

Regulation of hematopoiesis and the hematopoietic stem cell niche by Wnt signaling pathways

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Hematopoietic stem cells (HSCs) are a rare population of cells that are responsible for life-long generation of blood cells of all lineages. In order to maintain their numbers, HSCs must establish a balance between the opposing cell fates of self-renewal (in which the ability to function as HSCs is retained) and initiation of hematopoietic differentiation. Multiple signaling pathways have been implicated in the regulation of HSC cell fate. One such set of pathways are those activated by the Wnt family of ligands. Wnt signaling pathways play a crucial role during embryogenesis and deregulation of these pathways has been implicated in the formation of solid tumors. Wnt signaling also plays a role in the regulation of stem cells from multiple tissues, such as embryonic, epidermal, and intestinal stem cells. However, the function of Wnt signaling in HSC biology is still controversial. In this review, we will discuss the basic characteristics of the adult HSC and its regulatory microenvironment, the “niche”, focusing on the regulation of the HSC and its niche by the Wnt signaling pathways.

Keywords: hematopoiesis, hematopoietic stem cell, Wnt proteins, osteoblast

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The hematopoietic stem cell

The function of the hematopoietic stem cell (HSC) is to initiate hematopoiesis, the process by which all mature blood cells, which have a limited life span, are continuously produced throughout the life of the organism. HSCs are the only bone marrow cells capable of differentiating into all blood cell lineages [1-3]. In the adult mouse, the frequency of HSCs is approximately 1 in 10 000 bone marrow cells (0.01%) [4-7]. Hematopoiesis is generally depicted as a hierarchical process (Figure 1) in which the HSC sits at the top of the hierarchy. HSCs differentiate into hematopoietic progenitor cells that are capable of exponential proliferation as well as continuing the process of differentiation. After terminal differentiation, the functional

cells of the hematopoietic system are generated. Terminally differentiated blood cells can be classified into myeloid and lymphoid cells. Myeloid cells include red blood cells, platelets, and cells responsible for cellular immunity such as macrophages and granulocytes. Lymphoid cells, which are involved in humoral immunity, are T, B, and natural killer cells. There are between 6 and 9×10^8 total cells (nucleated white blood cells and red blood cells) in the mouse bone marrow, a ratio greater than 10^4 bone marrow cells per single HSC [8].

The life span of differentiated hematopoietic cells can range from years in the case of T and B cells involved in immunological memory, to 3 months in the case of red blood cells, to days, in the case of granulocytes. Therefore, HSCs are constantly called upon to supply a steady stream of hematopoietic progenitors that can generate new hematopoietic cells. Given the massive rate of hematopoietic cell turnover (e.g., daily turnover in the human body is estimated to be 1×10^{12} cells [9]), there are not nearly enough HSCs to continuously replenish mature blood cells

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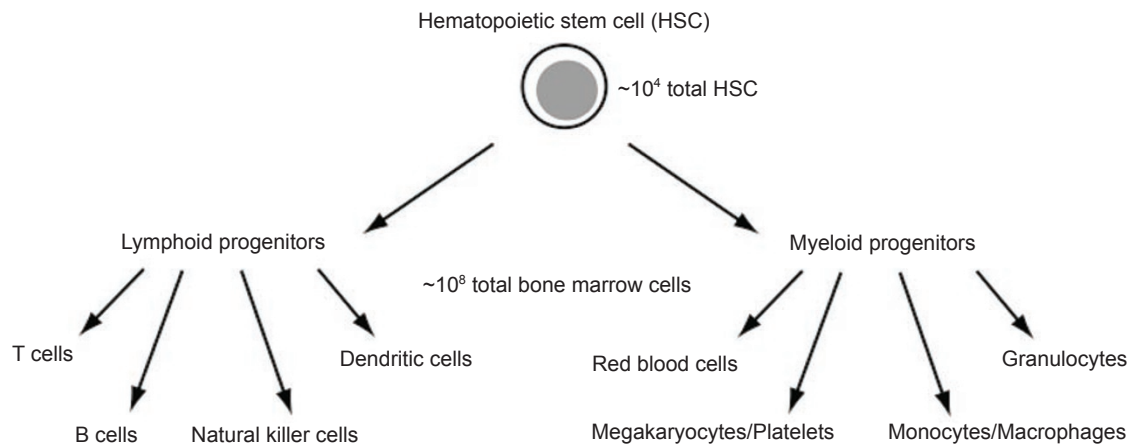


Figure 1 A simplified schematic diagram of the hematopoietic hierarchy. The hematopoietic stem cell (HSC) sits at the top of the hierarchy. Upon activation, the HSC is capable of differentiating into clonal progenitors that can expand exponentially as well as continue the process of differentiating. Hematopoietic cells are broadly divided into “lymphoid” and “myeloid cells”. Lymphoid cells include T cells, B cells, natural killer cells, and dendritic cells. Myeloid cells include red blood cells, platelets, monocytes/macrophages, and granulocytes (as well as other cell type such as eosinophils, mast cells, and basophils). A more detailed description of the initial stages of HSC differentiation is provided in Figure 2.

over a lifetime. Therefore, a stable pool of functional HSCs must be continuously maintained.

