

Wnt signaling and neural stem cells: caught in the Wnt web

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Abstract Wnt proteins have now been identified as major physiological regulators of multiple aspects of stem cell biology, from self-renewal and pluripotency to precursor cell competence and terminal differentiation. Neural stem cells are the cellular building blocks of the developing nervous system and provide the basis for continued neurogenesis in the adult mammalian central nervous system. Here, we outline the most recent advances in the field about the critical factors and regulatory networks involved in Wnt signaling and discuss recent findings on how this increasingly intricate

pathway contributes to the shaping of the developing and adult nervous system on the level of the neural stem cell.

Keywords Signaling · Wnt · Stem cell · Neurogenesis · Development

Introduction

In order to generate the vast number of neurons and glia of the mature nervous system, proliferation and maintenance of neural stem cells has to be balanced against their commitment towards a neural lineage. These decisions as well as the subsequent differentiation and maturation of the neural stem cell progeny are largely controlled by extrinsic signals. Wnt ligands are secreted proteins that are characterized by a high number of conserved cysteine residues. The founding member of the Wnt-protein family, i.e. Wnt-1, was identified in 1982 by Nusse and Varmus (Nusse and Varmus 1982) as a preferential integration site for mouse mammary tumor virus-induced breast tumors. Since then, numerous Wnt proteins have been described including 19 human and murine Wnt proteins (for additional information see Wnt homepage: <http://www.stanford.edu/~rnusse/wntwindow.html>). Work over the last 25 years has established Wnt proteins as essential regulators for the development of various organs including the nervous system as well as for adult tissue homeostasis (for review see, e.g., (Logan and Nusse 2004; Clevers 2006)). Wnt proteins participate in the regulation of almost every aspect of neural development including patterning of the neural tube, neural stem cell maintenance, proliferation, fate determination, axon guidance, dendrite development, and synapse formation. The ability of Wnt proteins to control these biologically

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divergent and sometimes opposing processes in neural development may be explained by their great potential to elicit several signaling cascades and coordinate multiple cellular signals and their downstream molecular targets.

At least two distinct pathways are activated by Wnts, the so-called canonical branch, which results in the activation of β -catenin/TCF transcriptional regulatory complexes (Clevers 2006), and the non-canonical β -catenin-independent branch, which involves a wide range of downstream signaling effectors (Klein and Mlodzik 2005; Kohn and Moon 2005). The canonical Wnt/ β -catenin branch is typically activated by the Wnt1 class (Wnt1, 2, 3, 3a, 8 and 8a), whereas the non-canonical pathway is triggered by the Wnt5a class of Wnt ligands (Wnt4, 5a, 5b, 6, 7a and 11). Activation of both branches is initiated by binding of the relevant Wnt ligands to the corresponding Frizzled receptors, which appear to play an active role in the final output of Wnt signaling (Mikels and Nusse 2006). Despite increasing evidence implicating the non-canonical signaling in the regulation of gastrulation and neurulation, there is only limited information with regards to the significance of this pathway in the biology of neural stem cells. Therefore, in this review we will first summarize the two Wnt branches and then focus on the critical components and interplays that adjust the output of the canonical, β -catenin-dependent pathway. We will subsequently discuss the diverse points of connection of canonical Wnt signaling with neural stem cell biology for which we have the most information and the greatest understanding.

The Wnt-signaling pathways

Canonical branch

In the absence of a Wnt signal, free cytoplasmic β -catenin is recruited in a large “scaffolding” complex consisting of Axin, APC (adenomatous polyposis coli), CK1 (casein kinase 1) and the serine/threonine kinase GSK (glucocin synthase kinase)-3 β . This cytoplasmic complex allows the sequential phosphorylation of β -catenin at the N-terminal “destruction box.” The phosphorylated β -catenin binds to the β -TrCP (β -transducin repeat-containing protein) component of a E3 ubiquitin ligase complex, which catalyses the ubiquitination of β -catenin and its subsequent destruction by the proteasome machinery. In the presence of Wnt, binding of the ligand to a Frizzled receptor and the LRP5/6 coreceptor triggers the recruitment of the two cytoplasmic components, Dishevelled and Axin, respectively. By an as yet ill-defined mechanism, GSK3 β is then released from the scaffolding complex, resulting in accumulation of unphosphorylated β -catenin, which enters the nucleus and forms complexes with a number of transcription factors, the

most common ones being the members of the Tcf (T-cell factor) and LEF (lymphocyte enhancer factor) family. In the absence of β -catenin, Tcf/LEF proteins act as transcriptional repressors by forming complexes with Groucho/TLE (transducin-like enhancer of split) proteins. The interaction with β -catenin converts these repressors into activators, which via recruitment of diverse coregulatory molecules, induce the expression of downstream target genes (for a comprehensive list, see the Wnt homepage: <http://www.stanford.edu/~rnusse/pathways/targets.html>). The ability to switch between a repressor and an activator status is a regulatory strategy that appears to be utilized also by other transcription factors mediating signaling (Barolo and Posakony 2002), and establishes a tight control of target gene expression at the transcriptional level (van Es et al. 2003).

Non-canonical branch

The non-canonical signaling branch has at least two intracellular signaling cascades, namely the Wnt/planar cell polarity (PCP) and the Wnt/ Ca^{2+} pathway. In the Wnt/PCP pathway, Wnt proteins bind to Frizzled receptors on the cell surface and activate Rho/Rac small GTPases (Habas et al. 2003) or the Jun N-terminal kinase (JNK) (Moriguchi et al. 1999), thereby regulating gene expression and subsequent cytoskeletal organization in crucial morphogenetic events during development (Veeman et al. 2003; Wang and Malbon 2003; Kuhl 2004). It is important to note that the precise orchestration of these signaling events is not yet fully characterized. In the Wnt/ Ca^{2+} pathway, the binding of Wnts to Frizzled receptors stimulates heterotrimeric G proteins and phospholipase C, thereby increasing intracellular Ca^{2+} release and decreasing cyclic guanosine monophosphate (cGMP) levels. This results in activation of Ca^{2+} -calmodulin-dependent protein kinase II (CamKII) and protein kinase C (PKC), which in turn can stimulate nuclear factor (NF)-AT and other transcriptional regulators (Veeman et al. 2003; Wang and Malbon 2003; Kuhl 2004). It is not yet clear whether the PCP and Wnt/ Ca^{2+} pathways are overlapping or represent distinct, context-specific noncanonical branches.

Critical players of the canonical signaling

The biogenesis of the Wnt ligands

The mechanisms that regulate synthesis, sorting and secretion of Wnts are particularly complex [for a recent review, see (Coudreuse and Korswagen 2007)]. For their secretion, Wnt proteins need to be post-translationally modified in the endoplasmic reticulum (ER) by cysteine palmitoylation (Willert et al. 2003), a modification which allows them to be loaded to lipoprotein particles (Panakova

et al. 2005). The relevant enzyme has been identified as *porcupine* in *Drosophila* (Hofmann 2000) and *mom-1* in *C. elegans* (Zhai et al. 2004). The intracellular trafficking requires a conserved seven-pass transmembrane protein, which is colocalized with Wnt in the Golgi apparatus. It is encoded by a conserved gene known as *wntless (wls)* or *evenness interrupted (evi)* (Banziger et al. 2006; Bartscherer et al. 2006). Another component of the Wnt secretory pathway is the protein VPS-35, a subunit of the “retromer” complex, which is essential for secretion of the ligand and formation of the long-range gradient (Coudreuse et al. 2006; Prasad and Clark 2006).

