resistance by promoting multidrug efflux [335]. Another study showed that, in a phase II clinic trial of treating AML patient with ribavirin, Gli1 and the UDP glucuronosyltransferase (UGT1A) family of enzymes are elevated in resistant cells [336]. Further experiments demonstrated that Gli1 is sufficient to drive UGT1A-dependent glucuronidation of ribavirin and thus drug resistance, and that genetic or pharmacological inhibition of Gli1 can overcome drug resistance [336].

## 5. Conclusion

Hh signaling pathway represents one of the best examples of how basic research initiated from model organisms such as fruit fly can be translated into novel strategies for cancer treatment. Despite decades of intensive investigation, Hh signal transduction mechanism is still not fully understood. For example, there are gaps between Smo and Gli in the mammalian pathway and the precise mechanism by which primary cilia orchestrate Hh signal transduction has remained poorly understood. In addition, how Gli proteins are regulated in the nucleus and how they influence chromatin landscape or communicate with basal transcriptional machinery have largely unexplored. Understanding the detailed molecular and biochemical mechanisms of these processes may provide new avenues for targeting the Hh pathway downstream of Smo. Although many Smo antagonists have entered clinic trial and several have been proved by FDA for cancer treatment, most of the downstream pathway inhibitors including small molecule Gli inhibitors are not suitable for clinical trial due to cytotoxicity or poor bioavailability; therefore, developing clinically actionable pathway inhibitors downstream of Smo has remained a high priority. This is an urgent issue because cancer patients treated with Smo inhibitors can quickly develop drug resistance and many cancers are driven by Smo-independent Gli activation. To overcome potential bypass mechanism or drug resistance, combinatory use to Smo inhibitors with

other pathway inhibitors could provide a more effective way to treat cancer. Although Smo inhibitors have been effective in treating ligand-independent cancers bearing Ptch1 or Smo mutations, early clinical trials using Smo inhibitors to treat ligand-dependent cancers where no Hh pathway mutations have been identified were disappointing. In the future clinical trials, cancer patients need to be stratified with better pathway biomarkers to ensure that their cancers are driven by activated Smo. In addition, better tumor models such as patient-derived xenograft (PDX) models and patient-derived tumor organoids can be used to test whether Hh pathway inhibitors, either alone or in combination with other pathway inhibitors, can inhibit tumor growth.

