

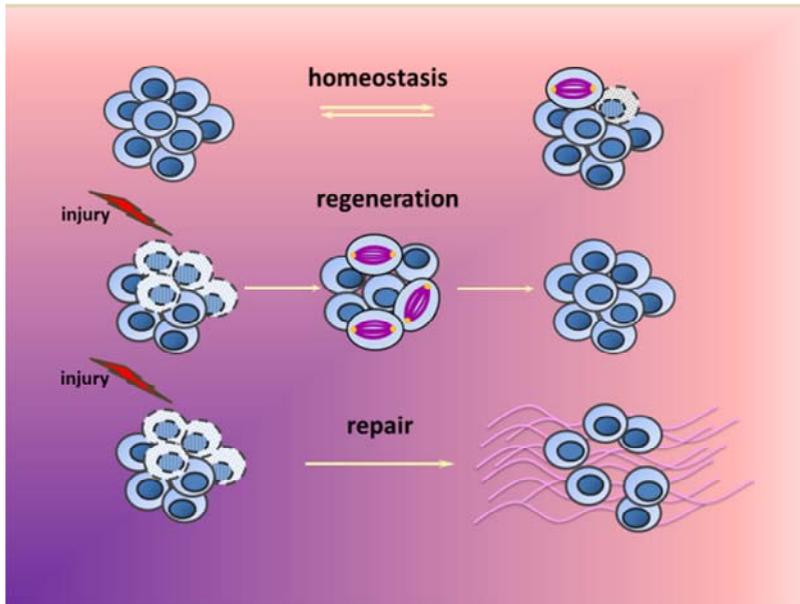
# Chapter Number

## Adult Stem Cells in Tissue Homeostasis and Disease

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### 1. Introduction

Stem cells (SCs) are a rare population of cells characterized by the ability to self-renew in order to preserve the SC pool and to differentiate in different lineage to produce progeny needed for the physiological functions of tissues and organs. SC can be classified as embryonic SC (ESC) and adult or somatic SC (ASC): ESC have been isolated from the inner cell mass of the blastocyst and are pluripotent cells, that is cells able to differentiate into all the cell types required to form an entire organism (Smith, 2001); ASC are tissue-resident SC that, based on their differentiation potency, can be classified as multipotent, oligopotent or even unipotent. It is still controversial whether every mammalian tissue and organ possesses an ASC, but many tissue-specific ASC have been successfully identified and isolated e.g., hematopoietic SCs (HSCs), mammary SCs, muscle SCs (satellite cells), intestinal SCs, and mesenchymal SCs. All these tissues need to constantly replace damaged or dead cells throughout the life of the animal. This process of continual cell replacement critical for the maintenance of adult tissues, is called tissue homeostasis, and is maintained through the presence of ASC (Fig. 1). The homeostatic replacement of cells varies substantially among different tissues. The epithelium of the intestine is one of the most rapidly self-renewing tissue in adult mammals and it completely self-renews in around 5 days (van der Flier & Clevers, 2009). By contrast, interfollicular epidermis takes 4 weeks to renew (Blanpain & Fuchs, 2009), whereas the lung epithelium can take as long as 6 months to be replaced (Rawlins & Hogan, 2006). Moreover, apart from the maintenance of tissue homeostasis, ASC are devoted to the regeneration and repair of highly specialized tissues. Regeneration refers to the proliferation of cells to replace lost structures, such as the growth of an amputated limb in amphibians. In mammals, whole organs and complex tissues rarely regenerate after injury, but tissues with high proliferative capacity, such as the hematopoietic system and the epithelia of the skin and gastrointestinal tract, renew themselves continuously and can regenerate after injury, as long as the SC of these tissues are not destroyed (Fig. 1). Repair most often consist of a combination of regeneration and scar formation by the deposition of collagen which relative contribution depends on the ability of the tissue to regenerate and the extent of the injury. For instance, in superficial injury of the skin, wound can heal through the regeneration of the surface epithelium. However, scar formation is the predominant healing process that occurs when the extracellular matrix framework is damaged by severe injury (Fig. 1). This last mechanism results in restoration of tissue continuity but with or without function (Gurtner et al., 2008).



1  
2 Fig. 1. Normal homeostasis and healing responses. In normal homeostasis a balance  
3 between proliferation and cell death maintains the tissue structure and function. Healing  
4 after acute injury can occur by regeneration, that restores normal tissue structure, or repair  
5 with deposition of collagen fibers and scar formation.

## 6 2. SCs and their niches

7 Self-renewal and differentiation of ASC are supported by two types of cell division known  
8 as symmetric and asymmetric (Morrison & Kimble, 2006). With symmetric division both the  
9 daughter cells acquire similar fates, while the asymmetric division, a fundamental and  
10 nearly universal mechanism for the generation of cellular diversity and pattern, gives rise to  
11 daughter cells with dissimilar fates. Divergent fates in daughter cells may be recognized by  
12 various characteristics: (i) morphological, such as cell size and shape; (ii) molecular, such as  
13 the segregation of proteins into only one daughter cell; or (iii) behavioural, such as the  
14 subsequent descendant types produced by either of the daughter cells. One mechanism for  
15 fate determination of daughter cells following symmetric and asymmetric cell divisions is  
16 the partitioning of fate-determining molecules during mitosis of the mother cell (Tajbakhsh  
17 et al., 2009). The idea that specific molecules can be partitioned unequally to daughter cells  
18 and behave as fate determinants had been hypothesized over a century earlier, following  
19 observations of cell divisions in simple organisms. When an intrinsic mechanism is used,  
20 cells establish an axis of polarity, orient the mitotic spindle along this axis and localize cell  
21 fate determinants to one side of the cell. During cytokinesis, determinants are then  
22 segregated into one of the two daughter cells where they direct cell fate (Betschinger &  
23 Knoblich, 2004). However, this hypothesis was only experimentally validated a little under  
24 two decades ago, with the identification of the first asymmetrically segregated cell fate  
25 determinant - Numb (Rhyu et al., 1994).

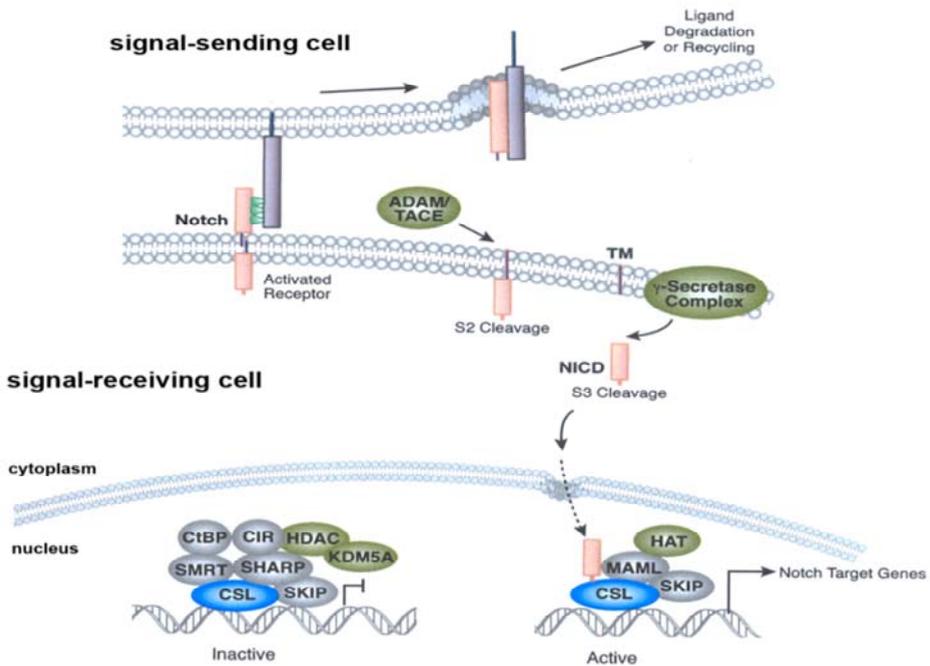
1 Alternatively, the SC depends on the contact with the surrounding microenvironment (the  
2 SC “niche”) for maintaining the potential to self-renew (Li & Xie, 2005). By orienting its  
3 mitotic spindle perpendicularly to the niche surface, the SC will place the two daughters in  
4 distinct cellular environments either inside or outside the SC niche, leading to asymmetric  
5 fate choice. However, when SC divides parallel to the niche it may also generate two  
6 identical SC in order to increase SC number or to compensate for occasional SC loss  
7 (Yamashita et al, 2010). The concept of the “niche” was proposed first by Schofield  
8 (Schofield, 1978) who hypothesized that proliferative, hematopoietic cells derived from the  
9 spleen displayed decreased proliferative potential when compared to HSC obtained from  
10 the bone marrow because they were no longer in association with a complement of cells, the  
11 “niche”, which supports long term SC activity. This concept subsequently has proven  
12 relevant to many different SC systems, and the definition of the niche has been expanded  
13 further to include functional regulation of SC by both cellular and acellular (extracellular  
14 matrix) component of the niche. Thus the niche comprises all the microenvironment  
15 surrounding SCs, which provides diverse external cues to instruct SC activities, preserve  
16 their proliferative potential and block maturation (Jones & Wagers, 2008).