Receptors and co-receptors

The main receptors of Wnts, the Frizzled proteins, consist of at least ten family members that share a highly conserved seven-transmembrane domain separated by short extracellular and cytoplasmic loops, a cysteine-rich extracellular N-terminal domain and a less conserved cytoplasmic domain of variable size. An additional level of complexity is provided by the fact that a single Wnt can bind to Frizzled proteins with different affinities, suggesting that the specific action of Wnt might be determined by the individual Frizzled receptor that is expressed in the target cell (Hsieh 2004; Kikuchi et al. 2007). For the canonical Wnt signaling pathway, Frizzled receptors synergize with a single-pass transmembrane protein of the low-density-lipoprotein receptor family (LRP) known as Arrow in *Drosophila* (Wehrli et al. 2000) and LRP5/6 in vertebrates (Pinson et al. 2000; Tamai et al. 2000). The surface expression of both types of receptors is essential for the initiation of the Wnt signal, and in the case of Arrow/LRP5/6, this is dependent on a chaperone called Mesd in mice (Hsieh et al. 2003). A second, recently identified coreceptor for both canonical and non-canonical Wnt signaling is a transmembrane tyrosine kinase receptor from the Ryk family. Like the LRP5/6 coreceptor, Ryk can form a complex with Frizzled proteins and initiate the canonical pathway (Lu et al. 2004). Interestingly, Ryk can also activate the non-canonical pathway through Frizzled-independent signaling cascades (Cheyette 2004; Bejsovec 2005); however the signaling events downstream of these cascades are not known. Ryk proteins contain an extracellular domain with homology to Wnt inhibitory factor (WIF1) and a conserved PDZ-binding motif, which links Ryk to downstream molecules of the canonical Wnt pathway, such as Dishevelled (Cheyette 2004; Lu et al. 2004; Bejsovec 2005).

Extracellular modulators of Wnt signaling

A common theme in many potent signaling pathways is the presence of regulatory proteins capable of dampening down the effects of the ligands. On this level, the Wnt activity is

controlled by transmembrane as well as secreted proteins. Secreted antagonists include soluble forms of Frizzled-related proteins (sFRPs), members of the Dkk family of proteins, Cerberus and WIF proteins, which inhibit Wnt signaling either by binding directly to Wnts or to the receptor components (Kawano and Kypta 2003). The sFRP proteins contain the cysteine-rich domain (CRD) of the Frizzled family that is sufficient and necessary for Wnt binding, but no transmembrane regions (Hoang et al. 1996). Therefore, they are able to bind and sequester Wnts preventing their interaction with Frizzled and LRP5/6 receptors and inhibiting both canonical and non-canonical signaling (Finch et al. 1997; Leyns et al. 1997; Hsieh et al. 1999). In contrast, Dkk proteins such as Dkk1 do not bind to Wnt ligands, but rather to the coreceptor LRP5/6, and therefore, they specifically inhibit the Wnt canonical pathway (Glinka et al. 1998). Through the interaction with LRP5/6, Dkk1 recruits a different class of transmembrane molecules, the Kremens (Mao et al. 2002). In the simplest model, the Dkk1-LRP5/6-Kremen complex is internalized and degraded, thus depleting the cell surface from the LRP5/6 coreceptor, which is essential for the canonical signaling. Interestingly, there are three members in the Dkk family. While Dkk1 acts as a specific Wnt antagonist, Dkk2 also binds to LRP5/6, but depending on the cellular context it can either activate or inhibit the canonical pathway (Li et al. 2002), whereas Dkk3 fails to bind to LRP5/6 and inhibit Wnt signaling (Krupnik et al. 1999). Cerberus functions as a more general, multivalent growth-factor antagonist, as in addition to Wnt it binds to Nodal and BMP ligands via independent sites (Piccolo et al. 1999). The synchronized inhibition of all three pathways by Cerberus results in simultaneous head formation and trunk inhibition. WIF1 also appears to antagonize Wnt signaling by sequestering Wnts from their Frizzled receptors; however in contrast to sFRPs, it lacks a CRD-like domain (Hsieh et al. 1999).

The regulation of the Wnt pathway at the extracellular level becomes even more complex considering that depending on the context, extracellular inhibitors can also enhance signaling by facilitating Wnt secretion, transport or stability (Logan and Nusse 2004). In addition, the canonical Wnts are sensitive to the action of other non-canonical Wnts, which are capable of interfering with the canonical pathway (Logan and Nusse 2004; He and Axelrod 2006). For example, Wnt5a can antagonize the Wnt3a canonical pathway via the tyrosine kinase receptor Ror2 (Mikels and Nusse 2006). Finally, the Frizzled/LRP receptors can also be activated by factors unrelated to Wnt such as the cysteine-knot protein Norrin, which induces the canonical Wnt pathway (Xu et al. 2004), and the R-spondins, which can activate β -catenin (Kazanskaya et al. 2004; Nam et al. 2006) and promote proliferation on the intestinal epithelium (Kim et al. 2005).

Downstream of the activated receptors, the complexity of Wnt signaling is conveyed in the regulation and subcellular distribution of the two crucial transducers, Dishevelled and β -catenin.

Dishevelled

In both canonical and non-canonical pathways the Wnt signal is transmitted through the cytoplasmic multifunctional phosphoprotein Dishevelled (a single member in *Drosophila*, *Dsh* and three members in mammals *Dvl-1*, *-2* and *-3*) (Wallingford and Habas 2005). The function of Dsh/Dvl is required for multiple Wnt/Frizzled cascades, and also in this case, the final response to Wnt activation depends on the cellular context (Ilyas 2005). Recent studies from numerous laboratories have revealed that Dsh/Dvl proteins act as core scaffolds for multicomponent signaling complexes, providing docking sites for a wide range of protein kinases, phosphatases, adaptor proteins as well as for other scaffolding molecules, such as Axin. Dsh/Dvl proteins can self-associate *in vitro* and *in vivo* and generate dynamic assemblies via their DIX (Dishevelled-Axin) domain, which are important for the efficient recruitment of Axin (Schwarz-Romond et al. 2005). These proteins display a remarkably dynamic spatial localization. Accordingly, Dsh/Dvl can act at the plasma membrane, in the cytoplasm or even within the nucleus with the nuclear import of Dsh/Dvl being essential for its function in the pathway (Habas and Dawid 2005; Itoh et al. 2005; Weitzman 2005). The Dsh/Dvl proteins comprise three highly conserved primary domains (Wharton 2003), which are involved in multiple protein-protein interactions with downstream effectors and are essential for subcellular trafficking. This modular structure allows the separate activation of at least three different signaling cascades: (1) the Wnt/ β -catenin canonical pathway that regulates nuclear translocation of β -catenin and activation of the Tcf/LEF transcriptional regulators, (2) the Wnt/ROCK (Rho-associated protein kinase)/JNK pathway that controls the non-canonical PCP cascade that modulates the actin cytoskeleton and (3) the Wnt/ Ca^{2+} /cGMP pathways that control the activation of Ca^{2+} -sensitive transcription factors as well as the cGMP-dependent responses that are involved in ventral axis specification (Malbon and Wang 2006). It therefore appears that Dsh/Dvl represents a crucial branching point relatively upstream on the Wnt signaling cascade, which is capable of interpreting the variety of Wnt-generated stimuli and transmitting them downstream into physiologically appropriate signaling routes.