In order to do this, HSCs establish a balance between the processes of self-renewal, in which the daughter progeny of a dividing HSC retains the stem cell phenotype, and hematopoietic differentiation. It is proposed that the HSC achieves this balance by deciding between symmetric and asymmetric cell divisions. In symmetric division, the stem cell gives rise to identical daughter progeny, either both stem cells (self-renewal) or differentiating hematopoietic progenitors. In asymmetric cell division, the stem cell gives rise to one daughter stem cell and one daughter cell that differentiates. It is unknown whether the HSC undergoes asymmetric division *in vivo* although several *in vitro* studies have demonstrated using single cultured hematopoietic progenitors that up to 20% of the cell divisions from one cell to two cells are asymmetric [10-13]. There are examples of asymmetric stem cell division in vertebrates, notably in neural progenitor cells in the cortex [14] and in basal cells in fetal epidermis [15]. HSCs are generally quiescent, with 75% residing within the G_0 phase of the cell cycle at any one time [16]. It has been estimated that about 8% of HSCs in mice enter the cell cycle every day and that every cell in the HSC population has gone through the cell cycle at least once every 3 months [16]. Regulation of proliferation is a key mediator of HSC numbers as mice deficient in the cell cycle inhibitory protein p21 show increased HSC numbers [17].

The functional definition of an HSC is the ability to en-

graft lethally irradiated recipients (the radiation treatment destroys the host bone marrow) and establish long-term (e.g., after 16 weeks in mice) multi-lineage hematopoiesis [18]. In such an assay, the donor cells must be detectable after 16 weeks in order to rule out any contribution by hematopoietic progenitors in the graft. Furthermore, the donor-derived cells must be detectable in all lineages, myeloid and lymphoid. These criteria can be met even when a single cell is transplanted, in which case a single transplanted HSC is responsible for generating approximately 1×10^8 cells [4, 19-21].

HSCs can be prospectively isolated from whole bone marrow through the use of flow cytometry to sort HSCs based on cell-surface phenotype (Figure 2). The depletion of lineage-committed blood cells (T and B cells, macrophages, granulocytes, red blood cell precursors, etc.) from bone marrow leaves behind the lineage-negative, or lin^- , fraction which contains all HSCs and hematopoietic progenitors. In mice, the population of lin^- cells that highly express the cell surface proteins c-kit and Sca-1 (Lin^- , c-kit^{HI}, Sca-1^{HI} or KSL) contain all HSCs [22]. Additional cell surface proteins such as Thy1.1, IL-7R α , Flt3, CD150, and endoglin or the distinct dye-efflux profiles of Hoechst or Rhodamine can also be used to further enrich for HSCs [23-28]. The cell surface antigen CD34 can discriminate between long-term HSCs, which are CD34⁻, and short-term HSCs, which are CD34⁺ [29, 30]. This contrasts with human long-term HSCs, which are enriched in a cell population with a Lin^- , CD34⁺, CD38⁻ phenotype [31, 32].