### 17 **3. Signaling pathways regulating SC function**

18 Despite morphological and functional differences among different ASC, common signaling  
19 pathways appear to control SC self-renewal, activation, and differentiation, including Notch  
20 and Wntless-type (Wnt).

#### 21 **3.1 Notch signaling pathway**

22 The Notch signaling pathway was discovered in flies more than 90 years ago (Morgan,  
23 1917), and it is among the most well-conserved signaling pathways in animals. It arose with  
24 the evolution of multicellular organisms and the concomitant need for juxtacrine cell-to-cell  
25 communication to coordinate development. In mammals, four Notch transmembrane  
26 receptors (Notch1-4) have been described. Notch ligands are also transmembrane proteins  
27 comprising two different subtypes (Delta, Jagged), each containing several members  
28 (Jagged1-2, Delta-like1, 3, and 4) (Kopan & Ilagan, 2009). In Notch signaling, a 'signal-  
29 sending cell' presents the Notch ligand to the 'signal-receiving cell', which expresses the  
30 Notch receptor. Triggering of Notch receptor by ligand binding promotes two proteolytic  
31 cleavage events at the Notch receptor (Fig. 2) (Kopan & Ilagan, 2009). The first cleavage is  
32 catalyzed by the ADAM-family of metalloproteases, whereas the second cleavage is  
33 mediated by  $\gamma$ -secretase, an enzyme complex that contains presenilin, nicastrin, PEN2 and  
34 APH1. The second cleavage releases the Notch intracellular domain (NICD), which is free to  
35 translocate to the nucleus where it engages CSL, converting it from a transcriptional  
36 repressor to an activator and activates transcription of genes containing CSL binding sites  
37 (Kopan & Ilagan, 2009). In the absence of a Notch signal, CSL represses transcription of  
38 Notch target genes by interacting with the basal transcription machinery and recruiting  
39 ubiquitous corepressor proteins to form multiprotein transcriptional repressor complexes  
40 (Lai, 2002). In the presence of a Notch signal, NICD binding to CSL displaces corepressors  
41 from CSL. The best characterized Notch target genes belong to the hairy enhancer of split  
42 (Hes) complex and consist of the b-HLH transcription factors Hes (1-7) and Hey (1-3) (Bray  
43 & Bernard, 2010).



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Fig. 2. Model of Notch signaling pathway. See the text for detail.

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### 3.2 Wnt signaling pathway

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The Wnt signaling pathway is a highly conserved developmental pathway, and orchestrates development and morphogenesis in many different tissues. Wnt proteins are secreted proteins, that bind to receptors of the Frizzled family (FZD) (Wodarz & Nusse, 1998), of which 10 members were found, and several coreceptors such as lipoprotein receptor-related protein (LRP)-5/6, (Pinson et al., 2000) Ryk, or Ror2 (Logan & Nusse, 2004). Wnt signals can be transduced to the canonical, or Wnt/ $\beta$ -catenin, pathway and to the noncanonical, or  $\beta$ -catenin independent, pathway.

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#### 3.2.1 Canonical Wnt signaling pathway

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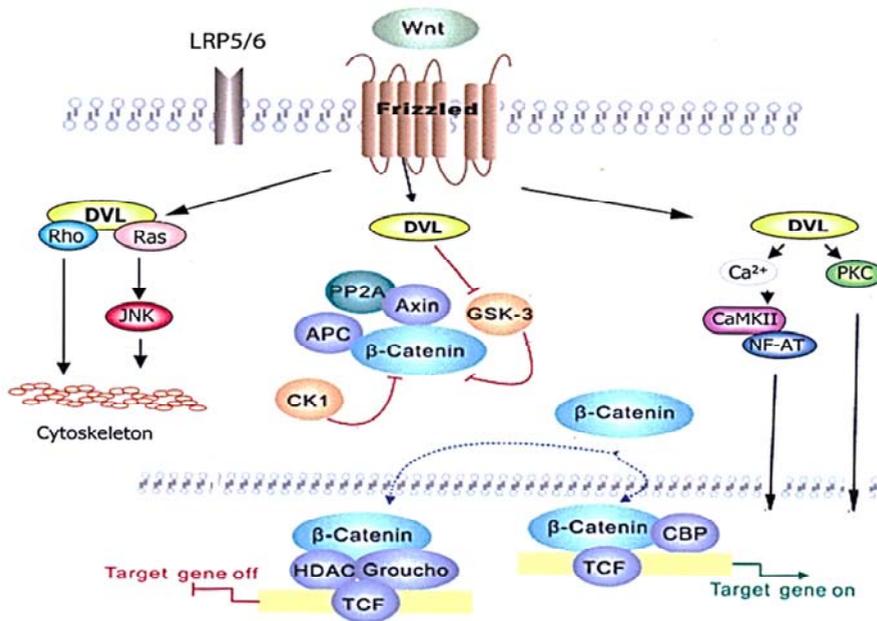
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The canonical Wnt pathway involves the multifunctional protein  $\beta$ -catenin (MacDonald et al., 2009). In the absence of Wnt,  $\beta$ -catenin is targeted to a multimeric destruction complex with adenomatous polyposis coli (APC) and Axin and is phosphorylated by casein kinase 1 $\alpha$ , followed by phosphorylation by glycogen synthase kinase (GSK)3 $\beta$  (Fig.34) (Ikeda et al., 1998). This phosphorylation targets  $\beta$ -catenin for ubiquitination and degradation by the proteasome. The binding of Wnt ligands to the FZD receptors results in the disassembly of the destruction complex and the stabilization of  $\beta$ -catenin. This process also involves the protein dishevelled (DVL). Cytoplasmic  $\beta$ -catenin accumulates and is eventually imported into the nucleus, where it serves as a transcriptional coactivator of transcription factors of the TCF/LEF family (Arce et al., 2006). TCF/LEF target genes are then involved in regulating cell proliferation, SC maintenance, or differentiation.

