



Research Article

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# Role of Tumor Microenvironment in Cancer Stem Cell and Clinical Application

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## Abstract

Cancer stem cells can differentiate and self-renew. Therefore, they are resistant to traditional therapies and cause cancer relapse. The most determinant factor for the CSCs resistance is the tumor microenvironment, which contains many aspects to prevent CSCs from being eradicated. In this review, we will introduce different aspects according to the tumor microenvironment (TME) like hypoxia, which allows CSCs to flourish in the TME; CAF, which contributes to the self-renewal quality of CSCs; immune cells, which could potentially incapacitate cancer cells and decrease the stemness of CSCs, and different major signaling pathways that help with the proliferation and survival of CSCs. We also conclude with the major clinical trials involved in each of the signaling pathways, which presents possibilities to assist with therapy.

**Keywords:** Cancer stem cell, Tumor Microenvironment, Hypoxia, Cancer-associated fibroblasts, Immune cells, Notch, WNT, Hedgehog.

**Abbreviations:** CSCs: Cancer stem cells; EMT: Epithelial Mesenchymal Transition; TME: Tumor microenvironment; HIF: Hypoxia-inducible factors; CAF: Cancer-associated Fibroblasts; MDSCs: myeloid-derived suppressor cells; TAMs: tumor-associated macrophages; TANs: tumor-associated neutrophils; BCC: Basal cell carcinoma; ECM: Extracellular matrix; ROS: reactive oxygen species; VEGF: Vascular endothelial growth factor; CCL2: C-C motif ligand 2; LOX: lysyl oxidase; nk cells: natural killer cells; mAbs: monoclonal antibodies; CML: chronic myeloid leukaemia; TKI: tyrosine kinase inhibitors; MM: Multiple myeloid; CLL: chronic lymphocytic leukemia.

## Introduction

Cancer is an illness without a completely effective cure yet. Statistically, in 2020, the four major cancer types alone resulted in the deaths of approximately 606,520 people in the US [1]. Not to mention, a tremendous number of patients are undergoing therapeutic resistance and even for “recovered” patients, which are mostly caused by cancer stem cells. Cancer stem cells (CSCs) are characterized by self-renewal and differentiation abilities [2]. It is tricky to identify CSCs. However, surface markers, like CD111 and CD44, allow the identification of CSCs [3]. Additionally, functional assays include ALDH1 and Hoechst Exclusion Assay, which have also been used to detect CSCs; all the markers present the possibility to eradicate CSCs [4].

The first origin theory for CSCs derivation is from stem cells, and another possibility is the development from progenitor cells, which are more abundant while still containing the ability of self-renew [5]. CSCs could also be developed from differentiated cells by de-differentiation. CSCs have been known to be resistant to traditional therapies like chemotherapy and radiotherapy [6]. There are many contributing factors including Epithelial Mesenchymal Transition (EMT), Detox proteins and multidrug resistance, dormancy, resistance to DNA damage-induced cell death, tumor environment, epigenetics, and signaling pathways [7]. For example, CSCs have the ability to proliferate slower to avoid being targeted by chemotherapy, which targets faster proliferating cells [8].



Possible solutions include immunotherapy, which targets the use of tumor antigens to affect the balance between apoptosis and proliferation [9]. However, immunosuppression presents conflicts to the success of immunotherapy, and furthermore, there are inhibitor therapy and nanotherapy [10]. Preclinical and clinical trials are being held for the testing of additional therapies. Investigating how CSCs are therapeutic-resistant and its functions will aid in the success of a therapy.

## Hypoxia

Hypoxic regions, along with acidic and necrotic regions are authentication marks of hostile solid tumors [11]. Specifically, interactions between the hypoxic niche and CSCs lead to therapeutic resistance, tumor heterogeneity, and stemness maintenance [12]. Hypoxic stress normally happens along with nutrient restriction and acidic stress, which stimulates the growth the subpopulations of cells that are adapted to survive in nutrient-restricted conditions [13]. In turn, the cells encourage shifts toward aerobic glycolysis and glutamine-mediated fatty acid production [14]. Because of this, CSCs can live and flourish in the nutrient-deprived regions, giving rise to stem cell characteristics.<sup>5</sup>