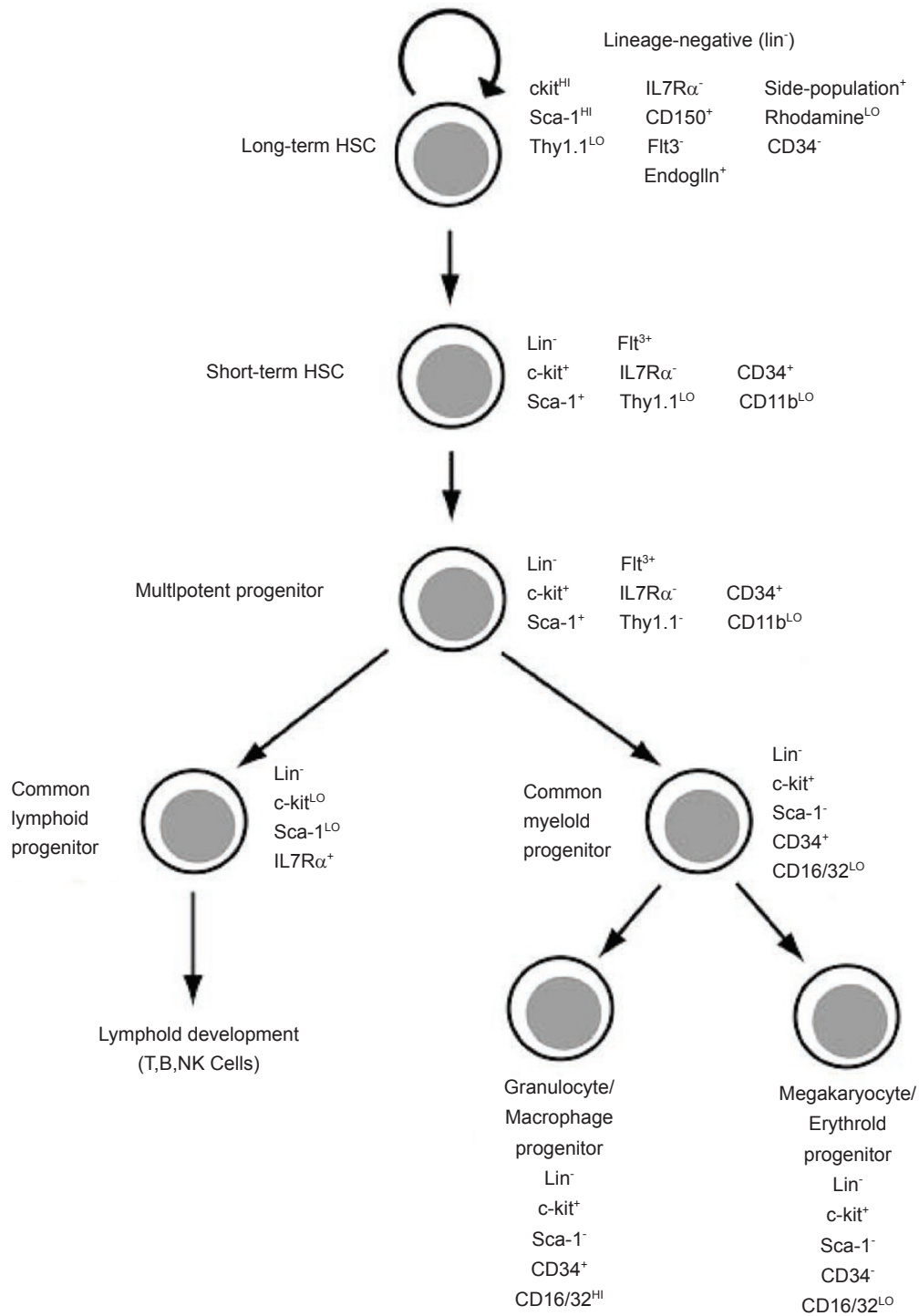


Figure 2 A model of the initial steps in hematopoiesis in adult mice along with some of the markers used to discriminate between HSCs and progenitors. “Side-population” refers to a distinct Hoechst efflux profile observed in long-term HSCs [27]. Long-term HSCs can be separated from short-term HSCs, which have limited self-renewal capacity (6-8 weeks) [23]. Multipotent progenitors are cells that can differentiate into all types of hematopoietic cells but have no self-renewal capability [156]. Common lymphoid progenitors can differentiate into all lymphoid lineages [24]. Common myeloid progenitors differentiate into progenitors that can differentiate into the granulocyte/macrophage and megakaryocyte/erythroid lineages, respectively [157]. The relationship between short-term HSCs, multipotent progenitors, and the oligopotent common lymphoid and myeloid progenitors is not definitively known and other studies have defined populations that fall outside those described in this figure (e.g., [158, 159]).

The ontogeny of HSCs is still a controversial topic (for an extensive discussion of this topic, please see Cumano and Godin [33]). During development, hematopoiesis takes place in different organs at different stages. The first stage of hematopoiesis, called primitive hematopoiesis, takes place in the blood islands (a distinct aggregation of cells in which erythrocytes are surrounded by endothelial vascular cells) of the extra-embryonic yolk sac starting at approximately 7.5 days-post-coitus (d.p.c.) in the mouse [34]. Primitive hematopoiesis produces primitive erythrocytes, which are nucleated and contain embryonic hemoglobin [35-37]. By d.p.c. 12 in the mouse, the fetal liver is the site of definitive hematopoiesis, which is marked by the appearance of functional HSCs capable of producing enucleated red blood cells, the full complement of myeloid cells, and at later time points, lymphoid cells [38-40]. HSCs from the fetal liver colonize the bone marrow (starting at approximately d.p.c. 16.0 in the mouse), which becomes the final primary site of definitive hematopoiesis [41].

Initially, it was postulated that hematopoietic cells from the yolk sac colonized later sites of hematopoiesis, such as the fetal liver. Recently, Samokhvalov *et al.* [42] used an *in vivo* model that traced the developmental lineage of labeled d.p.c. 7.5 yolk sac cells to demonstrate that these cells produced hematopoietic progeny in fetal and adult mice indicating that hematopoietic cells in the yolk sac contribute towards the establishment of definitive hematopoiesis. However, these studies do not exclude the possibility that there is *de novo* generation of adult HSCs at other tissue sites. Definitive HSCs (defined by the ability to repopulate adult recipients) were observed at d.p.c. 10.5 near the aorta in a mesoderm-derived domain of the developing embryo called the aorta-gonad mesonephros (AGM) region and in the placenta [43-45]. Since circulation is established around d.p.c. 8.5, it is unclear whether the yolk sac, AGM, and placenta represent three independent sites of HSC development or whether colonization of one site by another has occurred [46].