### 3.2.2 Noncanonical Wnt signaling pathway

1 Different noncanonical Wnt signals are transduced through FZD receptors and coreceptors.  
 2 Depending on the major intracellular mediators used, those are called the Wnt/JNK  
 3 (Veeman et al., 2003) or Wnt/calcium pathway (Fig. 3). The core element of the Wnt/JNK  
 4 (or planar cell polarity –PCP- pathway) includes the activation of small GTPases of  
 5 the rho family, such as rac, cdc42, and rhoA. The GTPases can activate more downstream  
 6 mediators like JNK or rho kinase (ROK). In this branch, Dvl is also recruited by a FZD  
 7 receptor and promotes the asymmetrical localization of the PCP core proteins within the cell  
 8 (Montcouquiol, et al. 2006). The asymmetrical subcellular localization of these elements in  
 9 an epithelial sheet directs cytoskeletal reorganization. The same mechanism is used in  
 10 mesenchymal cells to direct cell movement and migration during gastrulation (convergent  
 11 and extension movements) (Roszko, et al., 2009).



13  
 14 Fig. 3. Model of canonical and noncanonical Wnt signaling pathway. See the text for detail.

15 The existence of the Wnt/calcium pathway was hypothesized because injection of RNA  
 16 coding for certain Wnts or FZD into early zebrafish embryos triggered intracellular calcium  
 17 release (Slusarski et al., 1997) and loss of Wnt-11 or Wnt-5A function resulted in reduced  
 18 intracellular calcium signaling (Eisenberg & Eisenberg, 1999; Westfall et al., 2003). This  
 19 finding was subsequently expanded by the observation that the Wnt-induced release of  
 20 intracellular calcium is sufficient to activate different intracellular calcium-sensitive  
 21 enzymes such as protein kinase C, PKC (Sheldahl et al., 1999), calcium-calmodulin-  
 22 dependent kinase II, CamKII (Kuhl et al., 2000) and the calcium-sensitive phosphatase  
 23 calcineurin (Saneyoshi et al., 2002). Through calcineurin the Wnt/calcium pathway connects  
 24 to NFAT (nuclear factor of activated T cells) transcription factor and gene expression.

1 Presently, a series of recent findings clearly indicate that different Wnt signaling pathways  
2 are simultaneously active within the same cell type, supporting the idea that Wnt pathways  
3 are highly connected to form a Wnt signaling network. This network seems to be activated  
4 by either one or more ligands acting on a certain cell type (Kestler & Kuhl, 2008).

### 5 **3.3 Wnt signaling inhibitors**

6 Secreted frizzled-related proteins (SFRP1, 2, 3, 4, 5), WIF1, DKK1, -2, -3, and -4 are secreted-  
7 type Wnt signaling inhibitors. WIFs and SFRPs can directly bind to Wnt proteins in the  
8 extracellular space, thereby affecting receptor occupancy and, ultimately, the cellular  
9 response (Bovolenta et al., 2008). DKK1 is among the best-characterized inhibitors of the  
10 canonical Wnt pathway. DKK1 itself is a target gene of Wnt/ $\beta$ -catenin signaling, thereby  
11 establishing a negative-feedback loop (Niida et al., 2004). There are two possible  
12 mechanisms by which DKK1 inhibits  $\beta$ -catenin signaling. One possible mechanism is that  
13 DKK1 prevents the formation of Wnt-FZD-LRP6 complexes on the cell surface by binding  
14 to LRP6 (Seto et al., 2006). Another possibility, which is related to the internalization of  
15 LRP6, is that DKK1 binds to another class of receptor, Kremen (Krm). In this model, the  
16 binding of DKK1 to LRP6 and Krm results in the formation of a ternary structure and  
17 induces rapid endocytosis and the removal of LRP6 from the plasma membrane, and  
18 thereby attenuates  $\beta$ -catenin signaling (Mao et al., 2002).

## 19 **4. Hematopoietic SCs**

20 In adult mammals, HSCs form a rare population of multipotent SCs that reside primarily in  
21 the bone marrow (BM). They have the capability to both self-renew and constantly give rise  
22 to lineage-specific progenitor cells and effector blood cells that perform the physiological  
23 functions of the hematopoietic system. Blood cells can be classified into various cell types,  
24 from the myeloid (monocytes and macrophages, neutrophils, basophils, eosinophils,  
25 erythrocytes, megakaryocytes/platelets, dendritic cells), and lymphoid lineages (T-cells, B-  
26 cells, NK-cells) (Liu et al., 2010).

27 HSCs are functionally defined by their capacity to reconstitute the hematopoietic system of  
28 immunodeficient animals such as NOD/SCID mice or contribute to functional  
29 reconstitution in human transplant settings. HSCs can be identified and isolated by a  
30 combination of presence and absence of cell surface markers. The most commonly used  
31 combination is characterized by the positive expression of the tyrosine kinase receptor c-Kit  
32 (CD117) and the membrane glycoprotein Sca-1 (Okada et al., 1992), together with the lack of  
33 markers of terminal differentiation (Ter119, Gr-1, Mac-1, B220, CD4 and CD8), collectively  
34 known as Lineage markers. The resulting c-Kit<sup>+</sup> Sca-1<sup>+</sup> Lin<sup>-</sup> population, is commonly  
35 referred to as KSL cells. More recently, an alternative method was described, using a  
36 signature of SLAM (Signaling lymphocyte activation molecule) family of cell surface  
37 molecules, CD150<sup>+</sup> CD244<sup>-</sup> CD48<sup>-</sup> (Kiel et al, 2005). This is the first family of receptors  
38 whose combinatorial expression precisely distinguishes HSCs from hematopoietic  
39 progenitor cells (HPC).

40 The BM microenvironment –also called niche- plays an important role in the regulation of  
41 self-renewal and differentiation of HSCs. It is composed of different types of cells and  
42 structures surrounding the bone, which regulates the fate of hematopoietic cells through

1 direct or indirect means, facilitating a stable generation of all the blood cells needed in a  
2 steady state situation. But the niche also adapts in times of hematopoietic stress. A failure to  
3 maintain a strict regulation of the hematopoietic cells can lead to a variety of malignancies  
4 such as leukemia, the most common form of cancer in humans (Renstrom et al., 2010).

#### 5 **4.1 Notch pathway as a regulator of HSC behavior**

6 All Notch receptors and ligands are expressed on HSCs (Singh et al., 2000) and it is now  
7 well established that Notch signaling is essential for the production of HSCs during  
8 embryogenesis. However, its role in subsequent stages of mammalian HSC development is  
9 still controversial (Liu et al, 2010; Radtke et al., 2010).

10 In adult hematopoiesis, activation of Notch signaling has been reported to promote HSCs  
11 self-renewal, proliferation and differentiation *in vitro* and *in vivo*, and in both mice and  
12 humans. Constitutive expression of NICD by HSCs, leading to the constitutive activation of  
13 the Notch pathway, enhances proliferation and consequently delays hematopoiesis.  
14 Conversely, it inhibits differentiation in response to various cytokines, mostly under  
15 myeloid promoting conditions (Carlesso et al, 1999). Several reports show that HSCs  
16 stimulated with soluble or membrane-bound Notch ligand Delta 1 (Karanu et al, 2001) or  
17 Jagged1 (Karanu et al. 2000) increase in expansion potential *in vitro* and in reconstitution  
18 capacity *in vivo*. Although these gain-of-function studies show an important role for Notch  
19 in expanding the HSC pool, they do not prove that Notch is essential for post-natal  
20 hematopoiesis. The controversy arises from several loss-of-function studies in mice that did  
21 not fully support the previous conclusions. In particular, inactivation of Notch receptors  
22 (Notch1, Notch2), ligands (Jagged1) or downstream effectors (CSL/RBPJ, Mastermind-like1)  
23 does not impair HSC function (Cerdan & Bhatia, 2010). Additional studies failed to identify  
24 a protective role for Notch when HSCs were exposed to oxidative stress. Taken together,  
25 these results show that Notch signaling is not a major regulator of adult HSC maintenance  
26 *in vivo*. Downstream of HSCs, Notch signaling plays a critical role in cell fate decision of a  
27 variety of oligopotent progenitor cells in the hematopoietic system, such as in T-cell  
28 development. Inactivation of Notch signaling in HPCs results in early blockade of T-cell  
29 lymphopoiesis, due to a failure in commitment to the T-cell lineage. Transgenic mice with a  
30 conditional deletion of Notch1 do not develop T-cells but develop ectopic B-cells in the  
31 thymus, while immunodeficient mice expressing a constitutively active form of Notch1  
32 develop ectopic T-cells in the bone marrow (BM) but no B-cell (Tanigaki & Honjo, 2007).  
33 Additionally, Notch1 signaling is necessary at various stages of T-cell development, such as  
34 progression through thymocyte maturation, regulation of T-cell Receptor  $\beta$  (TCR- $\beta$ ) gene  
35 rearrangement, regulation of lineage decisions between  $\alpha\beta$  and  $\gamma\delta$  lineages (Tanigaki &  
36 Honjo, 2007).