Activation and transcriptional properties of β -catenin

In the absence of the ligand, the cytoplasmic levels of β -catenin are constantly low via a mechanism that involves its

continuous phosphorylation, ubiquitination and degradation by the 26S proteasome. Upon binding of Wnts to their receptors two critical events take place: (1) LRP5/6 becomes sequentially phosphorylated by GSK3 β and CK1- γ (which is anchored in the membrane through C-terminal palmitoylation), thereby generating a high affinity docking site for recruitment of Axin to the cell membrane and its subsequent destabilization (Mao et al. 2001; Davidson et al. 2005; Zeng et al. 2005), (2) Dsh/Dvl is recruited to the membrane where it is hyperphosphorylated by CK1- ϵ and CK2, resulting in recruitment of Frat-1 (Kishida et al. 2001; Lee et al. 2001; Hay et al. 2005) and release of GSK3 β from the scaffolding complex (Li et al. 1999; Ferkey and Kimelman 2002). The destabilization of Axin in combination with the inhibition of GSK3 β activity results in the rapid accumulation of free β -catenin and its translocation into the nucleus where it potently controls transcriptional events. Upon removal of the Wnt source, β -catenin is exported from the nucleus by the APC, which is a key negative regulator of the cascade. Importantly, in addition to promoting the nuclear export of β -catenin (Bienz 2002), nuclear APC was recently shown to counteract the transcriptional activity of β -catenin and to control the periodic exchange of β -catenin-associated coregulatory complexes on the responsive promoters (Sierra et al. 2006).

In the nucleus, β -catenin regulates the expression of Tcf/LEF-dependent target genes by two distinct mechanisms. First, it displaces the Groucho/TLE repressors from the Tcf/LEF proteins via competition for overlapping binding sites, which are located at the Tcf/LEF's N-terminus (Daniels and Weis 2005; Sierra et al. 2006). Second, it recruits regulatory proteins to Tcf/LEF-bound chromatin through two potent transcription activation domains that are present at its N- and C-termini. The N-terminus interacts directly with the adaptor protein Bcl-9/Lgs (Legless) (Stadeli and Basler 2005), and in this way connects LEF-1 to the PHD finger protein Pygopus (Pygo), a transcriptional activator (Willert and Jones 2006; Hoffmans and Basler 2007). By forming this trimeric complex, Bcl-9/Lgs and Pygo proteins have also been implicated in the nuclear localization of β -catenin (Brembeck et al. 2004; Townsley et al. 2004). On the other side, the C-terminus of β -catenin recruits multiple complexes that are capable to modify and to reorganize the chromatin structure [reviewed in (Stadeli et al. 2006; Willert and Jones 2006)].

The activation of Tcf/LEFs by β -catenin can be disrupted by certain inhibitory proteins such as ICAT (inhibitor of β -catenin and Tcf) (Tago et al. 2000) or Chibby (Takemaru et al. 2003). The ICAT-mediated inhibition appears to be crucial for the specification of the fate of neural progenitor cells along the anterior-posterior axis. Indeed, in an *in vitro* system in which Wnt3a was

capable to redirect the fate of neural progenitors to a posterior character, ICAT could directly induce forebrain cells via its inhibitory effect on Wnt (Sato et al. 2004). Importantly, in addition to the Tcf/LEF key DNA-binding partners, β -catenin can also interact with other DNA-binding proteins, such as members of the SRY-box containing (Sox) family of transcription factors (Zorn et al. 1999; Sinner et al. 2004), the bicoid-related protein Pitx2 (Kioussi et al. 2002) and the paired-like homeodomain transcription factor Prophet of Pit1 (Prop1), which was recently found to be important for pituitary cell fate determination (Olson et al. 2006)(see later), thereby providing additional mechanisms that might contribute to the precise control of Wnt/ β -catenin-mediated cell fate decisions.

As is evident from the above, the ability of β -catenin to shuttle between the cytoplasm and the nucleus, interacting with a diverse inventory of proteins ranging from protein kinases to chromatin remodeling factors and chromatin-modifying enzymes as well as to cooperate with different DNA-binding partners in the nucleus, enables the dynamic and precise translation of the extracellular Wnt signal to a specific transcriptional output. It also reflects the competence of β -catenin to act as an additional integration point for various Wnt-induced developmental pathways downstream of Dishevelled.

The Tcf/LEF transcription factors

Another major determinant of the ability of Wnt proteins to regulate a wide range of biological processes is the remarkable diversity of the Tcf/LEF actions in the nucleus (Arce et al. 2006). This complexity is partly due to the occurrence of multiple isoforms for these transcription factors, which in combination with the diverse interactions with the DNA and a wide range of coregulatory proteins can differentially affect the expression of various target genes. Whereas nonvertebrate organisms such as flies and worms carry a single Tcf/LEF gene, higher organisms express at least four family members: Tcf-1, LEF-1, Tcf-3 and Tcf-4 (Hurlstone and Clevers 2002). Furthermore, a large number of isoforms is generated through a combination of alternative splicing and differential promoter usage (Van de Wetering et al. 1996). In addition, Tcf/LEF proteins are characterized by both redundancy and functional diversity. For example, in *Xenopus*, LEF-1 functions as a Wnt-dependent activator, whereas the Tcf members act both as repressors and activators (Dorsky et al. 2002; Gradl et al. 2002; Houston et al. 2002; Standley et al. 2006). In early mouse embryogenesis, Tcf-1 and LEF-1 appear to be redundant since both genes have to be deleted in order to phenocopy the *Wnt3a*^{-/-} knockout at E9.5 (Galceran et al. 1999). In the intestine, disruption of the Tcf-4 gene was

found to deplete the epithelial stem cell compartments (Korinek et al. 1998), whereas deletion of Tcf-1 resulted in tumor formation several months after birth (Roose et al. 1999), suggesting that in this system, Tcf-4 promotes stem cell maintenance, whereas Tcf-1 exerts the opposite effect. The fourth member of the family, Tcf-3, is widely expressed at early developmental stages and exhibits strong and unique actions, behaving either as an activator or a repressor. Notably, Tcf-3 inhibits the expression of genes that are activated not only by Wnt, but also by other signaling pathways (Merrill et al. 2004; Pereira et al. 2006). In vitro, Tcf-3 was recently shown to limit ES self-renewal by repressing *nanog* expression (Pereira et al. 2006), whereas its repression activity was found to be important for the maintenance of a stem cell niche in the hair follicles (DasGupta and Fuchs 1999; Merrill et al. 2001). Note that some of the splice variants that are produced by the Tcf/LEF loci act as natural dominant negative isoforms, and there is evidence that the relative ratio in isoform abundance may play an important role in proliferation and differentiation (Hovanes et al. 2001; Weerkamp et al. 2006; Willinger et al. 2006).