Wnt signaling pathways in hematopoiesis

The maintenance of HSC pool requires a complex set of signals. Due to their ability to regulate multiple types of stem cells, the signals transduced by the Wnt family of proteins have proven to be of great interest in the study of HSC biology. Wnt ligands are a family of secreted glycoproteins (19 different Wnt genes in the mouse and human genomes) that are critical for normal development [47]. Multiple *Wnt* genes are expressed in bone marrow tissue, including *Wnt2b*, *Wnt3a*, *Wnt5a* and *Wnt10b* [48-50]. Wnt ligands can activate multiple signaling pathways by binding to a member of the Frizzled family of receptors (10 different

Frizzled genes found in the mouse and human genomes) and the lipoprotein receptor-related protein (LRP) 5/6 coreceptors [51-53] (Figure 3). One Wnt signaling pathway, termed the canonical pathway, uses β -catenin as the critical signal transducer and is necessary for the formation of mesoderm, from which the hematopoietic system is derived [54]. In the absence of Wnt ligand binding, cytoplasmic β -catenin is sequestered in a multi-factor complex that includes the adenomatous polyposis coli (APC) tumor suppressor protein, the scaffold protein Axin, and glycogen synthase kinase-3 β (GSK-3 β) and casein kinase 1 (CK1) [55-58]. GSK-3 β and CK1 phosphorylate β -catenin, which is recognized by the β -transducin repeat-containing homolog protein (β -Trcp) [59, 60]. β -Trcp targets β -catenin for degradation by the ubiquitin pathway [61-63]. Wnt binding to Frizzled induces phosphorylation of LRP 5/6 by membrane-bound GSK-3 β and CK1 γ (as opposed to the cytosolic forms that phosphorylate β -catenin and target it for degradation), which recruits Axin to the membrane where it physically interacts with LRP5/6, disrupting the multi-factor complex, and leading to β -catenin stabilization [64-66]. The intracellular Dishevelled protein is necessary for the recruitment of Axin to the membrane [67]. Upon stabilization, β -catenin translocates to the nucleus where it interacts with members of the T-cell factor (TCF)/lymphoid enhancer factor (LEF) family of transcription factors to induce target gene expression [68-70].

Initial experiments that studied the role of Wnt signaling in hematopoiesis focused on the functions of specific Wnt ligands found in the bone marrow rather than on the signaling pathways that they induced. Hematopoietic progenitors from mouse fetal liver displayed a three- to four-fold increase in the ability to form colonies of hematopoietic cells *in vitro* when cultured with conditioned media containing Wnt5a [50]. A similar experiment performed with Lin^- , CD34 $^+$ human hematopoietic progenitors co-cultured with stromal cells transfected with *WNT2B*, *WNT5A*, or *WNT10B* cDNA showed a 1.4- to 1.8-fold increase in the frequency of primitive CD34 $^+$ cells *in vitro* [48]. Murdoch *et al.* [71] went on to show that injecting mice with Wnt5a-conditioned media prior to transplant of human umbilical cord blood cells increased engraftment more than three-fold.

Reya *et al.* [72] isolated Lin^- , c-kit $^{\text{HI}}$, Sca-1 $^{\text{HI}}$ and Thy1.1 $^{\text{LO}}$ (KTSL) cells from mice overexpressing the anti-apoptotic *BCL-2* gene and transduced them with a constitutively active form of β -catenin. This resulted in 20- to 48-fold *in vitro* expansion of KTSL cells for up to 2 months (compared to control KTSL cells which did not survive past 48 h). KTSL cells transduced with constitutively active β -catenin and cultured for 1 week engrafted lethally irradiated recipients, while untransduced cells did not engraft. Willert *et al.* [73] cultured single KTSL cells with recombinant Wnt3a,