#### 37 **4.2 Role of Notch in T-cell leukemia**

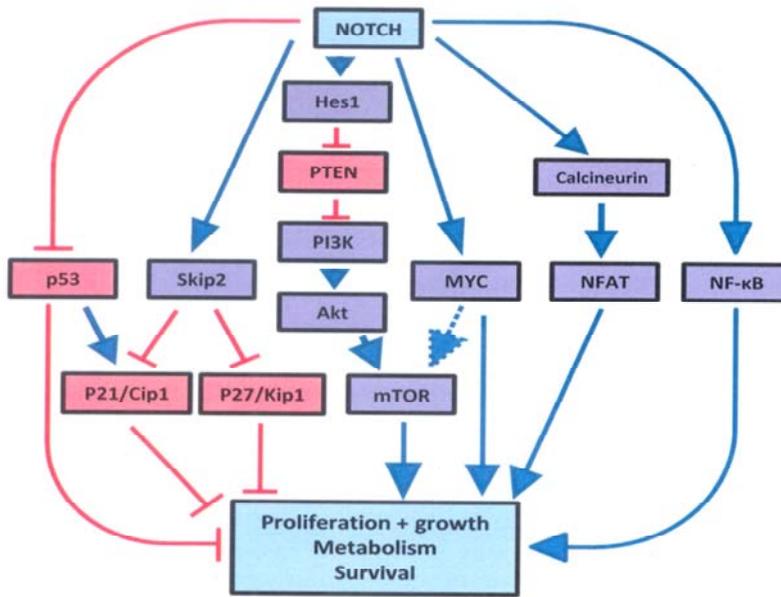
38 The pathological role for a deregulated Notch signaling was first described in a rare human  
39 T-cell acute lymphoblastic leukaemia/lymphoma (T-ALL), in which a t(7;9) chromosomal  
40 translocation results in the generation of a constitutively active, but truncated form of the  
41 Notch1 receptor named TAN1 (Translocation Associated Notch homolog) (Ellisen et al.,  
42 1991). Evidence that constitutively active Notch1 is responsible for disease development was  
43 provided by murine BM reconstitution experiments. Irradiated mice transplanted with BM

1 progenitors expressing activated forms of Notch1 developed clonal hematopoietic tumors  
2 characterized as T-ALL. Experiments performed using other truncated Notch isoforms,  
3 including Notch2 and Notch3, showed similar results. However, mice having a defect in T-  
4 cell development failed to produce tumors. These results reveal that Notch1 has a special  
5 oncotropism for T-cell progenitors (Radtko et al., 2010). These findings became extremely  
6 relevant when a study of a large number of T-ALL patients revealed in more than 50% of  
7 them the presence of at least one gain-of-function mutation in the Notch1 receptor,  
8 emphasizing the oncogenic role of Notch (Weng et al., 2004). Notch1 mutations found in T-  
9 ALL affect critical domains responsible for preventing the spontaneous activation of the  
10 receptor in the absence of ligand or for terminating Notch1 signaling in the nucleus.

11 Studies of the genes and pathways controlled by Notch in T-ALL identified Notch1 as a  
12 central regulator, promoting leukemia cell growth by multiple direct and indirect  
13 mechanisms (Fig. 4) (Paganin & Ferrando, 2011). Analysis of Notch1 expression in T-ALL  
14 showed that it acts as a direct transcriptional activator of multiple genes. Notch1 also  
15 promotes the expression of the MYC oncogene, which in turn further enhances its direct  
16 effect on anabolic genes and facilitates cell growth. Indeed, many of the anabolic genes  
17 directly controlled by Notch1 are also direct targets of MYC, creating a feed-forward-loop  
18 transcriptional network that promotes leukemic cell growth (Palomero et al., 2006).  
19 Additionally, Notch1 facilitates the activation of the PI3K-AKT-mTOR signaling pathway, a  
20 critical regulator of cell growth and metabolism, via transcriptional downregulation of the  
21 PTEN tumor suppressor gene by Hes1, a transcriptional repressor directly downstream of  
22 Notch1 signaling (Palomero et al., 2007). The mTOR signaling was suppressed in T-ALL  
23 cells upon inhibition of Notch signaling, illustrating the importance of this indirect  
24 mechanism of regulation. The transcriptional program activated by oncogenic Notch1 also  
25 has a direct effect on cell cycle progression, promoting of G1/S cell cycle progression in T-  
26 ALL. This effect is mediated in part by transcriptional upregulation of CCND3, CDK4 and  
27 CDK6. Moreover, Notch1 induces the transcription of the S phase kinase-associated protein  
28 2 (SKP2), which mediate the proteasomal degradation of CDKN1B (p27/Kip1) and  
29 CDKN1A (p21/Cip1), promoting premature entry of the cells into S phase (Sarmento et al,  
30 2005). Notch1 can also modulate the survival of T-ALL cells by interacting with NF- $\kappa$ B,  
31 upregulating its activity by increasing expression of I $\kappa$ B kinase and upregulating both the  
32 expression and the nuclear localization of NF- $\kappa$ B. Inhibition of NF- $\kappa$ B in T-ALL can  
33 efficiently restrict tumor growth both *in vitro* and *in vivo* (Vilimas et al., 2007).

34 In addition, Notch1 modulates the NFAT cascade through the activation of calcineurin,  
35 which is a calcium-activated phosphatase that is important for the activation and  
36 translocation of NFAT factors to the nucleus. Calcineurin inhibition resulted in T-ALL cell  
37 death, as well as tumor regression and prolonged survival of leukemic mice (Medyouf et al.,  
38 2007). Finally, Notch1 regulates the activity of p53, lowering its expression through  
39 repression of the ARF-mdm2-p53 surveillance network. Attenuation of Notch signaling led  
40 to increase p53 expression and to tumor regression by inducing apoptosis (Beverly et al.,  
41 2005). A strong body of evidence supports a central role of Notch1 in promoting cell  
42 metabolism, growth and proliferation, as well as in enhancing the activity of signaling  
43 pathways that reinforce these functions and also promote cell survival. These results suggest  
44 that blocking Notch1 signaling may reduce the self-renewal capacity of T-ALL cells and/or  
45 selectively affect the leukemia initiating cell population.

1 Only few Notch mutations have been reported in myelogenous leukemias, but it is unclear  
 2 whether Notch aberrant expression is responsible for the disease.