All Tcf/LEF isoforms bind β -catenin with their first 50 N-terminal amino acids. The downstream-located CRD domain that mediates the recruitment of the Groucho/TLE repressor as well as the cooperation with transcriptional activators separates the β -catenin-binding region from the high-mobility group (HMG) DNA-binding domain and the nuclear localization signal (NLS). At the C-terminus of some members, downstream of the NLS, we find the so-called “E” tail, which is amenable to alternative splicing in vertebrates and may confer selectivity in the regulation of the target genes. This region is present only in the Tcf genes (not in LEF-1) and encodes a DNA-binding domain with little sequence specificity, which can stabilize the association with certain DNA response elements, as well as a second domain that facilitates the interaction with CBP/p300. For example, two Wnt target genes, LEF-1 and *Cdx-1* (caudal-related homeobox), are activated by β -catenin only when the latter is recruited to the corresponding promoters by the Tcf-1 and Tcf-4 splice variants carrying the E tail (Atcha et al. 2003; Hecht and Stemmler 2003). The E-tail has two motifs for transient binding of CtBP (C-terminal binding protein), a particularly interesting protein that can act as a transcriptional corepressor of Wnt signaling (Valenta et al. 2003; Hamada and Bienz 2004) influencing epigenetic chromatin modifications through interaction with Polycomb corepressors (Chinnadurai 2002), but also as a transcriptional co-activator of some Wnt targets (Fang et al. 2006). A rather unusual property of CtBP is that its activity is regulated by the nuclear NADH/NAD⁺ ratio, and therefore its impact on Wnt signaling might be controlled by the metabolic status of the cell. In

addition, CtBP, in cooperation with APC, was recently found to participate in the clearance of β -catenin from transcriptionally active Tcf/LEF/ β -catenin complexes bound on the target promoter (c-Myc), a step that is thought to be a prerequisite for the subsequent recruitment of the Groucho/TLEs and Hdac1 (histone deacetylase 1) by the enhancer bound Tcf/LEFs and termination of transcription (Sierra et al. 2006). Interestingly, mouse embryos that lack the CtBP2 isoform display delayed neural development, axial truncations and reduced Brachyury (T) expression, resembling the phenotype of the Wnt3a mutants (Hildebrand and Soriano 2002).

Interactions of Tcf/LEFs with other transcriptional regulators

The relatively weak recognition of chromatin DNA by the Tcf/LEF proteins requires the cooperation with other transcription factors to increase binding affinity and specificity. This strategy allows other pathways to integrate on Tcf/LEF activity, thereby contributing further to the amazing complexity of the Wnt signaling in vertebrates. Of particular importance for the cross talk between Wnt and other major developmental pathways such as the TGF- β /BMP is the cooperation of Tcf/LEFs with the SMAD transcription factors that are bound to adjacent elements, thereby allowing the coordinated regulation of target genes (Riese et al. 1997; Labbe et al. 2000; Nishita et al. 2000), for example, Msx2 (Hussein et al. 2003) or c-Myc (Hu and Rosenblum 2005). Importantly, synergistic interactions occur also with homeodomain family proteins such as Alx4 on the NCAM promoter (Boras and Hamel 2002), Pitx2 on LEF1 (Vadlamudi et al. 2005) and Cdx1 on its own promoter (Beland et al. 2004). Another tempting Tcf/LEF-interacting partner that can significantly enhance transcriptional activation of target genes (Feng et al. 2007) is the *Drosophila split ends (spen)* homologue, known as MINT (Msx2-interacting nuclear targeting protein) in mouse or SHARP (SMRT/Hdac1-associated receptor protein) in human. The functional interaction between SHARP and Tcf/LEF was shown to be independent on β -catenin. Interestingly, the *Drosophila* homologue has been previously involved in neuronal cell fate specification and axonal guidance (Chen and Rebay 2000; Kuang et al. 2000) as well as in cell cycle regulation (Lane et al. 2000), possibly via the ability of Spen to interact with Notch and EGF (epidermal growth factor) signaling pathways (Chen and Rebay 2000; Kuang et al. 2000). Targeted ablation of the mouse homolog MINT conditionally in the brain resulted in severe reduction in hippocampal size and brain hypoplasia (Yabe et al. 2007). It is worth mentioning that SHARP was originally discovered as a corepressor for nuclear hormone receptors (Shi et al. 2001) and the DNA-

binding protein RBP-Jk, a component of Notch signaling (Oswald et al. 2002). Although the underlying mechanism of SHARP action on Tcf/LEF activity is still unknown, it may involve some of the interesting properties of this large protein, such as its ability to act as a nuclear matrix-associated scaffolding factor organizing the promoter region of target genes (Sierra et al. 2004) or bind RNA coactivators (Shi et al. 2001) and participate in RNA splicing and nuclear export (Hiriart et al. 2005). Of relevance to Wnt signaling, but from a different point of view, is the ability of the aforementioned Tcf/LEF-interacting protein CtBP to increase significantly SHARP-mediated repression on Notch target genes (Nagel et al. 2005; Oswald et al. 2005) as well as to inhibit key players of BMP signaling such as Id1 in response to the SMAD6 component of TGF β pathway (Lin et al. 2003). Considering the above observations we may infer that SHARP and CtBP may act as convergence points for most, if not all, the major developmental pathways that are known to influence the maintenance and fate determination of neural stem cells.

Finally, another layer for regulation of Tcf/LEF activity is provided by proteins that bind on these transcription factors and inhibit their activity directly or sequester them away from their target promoters or result in their covalent modification. An example of the first category includes the Frodo proteins, which were originally identified as proteins interacting with Dishevelled. These proteins appear to act as signaling adaptors involved in both, Wnt signaling and Nodal, another major pathway operating during vertebrate development, and are also important for neural tissue specification (Hikasa and Sokol 2004; Brott and Sokol 2005). Moreover, besides the recruitment of Groucho/TLE repressors, which is a common property of all Tcf/LEF proteins, some members of the family interact also with certain co-repressors such as Kaiso, a BTB/POZ protein that acts first by antagonizing the recruitment of β -catenin on the target promoter (Siemois) and then cooperates with a Tcf/LEF member (xTcf3) to repress transcription (van Roy and McCrea 2005). Examples of the second category include the Kaiso-related protein HIC1, which together with CtBP, sequesters Tcf-4 to nuclear bodies (Valenta et al. 2006), the LIM-containing HIC5, a nuclear hormone receptor coactivator, which inhibits Tcf/LEF activity (Ghogomu et al. 2006), and the proteins I-mfa and HIC, which bind to the HMG domains of Tcf-3 and Lef-1 and prevent DNA binding (Snider et al. 2001). Lastly, covalent modifications of Tcf/LEFs include acetylation by CBP/p300 (Gay et al. 2003), sumoylation by PIASy (Sachdev et al. 2001) and phosphorylation by CK1 (Hammerlein et al. 2005), CK2 (Miravet et al. 2002) as well as the Nemo-like kinases, which decrease the DNA-binding affinity of the Tcf/LEF/ β -cat complex (Ishitani et al. 2003; Lo et al. 2004). These posttranslational modifications can influence

the DNA-binding properties of Tcf/LEFs, their interaction with other partners, the nucleocytoplasmic shuttling or subnuclear localization, and while in most cases they decrease Wnt target gene expression, such modifications may also lead to increased activation. The potential intersection points between Wnt and other major developmental pathways in the nucleus that were discussed above are schematically illustrated in Fig. 1.