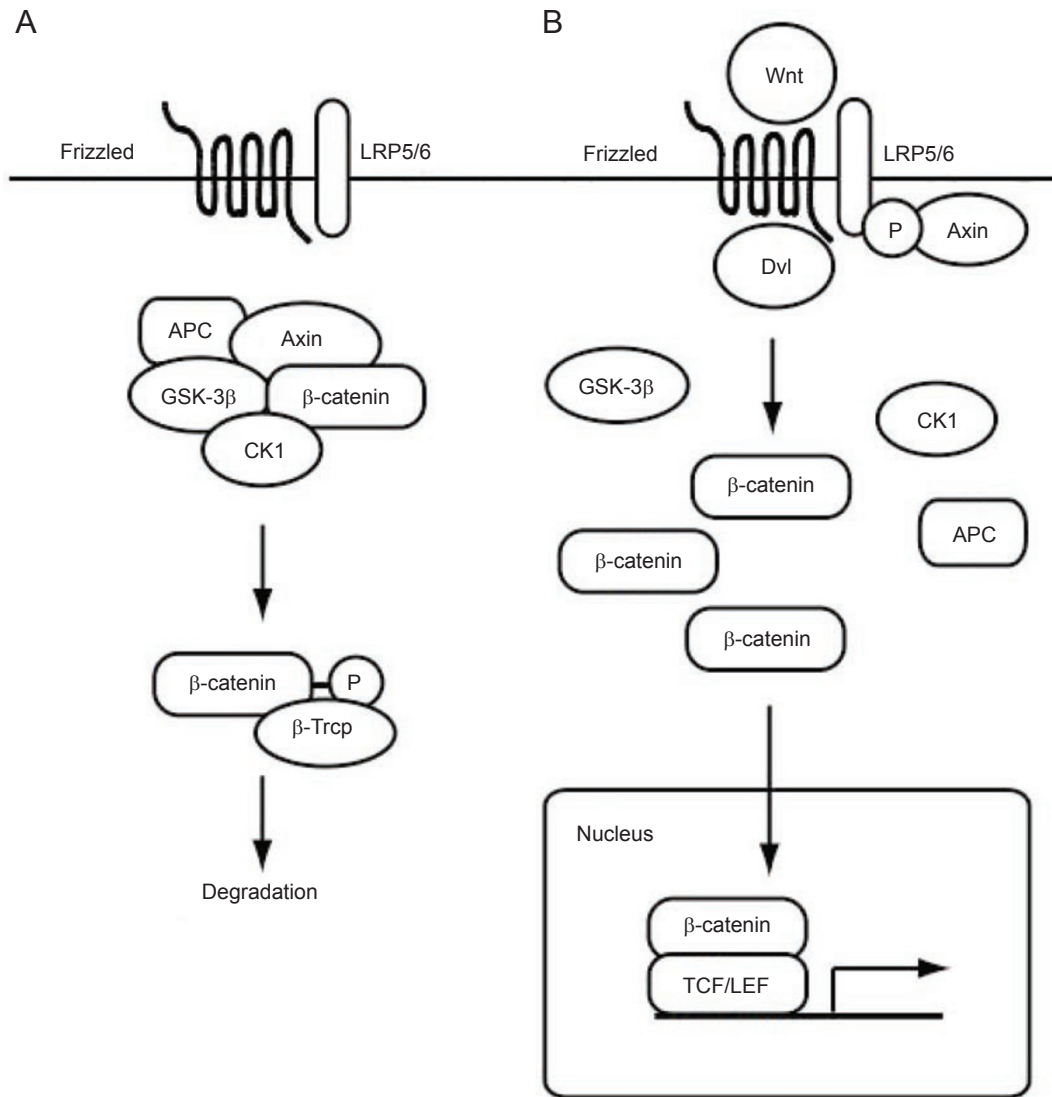


Figure 3 A schematic diagram of selected components of the canonical Wnt signaling pathways. **(A)** The absence of Wnt ligand binding to the Frizzled receptor and LRP 5/6 co-receptor enables the formation of a multi-protein complex (which includes APC, Axin, GSK-3β, and CK1) that promotes the phosphorylation and subsequent degradation of β-catenin. In the absence of β-catenin translocation, repressor proteins bind to TCF/LEF transcription factors and prevent transcription from occurring. **(B)** In the presence of Wnt ligand, the LRP co-receptors are phosphorylated by membrane-bound casein kinase 1γ and GSK-3β (not depicted), which recruits Axin to the cell membrane, disrupting the multi-protein complex. The Dishevelled protein (Dvl) is necessary for this process to occur but the mechanism is undefined. The disintegration of the multi-protein complex ultimately results in the accumulation and translocation of β-catenin to the nucleus. β-Catenin interacts with TCF/LEF and transcription occurs.

an activator of the canonical Wnt pathway, prior to transplant and showed that the presence of Wnt3a increased the frequency of hematopoietic reconstitution. HSCs deficient in the chromatin-binding protein Hmgb3 show increased expression of *Dvl1* (which encodes for Dishevelled 1) and exhibit increased canonical Wnt signaling which correlated with a bias towards self-renewal [74].

However, more recent studies have produced results that conflict with earlier interpretations on the actual role of the canonical Wnt pathway. Cobas *et al.* [75] showed that HSCs deficient in β-catenin retain their ability for self-renewal and multilineage differentiation. However, this study did not address whether canonical Wnt signaling was also absent in β-catenin-deficient HSCs, leaving open the

possibility that an alternative protein, such as γ -catenin, or an alternative signaling pathway, such as the TGF pathway which can also signal through TCF/LEF factors [76], might be able to partially compensate. Furthermore, this study only looked at whether the loss of β -catenin affected the ability of the HSC to reconstitute hematopoiesis in primary recipients and did not analyze whether β -catenin null HSCs from primary recipients could subsequently repopulate secondary or tertiary recipients, a more rigorous test of HSC function. Kincade and colleagues [77] showed that while transduction of an alternative form of constitutively active β -catenin prolonged survival (up to 5 months) and differentiation into multiple lineages of KSL cells *in vitro*, these cells were unable to engraft mice. Finally, Kirstetter *et al.* [78] and Scheller *et al.* [79] used two different transgenic models in which β -catenin was constitutively activated within HSCs. In both studies, constitutive canonical Wnt signaling inhibited multilineage differentiation and HSC self-renewal, leading to bone-marrow failure, indicating that too much canonical Wnt signaling has an adverse effect on HSC function. This suggests a model in which other signaling pathways act to balance the canonical Wnt pathway, either directly or indirectly.