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5 Fig. 4. Genes and pathways controlled by Notch in T-ALL

### 6 4.3 Wnt pathway and HSC

7 In hematopoiesis, Wnt pathway activity is required in the BM niche to regulate HSC  
 8 proliferation and preserve self-renewal capacity (Malhotra & Kincade, 2009). Even though  
 9 the role of canonical signaling on the regulation of adult hematopoiesis has been studied  
 10 in great detail, controversy remains, possibly explained by differences in strength and  
 11 duration of Wnt signaling or redundancy with other pathways. A role for Wnt signaling  
 12 in hematopoiesis is supported by observations that Wnt ligands enhance proliferation of  
 13 HSCs *ex vivo* (Van Den Berg et al, 1998) and that Wnt antagonists inhibit HSC  
 14 proliferation and reconstitution. In particular, only short-term repopulation was reported  
 15 using HSCs from normal mice cultured with Wnt3A (Reya et al., 2003; Willert et al., 2003).  
 16 Subsequent studies reported that noncanonical Wnt5a inhibited canonical Wnt3a-  
 17 mediated signaling to promote the maintenance of quiescent, functionally transplantable  
 18 HSCs. In addition constitutively active nuclear  $\beta$ -catenin signaling reduces HSC  
 19 quiescence and blocks HSC differentiation (Kirstetter et al., 2006). On the other hand,  
 20 osteoblast-specific expression of Dkk1 results in increased HSC cycling and reduced  
 21 regenerative capacity (Fleming et al, 2008). These findings suggest that Wnt pathway  
 22 activation in the niche limits HSC proliferation and preserves self-renewal. These  
 23 observations suggest that fine-tuning of Wnt/ $\beta$ -catenin activity in the microenvironment  
 24 is crucial for maintaining SC quiescence.

1 The canonical Wnt pathway has also been shown to be necessary for appropriate HSC  
2 development (Zhao et al., 2008). In this model, *Ctnnb1*<sup>-/-</sup> bone marrow cells are deficient in  
3 long-term HSC maintenance and compete poorly against wild-type cells. However,  
4 experiments in adult HSC revealed that *Ctnnb1* is dispensable for HSC maintenance in fully  
5 developed HSC (Koch et al., 2008). This indicates differential requirements for self-renewal  
6 pathways in development versus maintenance of HSC.

7 In the context of development, genetic studies have demonstrated the requirement for  
8 canonical signaling in the formation of mesoderm (Kelly et al., 2004; Liu et al., 1999). Recent  
9 advances have provided insights into the uniqueness of the biological functions of canonical  
10 and noncanonical pathways. It has been found that non-canonical and canonical Wnts  
11 affected different target populations and stages of hematopoietic development  
12 (Vijayaragavan et al., 2009). Consistent with its previously defined role in human adult cells  
13 (Van Den Berg et al., 1998), canonical signaling increased proliferation of blood committed  
14 progenitors when administered during the proper window of time during EB development.  
15 However, a short pulse of non-canonical signaling was necessary and sufficient to control  
16 exit of hESCs from the pluripotent state and subsequent entry into the  
17 mesendoderm/mesoderm lineages (Vijayaragavan et al., 2009). Taken together, these  
18 findings provide the first evidence of a unique role for non-canonical signaling in early  
19 specification of hematopoiesis from hESCs, whereas canonical signaling affects the  
20 proliferation of cells already fated to blood. These studies provide a valuable model system  
21 for examining the possibility of chronological activation and interaction between non-  
22 canonical and canonical signaling in the cellular progression from mesoderm to blood. The  
23 controversial function of canonical signaling on the reconstituting capacity of adult HSCs,  
24 combined with these present findings in hESCs, underscores the importance of fine tuning  
25 the strength and duration of Wnt signaling towards therapeutically exploiting the balance  
26 between self-renewal and lineage commitment of HSCs.

27 However, there are conflicting reports on the requirement for Wnt/ $\beta$ -catenin signaling in  
28 basal hematopoiesis: conditional disruption of  $\beta$ -catenin in adult HSCs does not affect their  
29 ability to self-renew and reconstitute hematopoietic lineages (Huang et al, 2009). In addition,  
30 although overexpression of stabilized  $\beta$ -catenin increases immunophenotypic HSCs, this is  
31 associated with a loss of repopulating activity and hematopoietic failure *in vivo* (Kirstetter et  
32 al., 2006), findings that appear incompatible with a positive role for  $\beta$ -catenin in  
33 hematopoiesis. A general conclusion from these apparently conflicting reports is that the  
34 role of Wnt signaling in hematopoiesis is complex and context dependent (Staal & Sen,  
35 2008). However, although the  $\beta$ -catenin loss-of-function studies suggest that canonical Wnt  
36 signaling is not essential for basal hematopoiesis in adults, they do not rule out a possible  
37 role for the Wnt/ $\beta$ -catenin pathway under nonbasal conditions and are still compatible with  
38 gain-of-function experiments in which the pathway is activated.

#### 39 **4.4 Wnt signaling and malignant HSC**

40 Stem cell quiescence is closely associated with protection from myelotoxic insults (Cheshier  
41 et al, 1999). Similar to the role of tissue SCs in normal tissues, several cancers are also  
42 propagated by small populations of quiescent cancer stem cells (CSCs) that are resistant to  
43 both conventional chemotherapy and targeted therapies, and are retained and contribute to  
44 relapse following discontinuation of therapy (Dick, 2008).

1 When *Ctnnb1* was deleted contemporaneously with activation of BCR-ABL using retroviral  
2 infection and transformation of HSC, chronic myeloid leukemia stem cell (CML-LSC) failed  
3 to engraft in secondary recipient mice (Hu Y et al., 2009). These experiments clearly indicate  
4 a pivotal role of Wnt signaling in CML-LSC development. More recently, *Ctnnb1* has been  
5 investigated in the maintenance of already engrafted CML-LSC. In this clinically relevant  
6 setting, pharmacologic or genetic inactivation of *Ctnnb1* after onset of the myeloproliferative  
7 disease acted synergistically with imatinib, reduced LSC numbers, and improved survival in  
8 a BM transplant model (Abrahamsson et al., 2009). Thus, despite its dispensability for adult  
9 HSC, CML-LSCs seem to retain dependency on canonical *Ctnnb1* to maintain self-renewal  
10 capacity. In human disease, *Ctnnb1* activation via the canonical Wnt pathway has been  
11 shown to occur in CML-blast crisis LSCs. Aberrant splicing of *GSK3* appears to contribute to  
12 this hyperactivation in blast crisis samples (Abrahamsson et al., 2009). Thus, there is  
13 growing evidence that canonical Wnt signaling is an attractive target pathway in the  
14 treatment of CML-LSC. Moreover, cell extrinsic inhibition of Wnt signaling through ectopic  
15 *DKK1* expression impairs leukemia cell proliferation *in vitro* (Zhu et al., 2009).