Wnt-signaling and patterning of the developing neural tube

Neural stem cells are considered the cellular building blocks of the developing nervous system and are characterized by their ability to undergo an extensive number of self-renewing divisions and to give rise to neurons or glia. Neural stem cells give rise to a great variety of neuronal subtypes along the entire neuraxis. Wnts and Wnt inhibitors are involved in generating this neuronal diversity by contributing to regional patterning of the neural tube in early embryogenesis. During *Drosophila* embryogenesis,

Wnt controls the organization of neuroblasts along the anterior/posterior (A/P) axis (Kaphingst and Kunes 1994; Song et al. 2000). In *Xenopus*, manipulation of the canonical pathway interferes with the A/P character of neuralized animal caps (McGrew et al. 1995; Kiecker and Niehrs 2001). Moreover, application of Wnts on rostral neural plate explants or on chick embryos inhibit ventral cell fate and induce an early dorsal character in telencephalic cells (Gunhaga et al. 2003). Moreover, loss of β -catenin in the telencephalon before the onset of neurogenesis leads to the downregulation of dorsal markers and the ectopic expression of ventral markers (Backman et al. 2005). Wnt1 and Wnt3a are components of roof plate signaling (Hollyday et al. 1995; Megason and McMahon 2002), and analysis of double knockout mice revealed severe defects in dorsal interneuron specification in the developing spinal cord (Muroyama et al. 2002). Finally, an elegant study showed recently that Wnt signaling may regulate fine scale cell fate choices along the A/P axis, in part by creating an adhesion gradient, thereby contributing to the fine-scale architecture of the nervous system (Hayden et al. 2007). For further detailed discussion of the role of

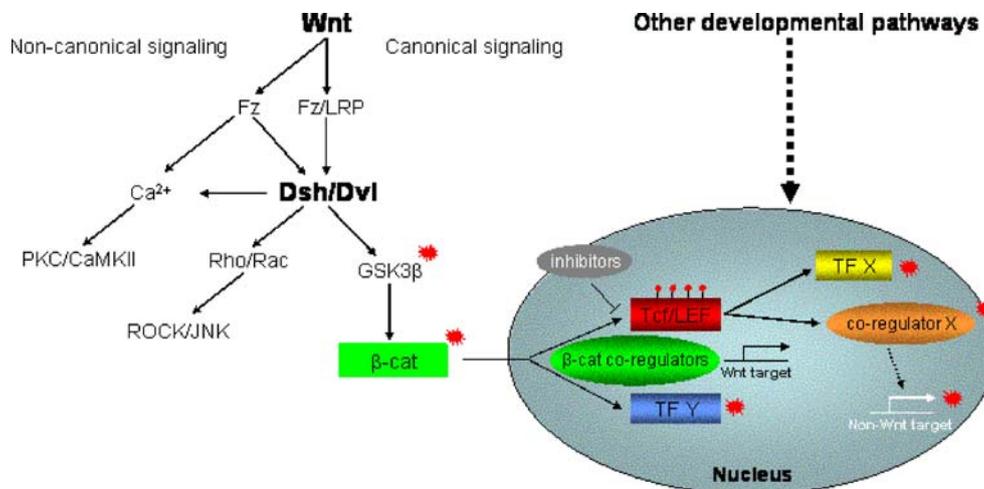


Fig. 1 Schematic representation of the potential intersection points between Wnt and other developmental pathways in the nucleus: Following the initial events that take place at the cell membrane (determined by the Wnt class, the available receptor/co-receptor complexes and the potential antagonists), the signal is first transmitted to Dsh/Dvl from which it is routed to different downstream effectors, resulting in the activation of non-canonical or canonical pathways. The hallmark of the canonical pathway is the nuclear translocation of β -catenin, which is also amenable to regulation by other signaling pathways (e.g., PI3K). In the nucleus, β -catenin exerts its regulatory effects on target promoters, which are recognized by Tcf/LEF (illustrated in red) or unrelated DNA-binding transcription factors (in blue; e.g., proteins of the Sox family or Prop1). On these promoters β -catenin acts by displacing available repressors (e.g., Groucho/TLE) and recruiting transcriptional activators (e.g., Pygopus) or variable chromatin remodeling complexes (in green). In the case of the Tcf/LEF proteins, the activation by β -catenin can be inhibited by other

proteins such as ICAT or Chibby (in grey). On the other hand, Tcf/LEFs can also associate with coregulatory molecules that are not dependent on β -catenin (in orange; e.g., SHARP) and they may cooperate with other DNA-binding transcription factors (in yellow; e.g., Smads, Alx4, Pitx2 or Cdx1) on composite target promoters. Such β -catenin-independent coregulators and unrelated transcription factors can be regulated by different developmental pathways (e.g., EGF, Notch, TGF β). Modulatory molecules that can sense the metabolic state of the cells such as CtBP may act as common regulators of Wnt target genes (in black) as well as of genes that are under the control of other developmental stimuli such as BMP or Notch (in white), thus allowing the coordination of their activities. Finally, covalent modifications of Tcf/LEFs such as phosphorylation, acetylation or sumoylation can influence their DNA-binding properties as well as the mode and place of interaction with their diverse partners. The potential points of intersection with other developmental pathways summarized here are illustrated with an *asterisk*. See text for details and references

Wnts in patterning of the neural tube, we would like to refer the reader to the excellent reviews by Ciani and Salinas (Ciani and Salinas 2005) and Chizhikov and Millen (Chizhikov and Millen 2005).

Wnt signaling and proliferation of neural stem cells

Tight regulation of the proliferation of neural stem and precursor cells is central for the control of the size of different CNS regions. Analysis of knockout mice has revealed a prominent function for Wnt proteins in the proliferation of neural precursor cells. During development, Wnt1 is expressed in the caudal midbrain. In the absence of Wnt1, neural precursor populations in the developing mid/hindbrain fail to expand, leading to an almost complete loss of the mid/hindbrain region (McMahon and Bradley 1990; Thomas and Capecchi 1990). Conversely, proliferation of isolated ventral midbrain precursors is stimulated by Wnt1 (Castelo-Branco et al. 2003), and increased expression of Wnt1 in the developing mid/hindbrain enhances proliferation of local precursors potentially through induction of the positive cell cycle regulator cyclin D1 and shortening of the cell cycle (Panhuysen et al. 2004). Wnt3a mutant mice display strongly reduced proliferation of precursor cells in the caudomedial cortical epithelium, which is the site from which the hippocampus arises. As a consequence, all layers of the hippocampus are greatly reduced (Lee et al. 2000). Similarly, conditional ablation of β -catenin in the developing hippocampus leads to disruption of all hippocampal subfields (Machon et al. 2003). The prominent role of Wnt signaling in the control of hippocampal development is underlined by the phenotype of the LRP6 (Zhou et al. 2004) and the LEF1 mutants (Galceran et al. 2000), which display strong hippocampal malformations. Curiously, these mutations specifically affect the proliferation of precursors to the dentate granule neurons and hence lead to loss of the dentate gyrus, but not of the pyramidal cell layers. In contrast, transgenic mice expressing a fusion gene that interferes with the transcriptional activation of all TCF/LEF family members results in the loss of all hippocampal subfields (Galceran et al. 2000). Taken together these results indicate that Wnt3a controls the proliferation of different hippocampal precursor pools through pathways that are dependent on intact β -catenin signaling, but that are distinct on the level of the receptor complex and the transcriptional complex.