Wnt ligands can also activate non-canonical signaling pathways; the pathway induced by a specific Wnt ligand mainly depends on the Frizzled receptor present. Several groups have shown that induction of non-canonical Wnt pathways can inhibit canonical signaling [80-83]. Topol *et al.* [82] has shown that induction of non-canonical Wnt signaling by Wnt5a promotes the GSK-3 β independent ubiquitination and degradation of β -catenin through an APC-Siah2-Ebi E3 ubiquitin ligase complex. To see if a similar mechanism occurred in HSCs, we have cultured KSL cells under serum-free conditions for 6 days with recombinant Wnt3a and/or Wnt5a (Nemeth *et al.*, manuscript submitted). While Wnt5a could promote β -catenin degradation and inhibit Wnt3a-induced canonical signaling, the presence of Wnt5a alone was sufficient to increase HSC engraftment efficiency and multilineage-repopulation compared to HSCs cultured without Wnt5a, indicating that non-canonical Wnt pathways are important for maintaining HSC function. Wnt5a enhanced the ability of HSCs to remain in the quiescent G₀ phase, which improved their engraftment efficiency. Multiple studies have shown that G₀ HSCs engraft and repopulate more efficiently than cycling HSCs [84-86]. The exact nature of the signaling pathway activated by Wnt5a in HSCs is still unknown. One possibility is a G protein coupled-increase in intracellular calcium (via cleavage of phosphatidylinositol 4,5-bisphosphate (PI(4,5)P₂) by phospholipase C- β), which then activates calcium-dependent kinases [87, 88]. There are similarities between the effects of Wnt5a on HSCs and the reported

functions of other G-protein coupled receptors (GPCRs) as pertains to cell proliferation and survival. CXCL12 is a chemokine that binds to the G protein-coupled CXCR4 receptor [89]. Induction of CXCL12 expression in human HSCs using DNA-damaging agents improved their engraftment and treatment of primitive hematopoietic progenitors with recombinant CXCL12 enhanced their *in vitro* survival in a p21-dependent mechanism [90, 91]. P2Y14, a member of a family of nucleotide GPCRs, is preferentially expressed in human fetal liver HSCs in the G₀ phase and ectopic expression of the receptor in primitive human progenitors enhanced *in vitro* HSC function [92]. GPCRs also regulate the adhesion of HSCs within the bone marrow microenvironment, which is critical for their long-term maintenance. The CXCL12-CXCR4 axis is necessary for colonization of bone marrow by fetal HSCs as well as retention of HSCs within the adult bone marrow [93-95]. Recently, the G-protein-coupled calcium-sensing receptor was demonstrated to have a critical function in regulating adhesion of HSCs to their microenvironment [96]. Although stimulation of HSCs by recombinant Wnt5a did not enhance HSC homing, it is possible that there is a similar function of Wnt5a *in vivo* in regulating adhesion of HSCs in the bone marrow via a G-protein-dependent mechanism

We also observed that Wnt5a can inhibit Wnt3a-mediated alterations in gene expression, such as increased *myc* expression [97], that have been linked to HSC differentiation, and this suggests a complementary *in vivo* model in which a balance between signaling by Wnt5a and Wnt3a is necessary for normal hematopoiesis to occur. This model may be especially relevant to the study of leukemias, hematologic disorders in which mutations (both somatic and germline) confer proliferative and survival advantages on HSCs and hematopoietic progenitors, inhibiting differentiation and promoting nearly limitless self-renewal. The clonal expansion of the malignant cells adversely affects the differentiation and function of the remaining normal hematopoietic cells, and these defects in normal hematopoiesis are the cause of the clinical symptoms. Mutations that activate canonical Wnt signaling have been reported for multiple solid tumors, e.g. *APC* in 85% of colorectal cancers [98, 99] and *CTNNB1* (which encodes for β -catenin) in 20% of hepatocellular carcinomas [100]. Therefore, it is not surprising that similar activation of the canonical Wnt pathway is observed in leukemic cells. Constitutive activation of the canonical Wnt pathway has been observed in samples from patients with acute myeloid leukemia (AML) and the expression of β -catenin correlates with poor prognosis [101, 102]. Thirty percent of AML patients bear the Flt3-ITD somatic mutation, the insertion of internal tandem duplications in the juxtamembrane domain of the Flt3 receptor [103]. This results in constitutive activation of the Flt3 receptor

and, consequently, increased proliferation and survival of transformed cells [104, 105]. The presence of Flt3-ITD is also associated with a poor prognosis [106]. Transfection of Flt3-ITD into 32Dcl3 cells activates canonical Wnt signaling, and β -catenin protein was present in 5/7 Flt3-ITD⁺ AML samples but absent in Flt3 wild-type AML samples, suggesting a mechanism for activation of canonical signaling in some AML sub-types [107].