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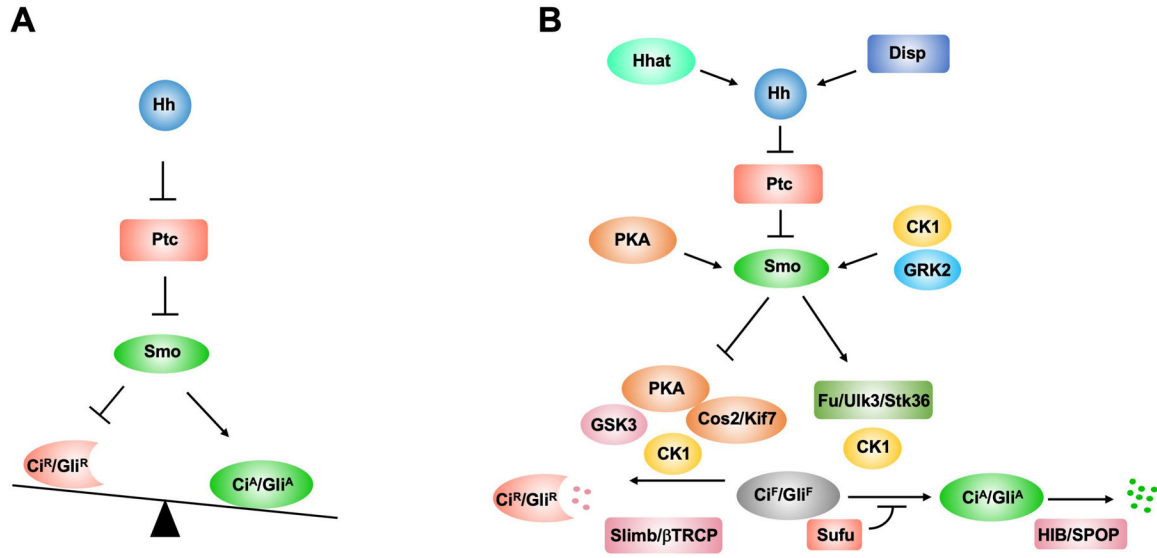
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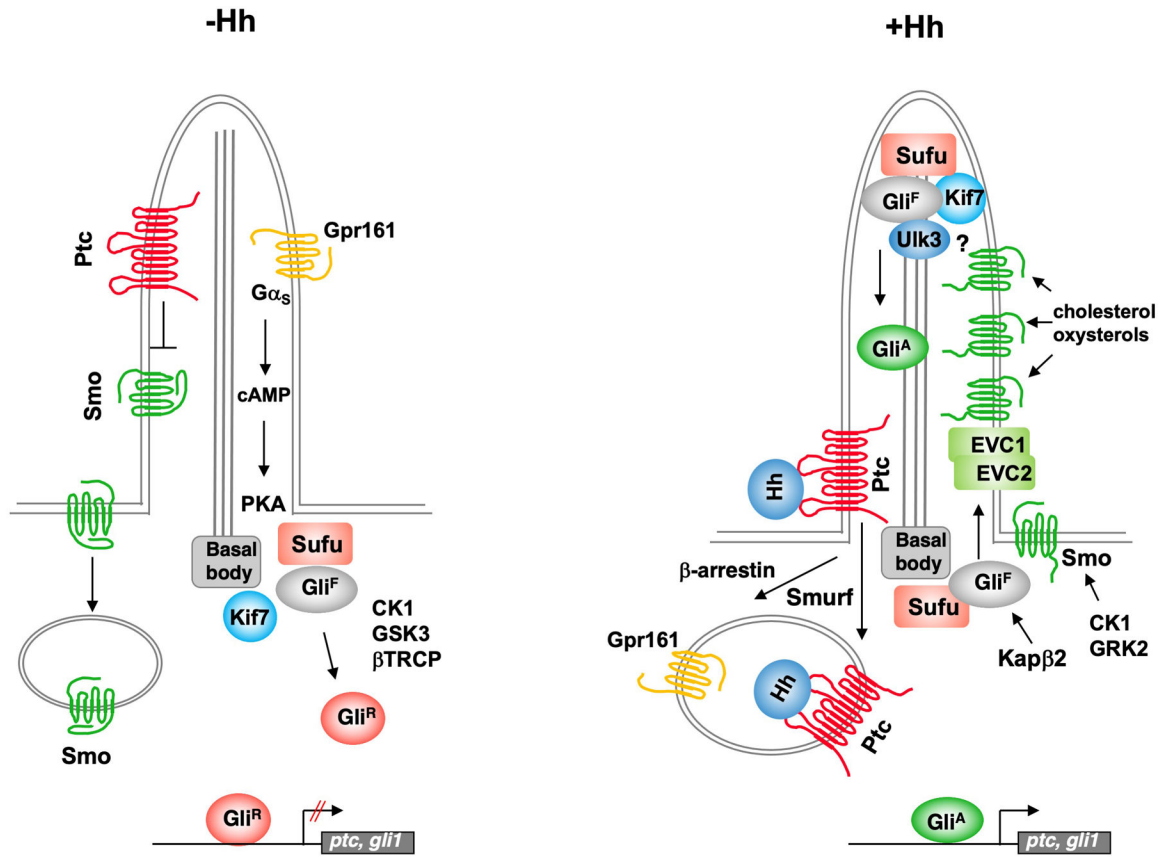
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**Figure 1. The conserved Hh signal transduction pathway**