Present work indicates that the proliferative action of Wnt proteins is predominantly mediated by the canonical Wnt/ β -catenin pathway. Loss of the Wnt-receptor Frizzled5 in *Xenopus* leads to decreased proliferation of retinal precursor cells. The Frizzled5 effect can be phenocopied by inhibition of the Wnt/ β -catenin pathway, indicating that

the Frizzled5 mediates proliferation through the canonical Wnt-signaling pathway (Van Raay et al. 2005). In the caudomedial cortical epithelium Wnt/ β -catenin signaling and the transcription factor *Emx2* collaborate in a positive feedback loop to control precursor proliferation (Tole et al. 2000; Theil et al. 2002; Muzio et al. 2005). The positive cell cycle regulators CyclinD1 and c-Myc have previously been identified as direct targets of Wnt/ β -catenin signaling. Indeed, mis-expression of a constitutively active form of β -catenin in neuroepithelial precursors causes a shift in the balance between cell cycle re-entrance and cell cycle exit and leads to expansion of the cortical precursor pool and enlarged cerebral cortical size at birth (Chenn and Walsh 2002). Conversely, loss of β -catenin in cortical precursors (Woodhead et al. 2006) as well as loss of the co-receptor LRP6 (Zhou et al. 2006), which leads to reduced Wnt/ β -catenin signaling, result in the premature differentiation of cortical precursors and cortical hypoplasia.

Previous studies have found that Wnt signaling and PI3 kinase signaling converge on the stabilization of β -catenin to control the proliferation of stem cells in the intestine (He et al. 2004), whereas the self-renewal of hematopoietic stem cells is controlled by combinatorial Wnt and Notch signaling (Duncan et al. 2005). The proliferative effect of β -catenin on neural precursors may also be dependent on the interaction of Wnt signaling with other pathways. In the developing spinal cord BMP-signaling inhibits Wnt-induced proliferation of dorsal precursors (Ille et al. 2007). In the presence of FGF2, cortical neural precursor cells show increased proliferation in response to Wnt7a/b overexpression (Viti et al. 2003) or activated Wnt/ β -catenin signaling (Israsena et al. 2004). In the absence of FGF2, however, cortical precursors will differentiate into neurons following stimulation of the Wnt/ β -catenin pathway (Israsena et al. 2004). One potential mechanism through which FGF signaling modulates the biological output of Wnt/ β -catenin signaling may be the cooperative activation of target genes, which control neural precursor cell proliferation. The transcription factor Sox2 prevents premature cell cycle exit of neural precursor cells in the developing spinal cord (Graham et al. 2003) and appears to be essential for proliferation of retinal precursor cells (Van Raay et al. 2005). Interestingly, Wnt and FGF signals converge to activate the expression of the transcription factor Sox2 in the neural plate of the chick (Takemoto et al. 2006). Curiously, it has been shown in other organ systems that activation of FGF signaling can increase the expression of Sox proteins (Mansukhani et al. 2005), which block the activation of canonical Wnt-signaling targets through sequestration of β -catenin (Zorn et al. 1999; Mansukhani et al. 2005) and may divert the transactivation potential of β -catenin towards different sets of downstream targets (Sinner et al. 2004). Such observations indicate that

context-dependent synergistic and inhibitory interactions among the relevant downstream components may control the biological output of Wnt and FGF signaling.

Wnt/ β -catenin signaling can also control the competence of precursor cells to respond to proliferative signals. Perturbation of Wnt/ β -catenin signaling in cardiac neural crest precursors leads to severe reduction of precursor proliferation and abnormalities in the cardiac outflow tract. Further analysis revealed that Wnt/ β -catenin signaling induces the expression of Pitx2, a transcription factor which is specifically expressed in precursor cells of the cardiac outflow tract and of the pituitary gland. The expression of Pitx2 in turn confers the competence to precursor cells to respond to growth factor signaling with the expression of the positive cell cycle regulator cyclin D2 (Kiousi et al. 2002). An additional level of complexity is added to the Wnt/ β -catenin controlled proliferation program by the ability of the Wnt/ β -catenin pathway to promote proliferation through increasing the mRNA stability of cyclin D1 and cyclin D2 (Briata et al. 2003).

Wnt signaling in the maintenance of the neural precursors and the control of neural cell fate decisions

Proliferation of neural precursor cells appears to be tightly linked with maintenance of the neural precursor state. This association is illustrated best by the observations that overexpression of the negative cell cycle regulator p27^{Kip1} enhances premature neuronal differentiation (Tarui et al. 2005) and that the fate of neural precursor cells, i.e., maintenance in a precursor state vs. neuronal fate commitment can be predicted from cell cycle length (Calegari et al. 2005). Therefore modulation of the expression of cell cycle regulators and of competence factors to respond to growth signaling pathways may be an eminent mechanism for maintenance of the neural precursor pool. However, observations in other organ systems strongly indicate that Wnt signaling controls stem cell maintenance also through molecular mechanisms which are independent of proliferative pathways. It has been demonstrated that β -catenin signaling is essential for the maintenance of quiescent or slowly dividing stem cells in the hair follicle (Lowry et al. 2005) and that Wnt/ β -catenin signaling sustains the expression of pluripotency factors such as Oct-3/4 and Nanog in embryonic stem cells (Sato et al. 2004). In the neural crest, combinatorial Wnt and BMP signaling leads to maintenance of neural crest stem cells, whereas Wnt signaling and BMP signaling alone will induce the differentiation of stem cells into sensory ganglion cells and autonomic neurons, respectively (Kleber et al. 2005).

It has been shown that Wnt/ β -catenin signaling positively controls the expression of the transcription factor

neuron restrictive silencer factor/repressor element 1 transcription factor (NRSF/REST) in spinal cord progenitor cells of the developing chick (Nishihara et al. 2003). NRSF/REST is a transcription factor which negatively regulates the expression of neuronal genes through binding to a neuron restrictive silencer element (NRSE) in the promoter of neuronal genes and the recruitment of transcriptional corepressors (Ballas and Mandel 2005). Expression of a dominant-negative NRSF/REST induces precocious differentiation of neural progenitor cells (Chen et al. 1998). Moreover, conversion of NRSF/REST in adult neural stem cells from a transcriptional repressor into a transcriptional activator through a non-coding RNA-dependent mechanism promotes neuronal differentiation (Kuwabara et al. 2004). These observations indicate that NRSF/REST may be essential for neural stem cell maintenance, and it will be interesting to examine whether the NRSF/REST activity is coordinated by Wnt/ β -catenin signaling, potentially in collaboration with other signaling pathways, to control neural stem cell maintenance.

A role for Wnt/ β -catenin signaling in neuronal fate determination *in vivo* was conclusively demonstrated for the first time in the development of neural crest derivatives. Expression of a stabilized form of β -catenin in neural crest stem cells results in increased generation of sensory neurons (Lee et al. 2004). Importantly, sensory neurogenesis in these transgenic mice occurs at the expense of other neural crest-derived lineages arguing that neural crest stem cells were induced to adopt a sensory fate.