Canonical Wnt signaling is also activated in cells from patients with blast-crisis chronic myeloid leukemia (CML) (i.e., CML in the terminal stages) [108]. Leukemic stem cells from CML patients exhibited decreased self-renewal and formation of hematopoietic colonies when transduced with a lentiviral vector expressing *Axin*, an inhibitor of canonical Wnt signaling. Ninety-five percent of CML patients carry the t(9,22) Philadelphia chromosome, a translocation event that results in the production of the BCR-ABL fusion protein, which contributes to the clonal expansion of malignant hematopoietic progenitors [109, 110]. Studies have demonstrated a link between BCR-ABL and canonical Wnt signaling. Wild-type BCR (breakpoint cluster region) protein can act as a negative regulator of canonical Wnt signaling through a direct interaction with β -catenin [111, 112]. The fusion of BCR and ABL (a tyrosine kinase) prevents this binding from occurring, possibly due to autophosphorylation, which allows Wnt signaling to proceed.

Approximately 3% of adults with acute lymphoblastic leukemia (ALL) display the E2A-Pbx1 fusion protein, which arrests normal B cell development [113]. E2A-Pbx1 induces expression of *Wnt16b* [114]. *Wnt16b* induces canonical Wnt signaling and inhibition of *Wnt16b* in ALL cell lines resulted in increased apoptosis [115]. Recently, it was demonstrated that promoters for canonical Wnt pathway inhibitory genes (e.g., *sFRP-1*, *Wif-1*, and *Dkk-3*) were abnormally methylated in ALL samples across a spectrum of genetic lesions [116]. This was associated with upregulation of canonical pathway genes *Wnt16*, *Frizzled 3*, and *Tcf-3* and nuclear localization of β -catenin. Abnormal methylation of Wnt pathway inhibitory genes was also associated with decreased rates of relapse-free and overall survival.

Finally, Liang *et al.* [117] showed that *Wnt5a*^{+/-} mice were predisposed for developing myeloid and lymphoid leukemias (17/77 mice) that exhibited loss-of-heterozygosity of the remaining wild-type allele. 10/10 AML samples and 8/10 ALL samples showed reduced or absent expression of *Wnt5a* and increased expression of cyclin D1, a canonical Wnt pathway target gene. This study did not directly test the hypothesis that *Wnt5a* acts as a tumor suppressor by inhibiting canonical Wnt signaling, although unfractionated fetal liver cells from *Wnt5a*^{-/-} mice contained equivalent levels of β -catenin as their wild-type counter-

parts. Ysebaert *et al.* [102] were unable to observe that expression of *WNT5A* strictly correlated with the presence or absence of β -catenin protein, although this study did not present data correlating quantified levels of *WNT5A* protein with levels of β -catenin protein.

Canonical Wnt signaling and the osteoblast HSC niche

Adult bone marrow is also home to non-hematopoietic cells, such as fibroblasts, adipocytes, endothelial cells, osteoblasts and stromal progenitors, which comprise the bone marrow microenvironment [118-120]. For over 30 years, it has been proposed that within the microenvironment, HSCs physically interact with biologically distinct cellular environments, called niches, which provide some of the external signals necessary for stem cell function [121]. The niche is a major determinant of whether a stem cell undergoes symmetric or asymmetric cell division. For example, in *Drosophila* ovaries and testes, the germ stem cell directly contacts a partner cell (cap cell in ovaries, hub cell in testes); after division, one cell remains in contact and has a stem cell phenotype whereas the daughter cell that is no longer in direct contact with its partner cell begins the differentiation program [122-124]. The mechanisms by which the niche regulates HSC fate at both the single cell and population levels are as yet incompletely defined.

Multiple cell types in the bone marrow microenvironment comprise the HSC niche. For example, recent studies have demonstrated that the bone marrow vasculature plays an important role in supporting HSCs [25, 125]. However, for the remainder of this review, we will focus on the osteoblast, which is derived from the mesenchyme and initiates the process of ossification. Osteoblasts support hematopoiesis through the production of growth factors and have also been demonstrated to be critical components of the HSC niche [126-129]. HSCs have been demonstrated to preferentially reside at the endosteal surface of trabecular regions of bone (regions of more rapid bone remodeling, such as the ends of long bones), in contrast to more differentiated hematopoietic progenitors that are localized to the center of the bone marrow [128, 130, 131]. Zhang *et al.* [128] demonstrated that the HSC can physically interact with osteoblasts, specifically N-cadherin⁺ osteoblasts found in the trabecular bone area.