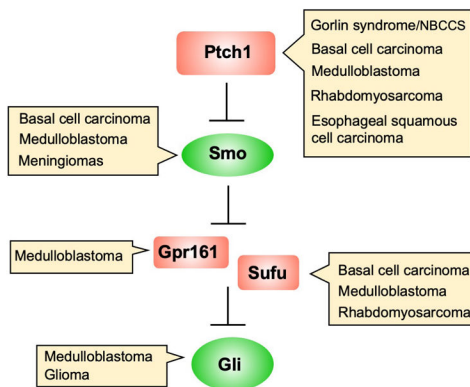
(A). A simplified scheme of Hh pathway in which Hh releases the inhibition of Smo by Ptc and activated Smo alter the balance between the activator (Ci<sup>A</sup>/Gli<sup>A</sup>) and repressor Ci<sup>R</sup>/Gli<sup>R</sup>) forms of Ci/Gli. (B) Hhat catalyzes the palmitoylation of Hh and Disp is involved in the secretion of lipidated Hh. Hh induces phosphorylation of Smo by multiple kinases including PKA (Drosophila only), CK1 and GRK2, which is required for Smo activation. In the absence of Hh, full length Ci/Gli is phosphorylated by multiple kinases including PKA, GSK3 and CK1 and subsequently targeted to ubiquitin/proteasome-mediated proteolysis through Slimb/βTRCP to generate Ci<sup>R</sup>/Gli<sup>R</sup>. Smo inhibits Ci/Gli phosphorylation by PKA/GSK3/CK1 to block the production of Ci<sup>R</sup>/Gli<sup>R</sup>. Furthermore, high levels of Hh stimulate Fu/Ulk3/Stk36-mediated phosphorylation Ci/Gli to promote the formation of Ci<sup>A</sup>/Gli<sup>A</sup> by antagonizing Sufu. HIB/SPOP targets Ci<sup>A</sup>/Gli<sup>A</sup> for degradation, which is attenuated by CK1. Cos2/Kif7 plays dual role by promoting the formation of Ci<sup>R</sup>/Gli<sup>R</sup> in the absence of Hh but Ci<sup>A</sup>/Gli<sup>A</sup> in the presence of Hh.



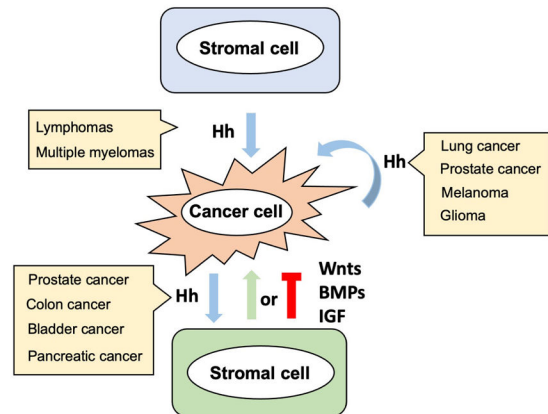
**Figure 2. Mammalian Hh signaling in primary cilia.**

In the absence of Hh, Ptc localizes to the primary cilia and inhibits Smo ciliary accumulation. Gpr161, a ciliary localized GPCR, is required for PKA activation. Kif7 is localized at ciliary base and both Sufu and Kif 7 are required for Gli<sup>R</sup> production. In the presence of Hh, Hh inhibits Ptc activity and promotes its ciliary removal depending on Smurf and, subsequently the accumulation of Smo into primary cilia depending on phosphorylation by CK1 and GRK2. Hh also promotes Gpr161 ciliary exit through Smo and β-arrestin. Smo is activated in the primary cilia by cholesterol and its derivatives oxysterols. Kif7, Gli and Sufu are localized at the ciliary tip where Gli<sup>F</sup> is converted into Gli<sup>A</sup>. The Evc1/Evc2 complex is localized near the ciliary base where it regulates Hh signal transduction downstream or in parallel to Smo in certain contexts. The nuclear import receptor Kapβ2 is required for Gli ciliary entry. See text for details.