When exposed to hypoxic stress, CSCs are enriched which leads to the resistance to traditional therapies.<sup>6</sup> Distinct resistance mechanisms have been proposed, like the induction of Hypoxia-inducible factors (HIF) signaling that ends with signaling pathways [15]. HIFs, such as HIF-1 and HIF-2, regulate the effects of hypoxia [16]. HIF-1 is globally expressed in multiple tissues when responding to acute hypoxia; narrowing in, HIF1a can activate Notch and WNT signaling directly, as well as regulating metabolic adaptations after nutrient deprivation [17]. In addition, HIF-2 is able to maintain stemness characteristics in neuro and glioblastoma cells, while remaining elevated under chronic hypoxia. Also, it upregulates key transcription factors controlling stem cell maintenance [18].

Since CSCs have a high capacity to thrive in nutrient-deprived regions, stemness programs are promoted along with phenotypes of dormancy and migration.<sup>11</sup> CSCs express high levels of HIF-1 in hypoxic conditions, which in turn elevates angiogenesis and VEGF expression in the region [19]. CSCs which reside in hypoxia also demonstrate different immunologic features and interactions within the niche. VEGF has many functions, including assisting PD-L1 expression and subduing the dendritic cell function, showing that therapies displaying T cell and dendritic cells will not be as effective when targeting the hypoxic niche [20]. CSCs that are in contact with hypoxia can increase and keep other niches. Hypoxic CSCs can migrate using upregulation of epithelial-mesenchymal signaling, or EMT signaling [21]. Their migration changes in adhesion receptor expression. Because of this, hypoxia furthers therapeutic resistance. They are distinctly placed to avoid the

therapeutic stressors contrasted with non-stem tumor cells in the hypoxic microenvironment because of the lower manufacturing of reactive oxygen species, or ROS [22].

## CAF

CAFs, or cancer-associated fibroblasts, are a cellular subtype being studied to create new target therapies along with anticipating patients' results. CAFs reside in the CSC microenvironment with differentiated neoplastic cells and normal cells [23]. They play an important role in the TME (tumor microenvironment) by being in a complex system of tumor-stroma evolution and angiogenesis [24]. Reciprocal crosstalk between CSCs and the cells mentioned above contributes to self-renewal ability. It is also possible that CAFs stem from resident fibroblast activation, as well as adipocytes, endothelial, and pericytes conversion [25]. In addition, CSCs secrete various cytokines and ligands that change ordinary fibroblasts to CAFs to reinforce self-renewal and proliferation. CAFs supply molecules such as soluble factors and proteases to assist in ECM synthesis or remodeling. Meanwhile, it also provides cytokines, growth factors, and chemokines [26]. A tight crosstalk with the CSCs concerns the CAF secreted factors that direct their plasticity, chemoresistance, and self-renewal capacity. The factors in turn regulate the CSCs stemness characteristics to support and induce aggressiveness.<sup>25</sup> Amid the different cytokines and growth factors that CAFs release, many studies emphasized the role of IL-6 and IL-8 in maintaining the stem-like characteristics of cancer cells and the induction of tumor growth, chemoresistance, and metastasis formation [27].

Additionally, research has shown that hyperactive NF-κB signaling drives the subset of CAFs while sustaining the cancer stemness by discharging IL6 and IL8 [28]. In line with this observation, Korkaya et al. have shown that in the subpopulation of resistant BC cells, the inflammatory loop IL-6/STAT-3/NF-κB can be activated by the trastuzumab treatment, which corresponds with the of CSCs [29]. Therapeutically, the management of anti-IL-6 receptor antibody returns the stemness phenotypes of tumor cells [30]. Aside from cytokines, CAFs also secrete growth factors, an example being hepatocyte growth factors, or HGF, which induces invasiveness of stem cells [31]. As an example, in hepatocellular carcinoma, activation of MET/FRA1/HEY1 cataract was used by HGF to sustain cancer cell stemness [32]. Consequently, HGF and CCL2, both examples of growth factors secreted by CAFs, upregulate the stem-like characteristics by the WNT and Notch, key stemness regulators.<sup>32</sup> Finally, in addition to cytokines and growth factors, CAFs secrete chemokine proteins, an example being SDF-1 [33]. It is highly exhibited on the surface of CSC, and it associates with CXCR4, its receptor, allowing the regulation of stem phenotype by the activation of PI3K/AKT and Wnt/b-catenin signaling pathways

[34]. It was found that CXCR4+ cells were more likely to achieve the stem properties and phenotypes compared to CXCR4- cells, while proliferation of CD44+ and CD24- BC cells is also boosted [35]. Another example of a chemokine, CCL2, assists CSC self-renewal that initiates NOTCH signaling pathway [12].