## 16 **5. Intestinal SCs**

17 Homeostasis of the intestinal epithelium is maintained by an intestinal SC (ISC)  
18 compartment that resides at the bottom of the crypt, safely far from the shear stresses and  
19 potentially toxic agents. These ISC are at the top of a cellular hierarchy and are crucial for  
20 the renewal of the differentiated progeny within the intestinal layer (Medema & Vermeulen,  
21 2011). Indeed, as they migrate out of their niche, they cease to proliferate and initiate  
22 differentiation into the different cell lineages of the mature villi: absorptive enterocytes,  
23 mucin-secreting-goblet cells, peptide hormone-secreting neuroendocrine cells, and  
24 microbicide-secreting Paneth cells. Until relatively recently, ISCs were a rather elusive  
25 entity at the bottom of the intestinal crypt, and the discovery of ISC markers has only partly  
26 detailed the organization of the intestinal crypt and villi. Briefly, the marker *LGR5* identifies  
27 crypt base columnar cells (CBCC) located in between the Paneth cells at the crypt bottom  
28 (Barker et al., 2007), whereas the markers *BMI1* and *TERT* identify the +4 position in the  
29 crypt, just above the Paneth cells (Montgomery et al., 2011; Sangiorgi & Capecchi, 2008).  
30 Knock-in constructs that allow expression of GFP and Cre from the *Lgr5* locus show that  
31 *LGR5* expression is confined to CBCCs, and that these cells give rise to the variety of  
32 epithelial cells present in crypts, proving that CBCCs function as ISCs as well (Barker et al.,  
33 2007, Sato et al., 2009). The existence of these different types of ISC remains a matter of  
34 debate and notably, remains to be determined whether and how *BMI1*+ +4 cells ISCs and  
35 *LGR5*+ ISCs relate to each other. Interestingly, recent data indicate that *TERT*-expressing  
36 ISCs can generate *LGR5*+ ISCs (Montgomery et al., 2011) suggesting that these different ISC  
37 types may act in a hierarchical fashion. Regardless of this dispute about ISC identity, there is  
38 a consensus that ISCs reside in a niche that provides the cells with essential signals such as  
39 Wnt, Notch and Hedgehog. Under normal circumstances, the Paneth cell signals dictate the  
40 size of the SC pool to maintain the total number of SCs within the niche constant. SCs may  
41 divide asymmetrically, so that one SC remains within the niche, resulting in self-renewal,  
42 whilst the other daughter cell gives rise to progenitor cells that can migrate up the crypt and  
43 become more differentiated as they reach the top. Alternatively, two recent studies (Lopez-  
44 Garcia et al., 2010; Snippert et al., 2010) support that SCs may divide symmetrically either

1 forming two daughter SCs (leading to expansion) or two daughter non-stem progenitor cells  
2 (leading to extinction). Several pathways play a role in maintaining and regulating stem  
3 ISCs, including Wnt and Notch.

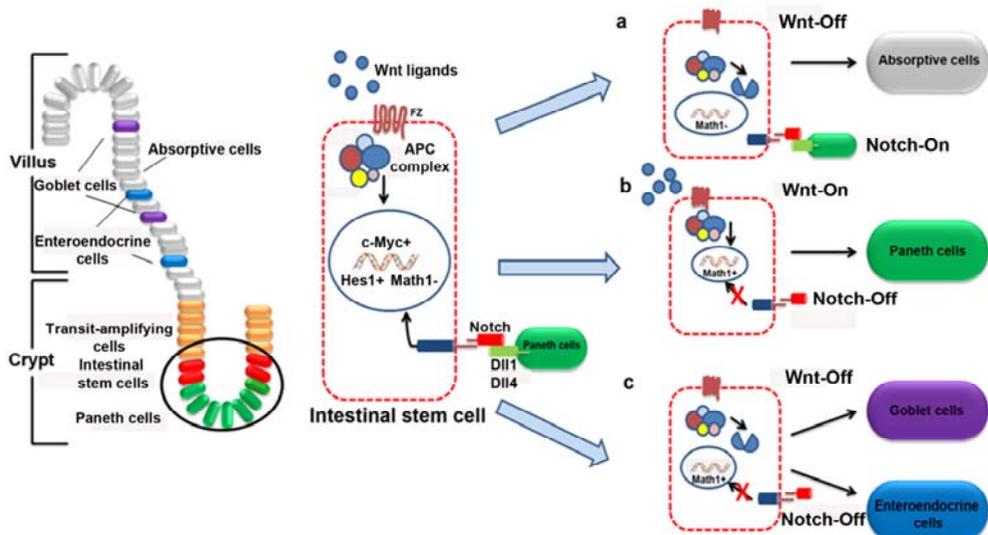
#### 4 **5.1 Notch signaling in intestinal epithelium**

5 In the intestine, Notch activity determines lineage decisions between enterocyte and  
6 secretory cell differentiation. Several components of the Notch pathway are expressed in  
7 adult intestinal crypt cells, suggesting a role for Notch signaling in gene expression  
8 programs in immature proliferating compartment cells (Sander & Powell, 2004; Schroder  
9 & Gossler, 2002). The first evidence that Notch signaling plays a role in cell-type  
10 specification in the intestine was reported in Hes1 knockout mice (Jensen et al., 2000). The  
11 deletion of the Hes1 gene resulted in the generation of excessive numbers of goblet cells,  
12 enteroendocrine cells, and Paneth cells. Subsequently, it was shown that Math1 (mouse  
13 atonal homolog1), one of the genes repressed by Hes1, is required for the differentiation  
14 into the three secretory lineages, because the intestinal epithelium of Math1-mutant mice  
15 is populated only by absorptive cells (Yang et al., 2001). These data suggest that the choice  
16 between the absorptive or secretory fate might be the first decision made by each  
17 progenitor cells, and that Hes1 and Math1 activated by Notch signal play opposite roles in  
18 this decision making. Recently, using the villin promoter to drive the expression of a  
19 constitutively active form of mouse Notch1 receptor, it was noticed an expansion of  
20 proliferating intestinal progenitor cells (Fre et al., 2005). Moreover, Notch activation  
21 inhibited the differentiation of secretory cells in the mouse intestine, as there was a  
22 complete depletion of goblet cells, a marked reduction in enteroendocrine cells, and a low  
23 expression of early marker for Paneth cells. These results clearly suggest that Notch  
24 signaling is required for maintaining crypt cells in a proliferative state, at least in part,  
25 through its negative regulation of Math1. Conversely, conditional removal of the Notch  
26 pathway transcription factor CSL/RBP-J increases the proportion of goblet cells in the  
27 murine intestine, and a similar phenotype was observed using a  $\gamma$ -secretase inhibitor (van  
28 Es et al., 2005). These results suggest that Notch pathway is not only a gatekeeper for  
29 proliferating crypt progenitor cells, but is also involved in controlling the balance between  
30 secretory and absorptive cell types. Data suggest that the ISC microenvironment delivers  
31 Notch-activating signals to maintain stemness, which is consistent with the observation  
32 that Paneth cells express Notch ligands (Sato et al., 2011). In particular, recent papers  
33 identified Dll1 and Dll4 as the physiologically relevant Notch1 and Notch2 ligands within  
34 the small intestine of the mouse. These ligands cooperate and exhibit a partial functional  
35 redundancy to maintain the crypt progenitor compartment (Pellegrinet et al., 2011).  
36 However, Notch seems to have dual functions in the crypt, as it acts together with Wnt to  
37 affect significantly crypt homeostasis (Fre et al., 2005; van Es et al., 2005).

#### 38 **5.2 Canonical Wnt signaling in intestinal epithelium**

39 The Wnt pathway proteins regulate cellular fate along the crypt-villus axis in normal gut  
40 epithelium and have been implicated in ISC self-renewal. The nuclear accumulation of  $\beta$ -  
41 catenin is preferentially observed in cells located at the base of crypts and decreases as cells  
42 move toward the top of the crypts (van der Wetering et al., 2002). Wnt target genes EphB2