The necessity of osteoblasts for the normal function of the HSC niche was demonstrated by Visnjic *et al.* [132] in which osteoblasts were ablated *in vivo* using a transgenic model wherein the osteoblast-specific promoter for the *Colla1* gene (which encodes for procollagen, type I, $\alpha 1$) was used to control the expression of thymidine kinase. Treating these mice with gancyclovir resulted in the loss

of osteoblasts and, subsequently, decreased bone marrow cellularity and KSL cell number. There were increased numbers of progenitors in extramedullary sites, e.g. the spleen, peripheral blood, and liver, suggesting that HSCs took up residence in other tissue sites. These findings were not replicated using a transgenic model in which only developmentally mature osteoblasts were deleted (using the promoter for the *Bglap1* gene, which encodes for osteocalcin and is induced during the onset of mineralization) [133]. This suggests that osteoblasts within HSC niches are developmentally immature. In the converse experiment, Calvi *et al.* [129] treated mice with parathyroid hormone, which at low doses leads to the anabolic formation of trabecular bone. This resulted in increased numbers of osteoblasts and HSCs in the bone marrow.

Several factors secreted by the osteoblast (as well as other cell types) have been implicated in the maintenance of HSCs. For example, osteoblasts produce Angiopoietin-1 (Ang-1), a soluble ligand that promotes angiogenesis by binding the receptor tyrosine kinase Tie2 [134]. The Ang-1-Tie2 signaling axis also maintains HSC adhesion within the niche and promotes HSC quiescence [135]. Osteoblasts also secrete Jagged-1, a ligand for the Notch signaling pathway [129]. Studies have shown that activation of Notch signaling results in increased numbers of HSCs and hematopoietic progenitors *in vitro* and *in vivo* [136-138]. Another critical function of the niche is the ability to regulate HSC homing, i.e., the recruitment of HSCs to unoccupied stem cell niches, where the HSC engraftment and retention takes place [139]. The ability to HSCs to home to sites where they can engraft and initiate hematopoiesis is necessary during development when HSCs sequentially colonize the fetal liver and then the bone marrow. Furthermore, homing of HSCs to the niche is critical in bone marrow transplantation. Osteoblasts contribute to the regulation of HSC homing through the production of adhesion molecules that facilitate retention of the HSC in the niche, such as vascular cell-adhesion molecule 1 [140-142]. Osteoblasts also secrete CXCL12.

Therefore, developmental pathways that regulate the composition of the bone marrow microenvironment of the stem cell niche may indirectly regulate HSC function. The canonical Wnt signaling pathway is an excellent candidate for testing this model since it regulates the development of mesenchymal tissue, including the specific cell types found in the HSC niche, e.g. the osteoblast [143, 144]. Recent studies have demonstrated that canonical Wnt signaling plays a critical role in maintaining normal osteoblast differentiation. Using different transgenic models, Day *et al.* [144], Hill *et al.* [145], and Rodda and McMahon [146] all demonstrated that the loss of β -catenin inhibited osteogenic development during embryogenesis. In developmentally

mature osteoblasts, the role of canonical Wnt signaling is less clear. In separate studies, deletion of β -catenin in mature osteoblasts led to osteopenia (reduced bone mass). Holmen *et al.* [147], using a *Bglap1*-Cre recombinase transgenic line to knockout β -catenin, detected decreased numbers of osteoblasts 4 weeks after birth. In contrast, Glass *et al.* [148], using a *Colla1*-Cre line, observed no decrease in osteoblast numbers and that the resultant osteopenia was due to increased numbers of osteoclasts (bone marrow-derived cells that assist in the reabsorption of bone tissue). In human genetics, loss-of-function mutations in the LRP5 co-receptor cause osteoporosis-pseudoglioma syndrome, characterized in part by decreased bone mass. A mouse model of LRP5 deficiency displays a similar phenotype [149]. Autosomal gain-of-function mutations in LRP5 result in enhanced canonical Wnt signaling and increased bone density due to inhibition of the Dkkopf (Dkk) protein, a negative regulator of the canonical Wnt pathway [150, 151].

Conclusions

Although the past 10 years have seen progress on the role of Wnt signaling pathways in hematopoiesis, important questions still remain. As canonical Wnt signaling is active in several types of leukemia, are there signaling pathways that can directly or indirectly interact with the canonical Wnt pathway to promote leukemogenesis? What are the mechanisms by which non-canonical Wnt signals can maintain HSC function? Can canonical Wnt signals simply regulate the composition of the bone marrow microenvironment (such as osteoblasts) or are they necessary for normal function of the niche cells as well?

As described above, the role of canonical Wnt signaling in leukemia is an active area of study and molecules designed to disrupt this pathway may see use in the clinic [152]. One of the prominent features of the malignant hematopoietic disorder multiple myeloma is the development of osteolytic lesions due to enhanced bone destruction. Recent studies have demonstrated that myeloma cells secrete Dkk-1, an inhibitor of both canonical Wnt signaling and osteoblast differentiation and a potential pharmacologic target [153-155]. Therefore, further study of the role of the Wnt signaling pathways in HSC regulation will not only elucidate the mechanisms by which these unique cells function but may also prove useful in the design of novel therapeutic strategies to treat hematologic disorders.

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