The key role of CAFs in the maintenance of CSC and drug disorderliness allows the utilization of therapeutic strategies. Blocking CAF and crosstalk from CSCs can be used to increase patients' survival. A new subpopulation of CAFs, CD10+ and GPR77+, was recognized and corresponds highly with decreased patient survival in different cancers [36]. Additionally, some *in vitro* experiments emphasized that CAFs assure a CSC reservoir in distinct tumors that increase stem marker expressions such as CD44, Sox2, and Bmi-1, assist CSC pool expansion, and self-renewal abilities [37]. Medium conditioned by CAF encouraged the tumorigenic behavior and the belligerence shown by CSCs [38].

### Immune Cells

A feature of cancer cells is the ability to lead infiltrating immune cells to protumorigenic and immunosuppressive conditions. Suppression of adaptive immunity can be caused by the polarization and activation of cells like myeloid-derived suppressor cells (MDSCs), tumor-associated neutrophils (TANs), tumor-associated macrophages (TAMs), and T cells, which impacts cell fate along with survival. These different kinds of immune cells can stimulate the dedifferentiation process of CSCs. Zoomed in, the induction of stemness was related to reduced anti-cancer immune cells like CD8+ T cells, polarization of infiltrating macrophages, B cells, and natural killer cells. The phenotypic plasticity displayed in CSCs can increase cancer hallmarks because of their ability to transdifferentiate into fibroblasts, pericytes, and endothelial cells, meaning it assists in tumor angiogenesis, inflammation, and cell niche development. Barring of immune cells from the TME has been related with inaccurate diagnosis in the bulk of cancers. When accounting for 21 solid cancer types, the exclusion of immune cells was shown to connect with the presence of stemness. Increase of stemness correlates with higher intratumoral heterogeneity, with the possibility of shielding antigenic clones from the immune system [39].

CSCs are known for recruiting and dividing TAMs, which originate from bone-marrow-derived macrophages, or BMDMs and local tissue inhabitant macrophages, which source from progenitors and hematopoietic stem cells. The recruitment is propelled by many different chemokines that are produced by macrophages, cancer cells, or other stromal cells, like C-C motif ligand 2 (CCL2), lysyl oxidase (LOX), or CCL3 [40]. In addition to the TAM's characteristics, because of their substantial plasticity and diversity, their populations can be diverged between two groups,

the M1 phenotype that's "classically activated" or the M2 phenotype, which is "alternatively activated". Microglia and macrophages are recruited to tumor sites where they acquire amoeboid morphology while adopting an M2 tumor-promoting phenotype, which in turn contributes to the immunosuppressive tumor environment [41]. When low levels of IFN- $\gamma$  and high levels of IL-10 are secreted by M2 TAMs, microglia behave like a potent Treg cell and supports suppression of immunity in the glioma environment. TAMs is closely related with the STAT3 pathways [42]. For instance, in pancreatic cancer, TAMs were discovered to assist CSC function with STAT3. In addition, TAM adhesion and immunosuppressive role in gliomas is positively correlated with STAT3 mediated vascular cell adhesion protein-1 expression [43].

Myeloid derived suppressor cells are a heterogeneous population of undeveloped myeloid cells composed of myeloid progenitors and precursors of granulocytes, macrophages, and dendritic cells. Recent studies have shown that when myeloid populations are expanded, they can sensitize tumors to traditional therapies [44]. The position of these populations has received a lot of attention in terms of comprehending protumorigenic immune cell function. For example, STAT3 in cancer cells can be activated by MDSC-derived interleukin-23, and the inhibition of MDSC by depletion or antibody blockage (anti-IL-23) can sensitize androgen deprivation therapy in autochthonous models. Similar results are found in pancreatic cancer [45]. CSC-derived exosomes can increase the survival of suppressive neutrophils that encourage cancer growth, which correlates with the discovery of the lack of natural killer (nk) cells. When there are surface activating receptors present without any signs of inhibiting receptors, nk cells can directly lyse MHC-I-deficient tumor cells or other pathogens. In the usual condition, binding surface inhibitory receptors that have HLA class I antigens inhibits the activation of nk cells. The purpose of the antigens is to maintain homeostasis and to defend non pathological cells [46].