1 and EphB3 control crypt cellular segregation (Batlle et al., 2002), Sox9 regulates Paneth cell  
2 differentiation (Mori-Akiyama et al., 2007), and Lgr5 (Barker et al., 2007). TCF4 null mice  
3 died shortly after birth and showed an embryonic epithelium made entirely of differentiated  
4 cells without proliferative compartments in the crypts (Korinek et al., 1998) suggesting that  
5 TCF4 maintains the proliferation of SCs in the murine small intestine. Notably, deletion of  
6 the Wnt/TCF4 target gene c-Myc led to a loss of intestinal crypts in a murine model  
7 (Muncan et al., 2006). The importance of the Wnt signaling pathway in maintaining the  
8 architecture and homeostasis of the adult intestinal epithelium was also shown in a murine  
9 model through adenoviral expression of Dkk1. This induced Wnt inhibition in fully adult  
10 mice, resulted in inhibition of proliferation in the small intestine and colon, with progressive  
11 loss of crypts, villi and glandular structure (Kuhnert et al., 2004). By contrast, when the Wnt  
12 pathway is overactivated by mutations in APC or  $\beta$ -catenin, many of the epithelial cells  
13 enter into the proliferative state and display a failure of the differentiation programs  
14 (Andreu et al., 2005; Sansom et al., 2004). According with these data, recent papers  
15 demonstrated that injection of R-spondin1 (R-Spo1), a potent activator of the Wnt signaling  
16 pathways, induced rapid onset of crypt cell proliferation displaying epithelial hyperplasia in  
17 the intestine of normal mice through  $\beta$ -catenin stabilization and subsequent transcriptional  
18 activation of target genes such as murine Axin2, Ascl2, and Lgr5 (Kim et al., 2005;  
19 Takashima et al., 2011). The effects of R-Spo1 administration determine protection against  
20 radiation-induced colitis by stimulating proliferation of intestinal SCs and protect them  
21 against a damage after allogeneic bone-marrow transplantation, suppressing inflammatory  
22 cytokine cascades and donor T cell activation (Takashima et al., 2011). These, *in vivo*, data  
23 suggest that Wnt signaling is directly linked to the promotion of cellular proliferation and,  
24 more specifically, the regulation of progression through cell cycle. In this regard, previous  
25 papers pointed to the downregulation of p21<sup>cip1waf1</sup>, a cyclin-dependent kinase inhibitor  
26 (CKI), as an important mechanism that might mediate Wnt-dependent growth promotion. A  
27 microarray analysis showed that p21<sup>cip1waf1</sup> was one of the genes whose expression was  
28 increased by inhibition of Wnt signaling in human colorectal cancer-derived LS174T cells  
29 (van der Wetering et al., 2002). Furthermore, the TCF4 target gene c-Myc has been shown to  
30 play a central role in Wnt-mediated repression of p21<sup>cip1waf1</sup> expression at the transcriptional  
31 level through its direct binding to the p21<sup>cip1waf1</sup> gene promoter (van der Wetering et al.,  
32 2002). These data suggest that the repression of p21<sup>cip1waf1</sup> by c-Myc might be the  
33 intracellular mechanism by which Wnt signaling regulates the G1/S transition and cell cycle  
34 progression. This signaling cascade has been shown to be functional *in vivo*, because  
35 abnormal features of proliferation/differentiation in the adult murine intestine, which occur  
36 with the single deletion of APC, are mostly rescued when c-Myc gene is simultaneously  
37 deleted (Sansom et al., 2007). Furthermore, this restoration of the morphologically normal  
38 phenotype in double mutant mice for APC and c-Myc is accompanied by restoration of p21  
39 expression within the crypts, suggesting the involvement of p21 in the Wnt-c-Myc pathway-  
40 mediated growth control of progenitor cells. Indeed, raises the possibility that p21 is an  
41 intracellular molecular switch between proliferation and differentiation. Moreover, it has  
42 been shown that conditional expression of p21<sup>cip1waf1</sup> alone allow cells to differentiate (van  
43 der Wetering et al., 2002) suggesting that the cell fate choice between proliferation and  
44 differentiation is regulated by modulation of the expression of p21<sup>cip1waf1</sup> via the direct  
45 induction of c-Myc by Wnt signaling.



1  
2 Fig. 5. The role for Notch and Wnt pathways in intestinal epithelial proliferation and  
3 differentiation. The ISC can give rise to four lineages of terminally differentiated cells: a is  
4 absorptive cells, b and c (Paneth, goblet and enteroendocrine cells) have secretory  
5 phenotypes. See the text for detail.

6 In general, the data strongly support a model in which Notch directs proliferation when  
7 Wnt signal activity is high, and directs enterocyte differentiation when Wnt activity levels  
8 drop towards the top of the crypt. The multipotent progenitors require both Wnt and Notch  
9 signals to be activated for fulfilling continuous proliferation without differentiation. Once  
10 some cells in this Wnt and Notch-activated population escape from the Notch signal, they  
11 stop proliferating and acquire the Math1 function. These cells raise the terminally  
12 differentiation in secretory cells in areas where the Wnt signal is not active (Pinto et al.,  
13 2003), whereas they differentiate in Paneth cells if they remain at the bottom of the crypt  
14 where Wnt ligands are abundant. By contrast, if cells in this Wnt and Notch-active  
15 population lose the Wnt signal, for example, because of their positional changes along the  
16 vertical axis, they differentiate as absorptive cells (Fig. 5).

### 17 5.3 SCs and the origin of intestinal cancer

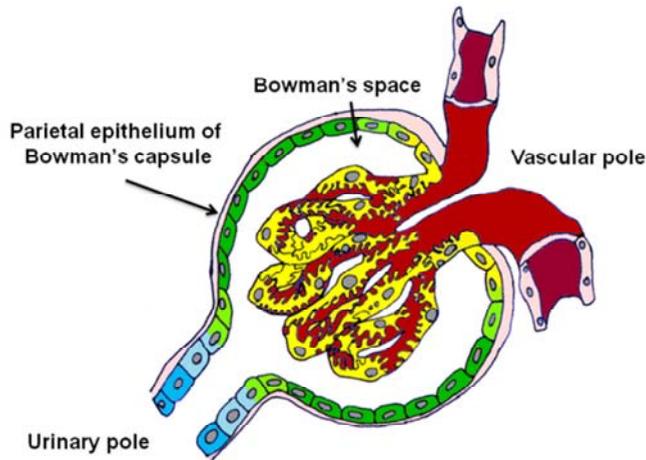
18 Despite stringent homeostatic maintenance in the intestine, the high number of patients  
19 with colorectal cancer (CRC) indicates that these regulatory mechanisms often fall short in  
20 protecting against malignant transformation. Both environmental and genetic risk factors  
21 have been defined for CRC, and deregulation of morphogenetic pathways plays a key part  
22 in cancer development. Notably, the vast majority of sporadic CRC cases carry Wnt  
23 pathway mutations, highlighting the importance of this pathway in CRC. The hit that  
24 induces transition from normal to polypoid tissue is accompanied by several changes in  
25 crypt appearance and behavior, cells show a more immature phenotype and a higher  
26 proliferative index which results in expansion of the pre-malignant clone. Although

1 mutation of APC or  $\beta$ -catenin is an early event in the transformation of colonic epithelial  
2 cells, studies have revealed that colon carcinomas do not contain nuclear  $\beta$ -catenin  
3 homogeneously (Fodde & Brabletz, 2007). This so-called  $\beta$ -catenin paradox indicate that  
4 Wnt signaling has a preponderant role only for a subset of tumour cells, cancer SCs (CSCs),  
5 which are endowed with tumorigenic capacity (Vermeulen et al., 2008). Indeed, the past  
6 decade has seen a shift in the way tumours are perceived, and the now widely accepted  
7 model is that tumours contain a small population of self-renewing CSCs, as well as a large  
8 compartment of more differentiated tumour cells (Vermeulen et al., 2008). Cellular hierarchy  
9 within CRC is maintained, at least in part, by microenvironmental factors regulating  
10 stemness and differentiation. In agreement, tumour cells located next to myofibroblast-rich  
11 regions, have a much higher incidence of nuclear-localized  $\beta$ -catenin, suggesting for  
12 microenvironment-modulated Wnt signaling (Fodde & Brabletz, 2007). A recent paper point  
13 to hepatocyte growth factor (HGF) as the myofibroblast-derived signal that, at least in part,  
14 orchestrates this intimate relationship and enhances Wnt activity in more differentiated  
15 tumour cells, thereby reinstalling CSCs features (dedifferentiation) (Vermeulen et al., 2010).  
16 Indeed, using a TCF/LEF reporter that directs the expression of enhanced green fluorescent  
17 protein, authors provided evidence that Wnt signaling activity is a marker for colon CSCs  
18 and is regulated by the microenvironment. Moreover, they show that differentiated cancer  
19 cells can be reprogrammed to express CSC markers and regain their tumorigenic capacity  
20 when stimulated with myofibroblast-derived factors (Vermeulen et al., 2010). Although,  
21 these data clearly ascertain a role for the Wnt pathway in CRC stemness, Notch inhibition  
22 with an antibody against the Notch ligand Dll4 results in human colon CSCs differentiation,  
23 reduction of CRC growth in a xenotransplantation model and chemosensitization (Hoey et  
24 al., 2009).