**A Ligand-independent group**



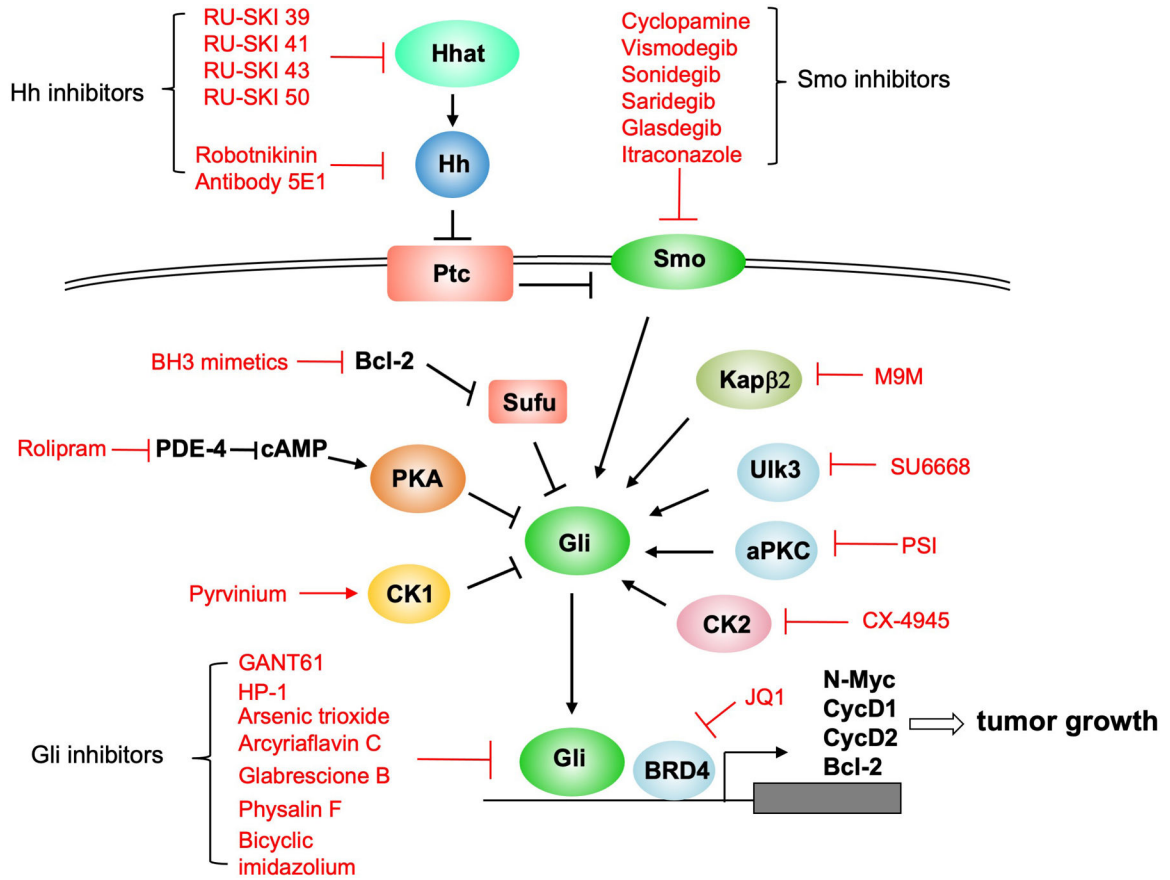
**B Ligand-dependent group**



**Figure 3. Hh signaling in cancer**

(A) In ligand-independent group of cancers, Hh pathway components are mutated or amplified (as in the case of Gli), leading constitutive pathway activation. (B) In ligand-dependent group of cancers, Hh derived from cancer cells act on stromal cells or cancer cells to regulate cancer progression. Cancer cells can also be regulated by Hh derived from stromal cells as in the case of lymphomas and multiple myelomas.





**Figure 4. Multiple strategies for inhibiting Hh signal transduction pathway**

Hh signal transduction can be blocked at multiple steps including Hh inhibitors that either inhibit the activity of Hh acyltransferase (Hhat) or directly bind and inhibit Hh, Smo inhibitors, Gli inhibitors as well as pathway modulators that inhibit Gli by regulating its kinases or binding partners. See text for details.