Immunotherapy has recently surfaced as a possible successful strategy for cancer treatment. Its effectiveness is because cancer cells usually upregulate immune-inhibitory cell surface signals like PD-L1, which is a programmed death ligand, to elude immune-mediated killing [47]. This suggests that checkpoint blockade could be a potent procedure for eliminating the subfraction. Immune checkpoint therapy anchors blocking antibodies in opposition to these inhibitory molecules, which in turn derepress the tumor's immune response. CSCs present in pancreatic cancer upregulate CD47 that allows the evasion of innate immune killing, which makes them a pertinent target for the CD47 blocking antibodies by increasing TAM1 population [48]. Targeting TANs and/or TAMs increase the sensitivity to chemotherapy both in *in vivo* and preclinical models [49]. In addition, CSCs urge resistance to

adoptive T cell transfer, referring to the engineer of patient-derived T cells to target a certain cancer antigen and create an immune response after re-transplant [50]. The findings of a population of CSCs in squamous cell carcinoma favorably eluded T cells by expressing CD80, which caused the fatigue and relapse of T cells suggesting that the potency of immunotherapy in targeting cancer cells with “stemness” differs by tissue and specific strategy. Because of immunotherapy’s recent surfacing, the effect of heterogeneous cancer cell populations on the clinical strategies is not fully comprehended yet. This means that a critical area for future study is studying the aggressive CSC populations and how they may elude immunotherapy with resistance [51].

## Signaling pathway

### Notch Signaling

Notch signaling is a crucial factor of stem cell preservation. It has been observed that Notch signaling ligand Jag1 presented in the vascular niche in cancer cells activate Notch signaling [52]. More specifically, Jag1 takes part in stem cell proliferation as well as stem cell niche formation in intestinal cancers models, which are absent of APC; an interesting observation about Jag1 is that it supports hair follicle stem cells proliferation when expressed by Tregs in a non-tumoral context [53]. These properties of Notch signaling pathway could increase stemness features in neighbor cells in cancer where TME cells express Jag1 [54]. In addition, recent studies proved that Notch signaling in mammary gland macrophages can be activated by DII1, which is derived from mammary stem cells [55]. This in turn fortifies mammary gland stem cells self-renewal by macrophage derived Wnt ligands [54].

Cell lineage specification in developing lymphocytes as well as the marginal zone’s regulation of B lymphocyte subsets involves Notch signaling [56]. In addition, Notch signaling is also involved in the differentiation of different cells, including helper, Treg, lymphoid, and dendritic cells. Notch signaling is important in many aspects [57]. For example, it regulates the main component of the anti-tumor immune function, the CD8+ cytotoxic T cell [58]. However, some functions of Notch signaling, such as instances in CD8+ T cells derived from colon cancer patients, need context and has the possibility of decreasing PD-1 expression to increase cytotoxic activity [59]. Furthermore, treatment that uses DII1, a multivalent protein to accelerate the reduction of tumor growth supports the role of Notch signaling to sustain antitumoral T lymphocyte activity by enhancing the antigen-specific cytotoxicity as well as evoking lymphocyte T differentiation [60]. In addition, Notch signaling is essential to regulate different elements of the immunosuppressive environment, with TAMs as an example [61].

Additional studies displayed that inducing the M1-macrophage phenotype involves Notch signaling. Macrophages lacking Notch signaling decrease the presentation activity of antigen [62]. When Notch is activated by force, expression of N1ICD suppresses tumor growth by revoking the function of TAM; in turn, TAM displays a transcriptomic signature connected to the Notch pathway [60].