## 25 **6. Identification of Renal SCs.**

26 The mammalian kidney shares with the majority of organs the ability to repopulate and at  
27 least partially repair structures that have sustained some degree of injury. Indeed, tubular  
28 integrity can be rescued after acute damage, and even severe glomerular disorders  
29 sometimes may undergo regression and remission, suggesting that glomerular injury is also  
30 reparable (Imai & Iwatani, 2007; Remuzzi, et al., 2006). However, the existence of renal SC  
31 (RSC) has been a matter of long debate. Recently, converging data definitively demonstrated  
32 the existence of a population of stem/progenitor cells in the parietal epithelium of the  
33 Bowman's capsule of adult human kidney (Sagrinati, et al., 2006) (Fig.6). These SC coexpress  
34 both CD24, a surface molecule that has been used to identify different types of human SC,  
35 and CD133, a marker of several types of adult tissue SC, lack lineage-specific markers,  
36 express transcription factors that are characteristic of multipotent SC, and exhibit self-  
37 renewal, high clonogenic efficiency and multidifferentiation potential. When injected  
38 intravenously in SCID mice that had acute kidney injury, RSC regenerated tubular  
39 structures from different portions of the nephron and also reduced the morphological and  
40 functional kidney damage (Sagrinati, et al., 2006).

41 In addition, it was demonstrated that RSC are arranged in a precise sequence within  
42 Bowman's capsule of adult human kidneys (Ronconi, et al., 2009) (Fig. 6).



1  
2 Fig. 6. Localization of RPC in the glomerulus. RPC (green) are localized in the Bowman's  
3 capsule epithelium. A transitional cell population (podocyte progenitors, green/yellow)  
4 displays features of either RPC or podocyte (yellow) and localize between the urinary pole  
5 and the vascular stalk. Cells that express only podocyte markers and the phenotypic  
6 features of differentiated podocytes (yellow) localize at the vascular stalk of the glomerulus.

7 These findings obtained in human kidneys were confirmed in a parallel study performed in  
8 murine kidney by Appel (Appel, et al., 2009), who also demonstrated the existence of  
9 transitional cells with morphological and immunohistochemical features of both parietal  
10 epithelial cells in proximity of the glomerular vascular stalk and that podocytes are  
11 recruited from parietal epithelial cells, which proliferate and differentiate from the urinary  
12 to the vascular stalk, then generating novel podocytes (Fig. 6). This occurs as the kidney  
13 grows, during childhood and adolescence, and may also take place following an injury  
14 which allows a slow, regulated generation of novel podocytes, such as uninephrectomy.  
15 Recently, a rare subpopulation of CD133+CD24+ cells has also been describe in renal  
16 tubules (Lindgren, et al., 2011). These cells are able to proliferate and differentiate after  
17 tubular injury. Accordingly, tubular epithelium regenerating on acute tubular necrosis  
18 displayed long stretches of CD133+CD24+ cells, further substantiating that the cells that are  
19 repairing tubular epithelium may simply represent the result of proliferation and  
20 differentiation of CD133+CD24+ tubular progenitors.

## 21 6.1 Involvement of RSC in glomerular disorders and cancer.

22 It has been widely recognized that a disruption in the strictly regulated balance of SC self-  
23 renewal and differentiation not only impairs regenerative mechanisms but can even  
24 generate disorders. In the glomerulus, the response to podocyte injury may cause aberrant  
25 epithelial cell proliferation, hypercellular lesions formation and Bowman's space  
26 obliteration, as seen in collapsing glomerulopathy and in crescentic glomerulonephritis  
27 (Albaqumi & Barisoni, 2008; Thorner, et al., 2008). Until now, theories explaining the origin  
28 of aberrant epithelial cells in collapsing glomerulopathy and crescentic glomerulonephritis  
29 have been controversial. One possibility is that these cells are exclusively of parietal  
30 epithelial origin (Thorner et al., 2008 ), while another is that some dedifferentiated

1 podocytes acquire markers of parietal epithelial cells (Moeller et al., 2004). It was recently  
2 demonstrated that the majority of cells present in the hyperplastic lesions in collapsing  
3 glomerulopathy or crescentic glomerulonephritis exhibits the RSC markers CD133 and  
4 CD24, with or without coexpression of podocyte markers (Smeets et al., 2009). Therefore, it  
5 is suggested that the glomerular hyperplastic lesions are generated by RSC of Bowman's  
6 capsule at different stages of their differentiation towards mature podocytes. Support for  
7 this hypothesis came from lineage tracing experiments performed in transgenic mice with  
8 genetically labeled parietal epithelial cells in a model of inflammatory crescentic  
9 glomerulonephritis, and of collapsing glomerulopathy (Smeets et al., 2009).

10 Finally, a close relationship between the transcriptome of CD133+ tubular progenitors and  
11 the one derived by papillary renal cell carcinomas was demonstrated (Lindgren et al. 2011).  
12 Moreover, a strong CD133 expression was observed in the papillary renal cell carcinomas  
13 analysed. Thus, these observations raise the provocative hypothesis that papillary renal cell  
14 carcinomas may directly derive from CD133+CD24+ renal tubular progenitors, whereas clear  
15 renal cell carcinomas may derive from other more differentiated proximal tubular cells.

## 16 **6.2 Signaling pathway regulating the RSC niche.**

17 The molecular mechanisms regulating the proliferation of RSC, as well as the cell fate  
18 determination in the podocyte lineage are unknown. We recently demonstrate the role of the  
19 Notch signaling pathway in both these processes (Lasagni et al., 2010). Notch activation  
20 triggers the expansion of renal progenitors by promoting their entry into the S-phase of the  
21 cell cycle and mitotic division. Moreover, Notch downregulation is required for  
22 differentiation toward the podocyte lineage. However, Notch downregulation was neither  
23 sufficient nor necessary for the acquisition of a podocyte phenotype, but an impaired  
24 downregulation of the Notch pathway led to podocyte death. Indeed, renal progenitor  
25 differentiation into podocytes was associated with cell cycle checkpoint activation and  
26 G<sub>2</sub>/M arrest, reflecting an intrinsic barrier to replication of mature podocytes. Persistent  
27 activation of the Notch pathway induced podocytes to cross the G<sub>2</sub>/M checkpoint, resulting  
28 in cytoskeleton disruption and cell death (Lasagni et al., 2010). Notch expression was  
29 virtually absent in the glomeruli of healthy adult kidneys, while a strong upregulation was  
30 observed in renal progenitors and podocytes in patients affected by glomerular disorders.  
31 Accordingly, inhibition of the Notch pathway in mouse models of focal segmental  
32 glomerulosclerosis ameliorated proteinuria and reduced podocyte loss during the initial  
33 phases of glomerular injury, while inducing reduction of progenitor proliferation during the  
34 regenerative phases of glomerular injury with worsening of proteinuria and  
35 glomerulosclerosis. Taken altogether, these results suggest that the severity of glomerular  
36 disorders depends on the Notch-regulated balance between podocyte death and  
37 regeneration provided by renal progenitors (Lasagni et al., 2010).

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