Wnt1-induced signaling is crucial at early stages for the specification of midbrain dopaminergic neuronal precursors and for the terminal differentiation of these precursor at later developmental stages (Prakash et al. 2006). *In vitro* work has suggested that the terminal differentiation of the midbrain dopaminergic precursors may also involve Wnt5a-induced non-canonical signaling pathways (Castelo-Branco et al. 2006) (although the relevance of Wnt5a for dopaminergic neurogenesis *in vivo* awaits further confirmation). The interplay of canonical and non-canonical signaling pathways in the control of fate specification and terminal differentiation appears to be a recurring theme in stem cell biology and development. For example, stimulation of non-canonical Wnt-signaling and inhibition of Wnt/ β -catenin signaling are required for the specification of ventral cell fates in developing vertebrates (Weidinger and Moon 2003; Westfall et al. 2003) and for the differentiation of chondrocyte precursors (Topol et al. 2003). Neural precursors in the developing mouse cortex on embryonic day 13.5 (E13.5) differentiate into neurons following activation of Wnt/ β -catenin signaling. In these precursors Wnt/ β -catenin directly activates the expression of the pro-neurogenic basic helix-loop-helix transcription factor Neurogenin1 (Hirabayashi et al. 2004), which in turn

initiates a neurogenic program. Interestingly, early cortical precursors (E10.5) show increased proliferation following stimulation of the canonical Wnt-signaling pathway *in vitro* and *in vivo*, demonstrating that the biological response of cortical precursor cells to Wnt/ β -catenin signaling is stage dependent (Hirabayashi et al. 2004; Hirabayashi and Gotoh 2005). As previously discussed, it is possible that the activity of interacting pathways differs at distinct stages and determines the response of the precursor cell. The observation that isolated cortical precursors respond under the same culturing conditions with proliferation or differentiation to increased Wnt/ β -catenin signaling depending on their developmental age strongly argues that extracellular cues are capable to generate steady epigenetic alterations in the nucleus of the cell precursors, thereby allowing the expression of the stage-dependent effects of Wnt/ β -catenin signaling. The molecular nature of these cell intrinsic changes is presently unknown. Some clues for potential cell intrinsic changes can be deduced by the following observations. The response of neural precursor cells to signals which induce astrocytic fate determination is stage dependent (Takizawa et al. 2001; Fan et al. 2005; He et al. 2005). *In vivo*, neural precursors give rise to neurons at early stages and will only later on generate astrocytes. *In vitro*, LIF signaling induces astrocytic fate commitment only in late neural precursors, but not in early neural precursors. The failure of early neural precursors to differentiate into astrocytes appears to be the consequence of stage-specific chromatin modifications of astrocytic promoters, which inhibit the expression of astrocyte-specific genes even in the presence of strong astrocytic-fate inducers. Whether chromatin-modifications in downstream targets of the Wnt-signaling cascade are involved in the regulation of the stage-specific response of neural precursor cells to activated β -catenin signaling remains to be determined.

The outcome of Wnt/ β -catenin signaling in stem cells may also be dependent on the type of transcriptional co-activator, which is recruited to the TCF/LEF/ β -catenin transcriptional complex. Using a small molecule driven approach, it was shown that the interaction of TCF/LEF/ β -catenin with the transcriptional co-activator p300 increases the differentiation of embryonic stem cells (Miyabayashi et al. 2007) and PC12 cells (Teo et al. 2005), while the interaction of TCF/LEF/ β -catenin with the transcriptional co-activator CBP promoted the undifferentiated state of these cells (Miyabayashi et al. 2007).

Cell fate decisions of neural precursors may also involve the interaction of stabilized β -catenin with transcription factors other than those of the TCF/LEF family. The generation of several hormone-producing cell types in the pituitary gland is dependent on the presence of the transcription factor Pit1. The expression of Pit1 is positive-

ly controlled by the transcription factor Prophet of Pit1 (Prop1) and negatively regulated by the transcription factor Hesx1. Loss of β -catenin in early pituitary precursors leads to a loss of Pit1 expression and loss of Pit1-dependent cell-lineages. Interestingly, the expression pattern of TCF transcription factors and the phenotype of the LEF1 mutant mice indicate that β -catenin is not interacting with TCF/LEF transcription factors in the control of Pit1 expression and establishment of Pit1-dependent cell lineages. Instead, it was found that β -catenin interacts with Prop1 to simultaneously activate the expression of Pit1 on the one hand and to repress the expression of Hesx1 on the other hand, which together results in the strong activation of Pit1 and the establishment of Pit1-dependent cell lineages (Olson et al. 2006). Thus, the coordinated transcriptional switch of two master transcription regulators allows Wnt to provide a key signal for cell fate determination during pituitary development via the synchronized activation and repression of specific gene targets. Considering that in addition to Tcf/LEFs or Prop1, β -catenin can interact with other DNA-binding transcription factors (Kioussi et al. 2002) that might also be expressed in a tissue- and/or developmental stage-specific manner, it is tempting to speculate that an analogous mechanism may contribute on the precise control of Wnt-determined cell fate decisions and the generation of neuronal subtype diversity. Based on the experimental evidence mentioned above, the potential mechanisms, which may determine the final output of Wnt/ β -catenin signaling considering (1) the link between stem cell maintenance and differentiation and (2) the interplay among Wnt and other major physiologically relevant extracellular cues, are schematically exemplified in Fig. 2. This paradigm may explain the competence of neural precursors to respond to Wnt with increased proliferation at early stages and to initiate a full neurogenic program later on.

Wnt signaling in the establishment of neuronal circuitries

Wnts also play a role in neurogenesis beyond the stage of neuronal fate determination of neural stem cells. Wnts participate in the establishment and refinement of neuronal circuits by controlling axon guidance, dendritic development, synapse formation and synaptic plasticity. Intriguingly, a number of these events are controlled by β -catenin independent pathways and involve a different set of co-receptors. Wnt7a mutant mice (Hall et al. 2000) display defects in the synapses of mossy fibers on cerebellar granule cells. Further analysis demonstrated that granule cells secrete Wnt7a, which stimulates axon and growth cone remodeling in mossy fibers. In this process, Wnt7a activates a pathway,