Aberrant Notch signaling has been recognized in different types of cancer. The Notch pathway’s pathogenic role potentially depends on the tumor type. In terms of clinical oncology, the inferences of the Notch signaling pathway complexity and diversity are a double-edged sword [63]. Initially, when the Notch pathway is targeted, it has the possibility to affect numerous cell types other than mature tumor cells and CSCs at the same, such as vascular endothelial cells and immune cells [64]. There are potential outcomes that turn out to be advantages, like the inhibition of angiogenesis, but there could also be drawbacks, including the toxicities or the repression of anticancer immunity [63]. To successfully develop therapeutic agents to target the Notch pathway, a complete comprehension of the mechanisms of the Notch signaling’s roles in certain cancers in addition to the utilization and development of mechanism-based combination regimens is required [65]. Currently, researchers have developed various divisions of Notch pathway inhibitors that have different targets and mechanisms of action, along with several agents that are at different periods of clinical development [66]. The oldest and the biggest class of agents that target Notch signaling are  $\gamma$ -secretase, also known as GSIs, which block the Notch receptors’ second proteolysis and releases the intracellular domain.<sup>66</sup> For example, the merging of GSI MRK-003 and trastuzumab completely cures HER2-positive breast cancer in mouse models. An additional example is BMS-906024, which has been tested with non-small-cell lung cancer in preclinical models [67]. Another approach to hinder aberrant Notch signaling is to target Notch ligands that have monoclonal antibodies, or mAbs [68]. Treatment involving anti-DLL4 mAbs impedes the development of functional capillaries, which causes disordered angiogenesis along with the immediate effects of Notch signaling in tumor cells [69]. In amalgamation with numerous treatments, like immune-checkpoint inhibitors, assorted studies of demcizumab, a humanized anti-DLL4 IgG2 mAb, have been finished with currently unavailable results.<sup>69</sup> However, this agent is not in clinical development anymore. Besides DLL4, researchers are pursuing DLL3 as a therapeutic target in small-cell-lung cancer [70]. In addition to mAbs targeting Notch ligands, there are also some that target Notch receptors. For instance, brontoctuzumab, an anti-Notch1 mAb with an average antitumor activity has been demonstrated in clinical studies throughout the years [71].



## Wnt signaling

Wnt signaling makes up one of the dominant mechanisms that regulate tissue morphogenesis while repair and embryogenesis take place. In addition to that, Wnt signaling controls the downstream signaling cascade, whether canonical or non-canonical, consequently has effect on the cellular cytoskeleton, as well as transcriptional control of differentiation and proliferation, along with organelle dynamics [72]. The three dominant pathways the Wnt signaling cascade encompasses the canonical Wnt pathway, the non-canonical planar-cell polarity pathway, and the non-canonical Wnt-calcium pathway [73]. The first pathway involves activating a transcriptional transactivation complex that consists of T cell-specific transcription factor,  $\beta$ -catenin, and lymphoid enhancer-binding factor [74]. The latter pathway is independent of  $\beta$ -catenin, and assists in the regulation of the cytoskeleton of the cell. The final pathway mentioned is involved in the regulation of intracellular calcium levels.<sup>74</sup> Irregular Wnt signaling has relations with various cancers, like breast, colorectal, oral, lung, hematopoietic, and cervical cancer [75]. The canonical Wnt pathway is generally involved in the development of numerous human cancers. The interchanges between receptor complexes and Wnt ligands interferes with the  $\beta$ -catenin destruction complex, which in turn leads  $\beta$ -catenin to build up in the cytoplasm [76]. Afterwards, the TCF—LEF transcription complex is activated by  $\beta$ -catenin transfer to the nucleus, which leads to the expression of diverse genes with functions; for instance, the enhancement of migration and proliferation [77]. The  $\beta$ -catenin-independent pathway uses different ways of downstream signaling that could obtain a transcriptional response instead of the utilization of  $\beta$ -catenin-LEF or  $\beta$ -catenin-TCF.<sup>73</sup> Overall, these pathways are classified based on the type of Wnt receptor and co-receptor they utilize the paired downstream receptors. The regulation of cell polarity during morphogenesis involves the PCP pathway [78]. In addition, the Wnt or Ca<sup>2+</sup> pathway is associated with inflammation, cancerogenesis, and neurodegenerative diseases [79].

The effects of the Wnt signaling pathway are expanded to tumorigenesis by modulating the tumor microenvironment using fine crosstalk between infiltrating immune cells like leukocytes and transformed cells [72]. Wnt signaling and the crosstalk with different immune cells affect tumor progression both positively and negatively [72]. Beneficially, it assists in the renewal and maintenance of leukocytes. However, it induces immune tolerance, which restricts antitumor response [80]. Stromal cells of TME secretes growth factors that take part in the activation of Wnt signaling in the nucleus. For instance, hepatocyte growth factor, or HGF stimulation in colorectal cancer cells increases its separation from Met and  $\beta$ -catenin phosphorylation in tyrosine residue [80].

This results in the upregulation of  $\beta$ -catenin expression in the PI3-K dependent pathway.<sup>81</sup> Several studies have been conducted, which present the possibility that  $\beta$ -catenin and Met help cells enter the cell cycle and prevent apoptosis [82]. For instance, cervical cancer progression has been proved to be correlated with c-Met overexpression [83]. Consequently, crosstalk between Wnt or  $\beta$ -catenin in CRCs and TME-released HGF promotes tumor growth and invasion [84]. An additional growth factor involved in the activation of  $\beta$ -catenin signaling is the platelet-derived growth factor, or PDGF for short. A study on this growth factor by Yang et al. implies that release of  $\beta$ -catenin is caused by PDGF treatment [85]. Wnt signaling is also involved in EMT, and in turn promotes the maintenance of CSCs.  $\beta$ -catenin interacts with LEF or TCF in the nucleus and begins the EMT process [86]. Moreover, TGF- $\beta$  and EGF increases p68 phosphorylation at tyrosine and needs p68 for initiating EMT. Therefore, the p-68- $\beta$ -catenin axis could correspond to a common product for different signaling pathways [87].

Conclusively, dysregulated Wnt signaling contributes to tumorigenesis in many different types of cancers. Targeting Wnt pathway is of great interest in oncology research [88]. Studies over this have given rise to different inhibitors related to Wnt pathway that are able to interfere in important carcinogenesis features, such as metastasis and tumor invasiveness [89]. Pharmacological antagonists of the Wnt pathway can be classified into four dominant groups. First, there are the agents that target transmembrane proteins or ligands that participate in Wnt signaling [90]. Second, Porcupine inhibitors that intrude on the processing and secretion of Wnt ligands [91]. Third, the agents that start caspases or hinder tankyrase, which keep the multiprotein destruction complex intact, therefore advancing the degrading of  $\beta$ -catenin. The last category contains the downstream  $\beta$ -catenin-TCF-LEF-dependent transcription inhibitors [92]. Every single one of these categories has been clinically tested <sup>88</sup>.

In addition, experimental antagonists of Wnt pathway associated with transmembrane ligands or proteins comprise of mAbs, decoy receptors, ADCs, and inhibitors of small molecules with several targets [93]. However, not all of these have reached clinical development yet [94]. More specifically, an example of a neutralizing humanized mAb to DKK1, an extracellular protein, is DKN-01, which functions like an endogenous Wnt-signaling antagonist by promoting LRP5/6 co-receptors internalization [95]. Preliminary results of a phase I study which combines DKN-01 with paclitaxel (NCT02013154) demonstrated that the patients are well tolerated, with minor side effects [96]. Another recombinant Wnt ligand decoy receptor, Ipafricept, includes the extracellular human Fzd8 part combined with IgG1 Fc fragment. Studies demonstrated that Ipafricept works well in a FIH phase

I trial involving patients suffering from advanced-stage solid tumors [97]. This trial led to extended SD in 3 patients who had germ cell cancer or desmoid tumors. In addition, Foxy-5 is a Wnt5A-mimicking peptide that activates Fzd2 and 5, which leads to the activation of downstream Wnt5A signaling [98]. There is a possibility that Foxy-5 has antimetastatic activity by hindering migration and endothelial tumor cell invasion with the induction of Wnt5A signaling [99]. Some  $\beta$ -catenin inhibitors have been studied as single agents or part of combination regimens. For instance, peptidomimetic drug CWP232291 activates caspases, which leads to  $\beta$ -catenin degradation, therefore reducing  $\beta$ -catenin target genes survivin and cyclin D1 expression [100]. It is currently being tested as monotherapy for patients with recurrent and/or refractory myeloid malignancies (NCT01398462) and in combination with lenalidomide and dexamethasone in patients with Multiple Myeloma (NCT02426723).101

### Hedgehog Pathway

The Hedgehog Pathway, otherwise known as the HH signaling pathway, contributes greatly to embryonic development. In addition, the aberrant activity of the HH pathway in adult tissues is connected to several solid neoplasms [102]. Different HH isoforms like Indian hedgehog, Sonic hedgehog, or Desert hedgehog have been processed and released by HH ligand-secreting cells [103]. The isoforms, mainly using paracrine signaling, bind to Patched 1, or PTCH1, and PTCH2, which are transmembrane receptors, which leads to the suppression of the inhibitory activity against a transmembrane protein, Smoothed (SMO) [102].

In addition, HH signaling participates in early haematopoietic development, and potentially in non-malignant haematopoiesis and the general preservation of haematopoietic stem cells [104]. Research also suggests that aberrant HH signaling has rudimentary roles in maintaining and inducing leukemia stem cells (LSCs) in several hematological malignancies [105]. For instance, unusual HH signaling has been recognized in myeloid LSCs, while increased expression of HH pathway is connected to chemotherapy resistance in acute myeloid leukemia (AML) cell lines [106]. Patients diagnosed with AML show that GLI1 upregulation is associated with disease relapse, low overall survival rate, and drug resistance [104]. Also, HH signaling is activated in chronic myeloid leukemia (CML) and assists BCR-ABL1-positive LSC expansion [107]. These cells are also resistant to BCR-ABL1 tyrosine kinase inhibitors (TKI). Consequently, it is involved with the progression of CML [108].

Likewise, the HH pathway is activated in Multiple Myeloma (MM) stem cell compartment, but the clonal expansion of MM can be rescinded by HH pathway's pharmacological inhibition in MM cell lines 107. However, in chronic lymphocytic leukemia

(CLL), downstream HH pathway molecules such as GLI1, 2, BCL2, and SUFU expression are upregulated and connected to disease progression [109]. The activation of dysregulated HH pathway is also prominently involved in tumorigenesis of basal cell carcinoma, or shortly BCC, of the skin [110]. Almost all these tumors have constitutive ligand-independent HH pathway activation because mutations in PTCH1 leads to loss-of-function, while mutations in SMO leads to gain-of-function [111]. Paracrine or autocrine signaling that are dependent on ligands is another process of HH pathway activation. Aberrant HH signaling has been involved in a medulloblastoma tumor subtype, defined as SHH [112]. This mainly happens in young patients and causes about 30% of all medulloblastomas. Several studies have shown decrease in heterozygosity and somatic mutation of PTCH1, which is an HH pathway negative regulator in this subset of medulloblastomas [105].

The exploration of pharmacological agents that target the HH pathway in solid and hematological malignancies has regulatory approval [113]. However, it is still being investigated. HH pathway targets SMO, HH ligands, and GLI transcription factors, while GLI and SMO agents have been tested in clinical research [114]. Some direct cyclopamine-competitive SMO inhibitors include sonidegib and Vismodegib, which have been FDA approved for metastatic BCC treatment along with recurrent locally advanced BCC in patients who aren't going to participate in surgery or radiotherapy [109]. Therefore, sonidegib and vismodegib have supplied comparable overall response rate for patients with locally advanced BCC. In addition, another inhibitor, Taladegib, has shown effectiveness in patients suffering from advanced-stage BCC [115]. Mutations in SMO have been found in around half of SMO inhibitor resistant BCCs. These mutations comprise of factors that affect four ligand binding pocket residues that are rudimentary to SMO autoinhibition, which consequently results in activation of this receptor [116]. Targeting GLI transcription factors are a promising therapeutic option because the HH pathway downstream effectors can also increase the upregulation of genes assisting in proliferation and survival without depending on the canonical HH pathway [117]. Agents that target GLI mediated transcription like GANT58 and 61 are focused on overcoming tumor resistance to SMO inhibitors [114]. In addition to that, researchers have observed promising responses to HH pathway inhibitors in patients with SHH-subtype medulloblastoma [114]

### Conclusion

Overall, after analyzing different components in the tumor microenvironment of CSCs and their clinical applications, there is a deeper understanding established on this topic. Since CSCs lead

to therapy-resistant factors for cancer, these different clinical trials present possible solutions to overcome this dilemma. Different factors in the tumor microenvironment have been addressed to eliminate CSCs, which provide new insights to improve prognosis of treatment in cancer patients.

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