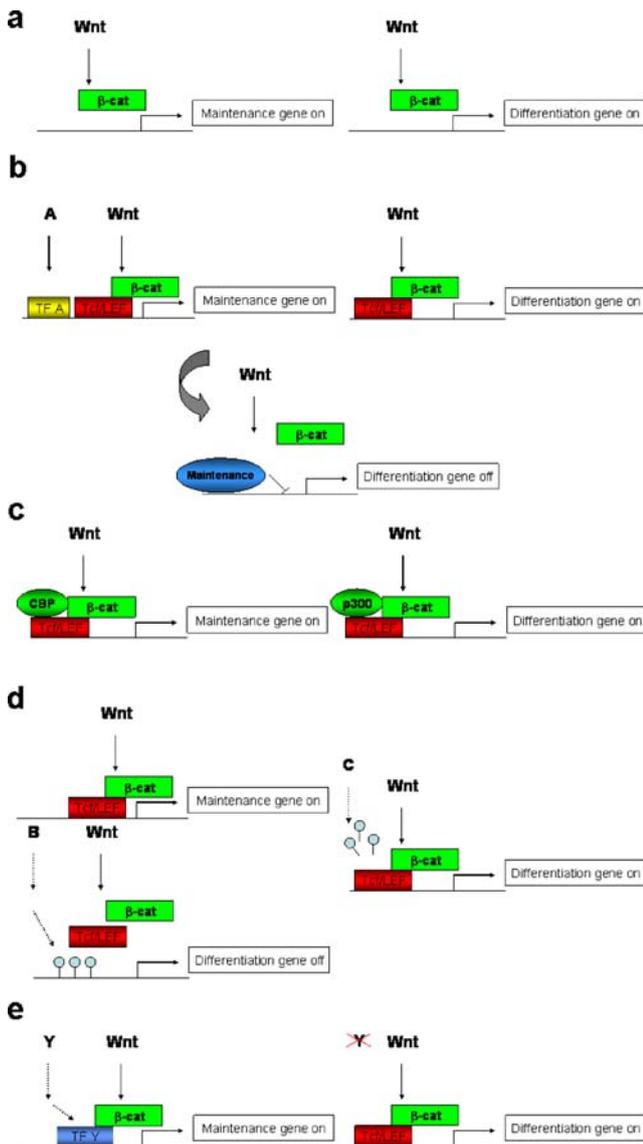


Fig. 2 Schematic representation of potential mechanisms leading to differential output of Wnt/β-catenin signaling using stem cell maintenance and differentiation as a model. **a** The expression of both maintenance and differentiation genes can require Wnt/β-catenin signaling. **b** The expression of maintenance genes is dependent on the cooperation of Wnt/β-catenin signaling with a second signal (A), which employs a second transcriptional activator (TF A) that also binds to the Wnt responsive promoter. Maintenance genes will repress the expression of differentiation genes by making their transcriptional regulatory region non-accessible to β-catenin recruitment. In the absence of A, repression will be relieved and Wnt/β-catenin signaling will predominantly lead to the expression of differentiation genes. **c** The expression of maintenance genes and differentiation genes can be differentially controlled by the selective recruitment of a specific co-activator. **d** Tcf/LEF cannot bind to the promoter of differentiation genes because of epigenetic modifications, which may potentially be induced by extrinsic signal B. In the presence of signal C the promoter becomes accessible to Tcf/LEF leading to the expression of differentiation genes. **e** Transcription factor Y (TF Y) is activated by an extrinsic signal Y. Stabilized β-catenin cooperates with TF Y to promote the expression of maintenance genes. In the absence of Y, stabilized β-catenin will associate with Tcf/LEF leading to the expression of differentiation genes

which diverges from the canonical signaling pathway at the level of GSK3β to change the phosphorylation status of the microtubule associated protein MAPIB, which in turn leads to modulation of cytoskeleton dynamics. A similar role as a target derived factor to control axonal remodeling and axonal branching has been proposed for Wnt3 in the formation of sensory-motoneuron connections in the developing spinal cord (Krylova et al. 2002).

Wnt signaling also appears to control axon guidance of long projection neurons along the rostro-caudal axis in the spinal cord. Frizzled 3 knockouts show guidance defects of sensory commissural axons in the spinal cord, which fail to project rostrally following crossing of the midline. Further analysis showed that Wnt4 is expressed in the ventral neural tube in an anterior-posterior gradient and that Wnt4 attracts commissural axons (Lyuksyutova et al. 2003). Wnt signaling also regulates the caudally directed outgrowth of the corticospinal tract. In this system, Wnts have a chemo-repulsive function. Interestingly, the repulsive activity can be blocked by antibodies to the Wnt coreceptor Ryk (Liu et al. 2005). Although in vitro assays have suggested that Ryk may be essential for Tcf/β-catenin activation, in vivo knockdown of Ryk using siRNA technology does not phenocopy Tcf/LEF or β-catenin mutants and only leads to defects in axon guidance and neurite outgrowth (Lu et al. 2004), suggesting that Ryk-dependent Wnt signaling is only involved in very specific developmental processes.

Wnt7b has been shown to increase dendritic arborization of hippocampal neurons in a GSK3β and β-catenin independent manner, indicating that dendritogenesis involves a non-canonical signaling pathway. Indeed, it has been demonstrated that Wnt7b activates JNK and that activation of JNK is sufficient to promote dendritic development (Rosso et al. 2005).

Finally, it has also been demonstrated that the expression of Wnt proteins can be enhanced by neuronal activity and that increased Wnt signaling enhance dendritic growth and facilitate long-term potentiation in the hippocampus (Chen et al. 2006; Wayman et al. 2006). Thus, Wnts appear to be activity-regulated signals which participate in the control of synaptic plasticity.

Wnt signaling in adult neurogenesis

Neural stem cells continue to generate new neurons in the adult mammalian brain in the subependymal zone (SEZ) of the lateral ventricles and the subgranular zone (SGZ) of the hippocampal dentate gyrus (Ming and Song 2005). In other regions such as the spinal cord, the striatum, and the substantia nigra neural precursor cells give rise exclusively to the glial lineage (Ming and Song 2005). In vitro analysis, however, showed that neural precursors from such non-

neurogenic regions have the potential to differentiate into neurons and glia on the clonal level (Shihabuddin et al. 2000; Lie et al. 2002). Importantly, neural precursors regardless of their origin differentiate into neurons following transplantation into the neurogenic regions and appear to adopt site-specific neuronal subtype identities; in contrast, neural precursors which have been transplanted into gliogenic regions do not differentiate into neurons, but will only give rise to glia (Suhonen et al. 1996; Shihabuddin et al. 2000; Lie et al. 2002). These results indicate that neural precursor cells in all regions of the adult central nervous system have the potential to give rise to neurons *in vivo* and that their fate is determined by signals provided by the environment.

Co-culture experiments have identified astrocytes in the SEZ and in the SGZ as a source for signals which promote neurogenesis. SEZ-derived astrocytes increase the formation of large neuroblast colonies from SEZ precursors *in vitro* (Lim and Alvarez-Buylla 1999). Similarly, hippocampus-derived astrocyte feeder layers promote the generation of neurons from adult hippocampus derived neural stem cells through increasing stem cell proliferation and induction of neuronal fate commitment (Song et al. 2002). Both membrane-bound factors as well as diffusible signals contribute to the neurogenic effect of hippocampal astrocytes. Importantly, spinal cord astrocytes do not promote neurogenesis from adult hippocampal neural stem cells, but rather promote their glial differentiation (Song et al. 2002). Thus, regional differences between astrocytes and astrocyte-derived signals appear to contribute to the spatial restriction of neurogenesis in the adult central nervous system.

Several Wnt family members are expressed in the adult dentate gyrus (Shimogori et al. 2004; Lie et al. 2005). Adult hippocampal neural stem cells express essential components of the Wnt/ β -catenin signaling pathway. Moreover, Wnt/ β -catenin signaling is active in proliferating cells and in a subset of newborn neurons. Interestingly, hippocampal astrocytes express at least one Wnt-family member, i.e., Wnt3, and activate Wnt/ β -catenin signaling in co-cultured adult neural stem cells. Inhibition of Wnt-signaling by sFRP reduces neurogenesis in hippocampal astrocyte/neural stem cell co-cultures. Similarly, expression of a dominant negative mutant of LEF1 in adult neural stem cells significantly reduces the neurogenic effect of hippocampal astrocytes on adult neural stem cells, demonstrating that astrocyte-derived Wnts promote neurogenesis through stimulation of the Wnt/ β -catenin signaling pathway (Lie et al. 2005).

Further *in vitro* analysis revealed that Wnt3-induced signaling is sufficient to stimulate the neuronal fate commitment of adult neural stem cells as well as the subsequent expansion of neuronally committed precursors. Overexpression of Wnt3 in the dentate gyrus of adult rats results in a two-fold increase in the number of newly generated immature neurons. In contrast, inhibition of Wnt signaling in the adult

dentate gyrus abolishes the generation of new neurons almost completely, indicating that Wnt signaling is essential for adult hippocampal neurogenesis (Lie et al. 2005).

The function of Wnt signaling in adult hippocampal neurogenesis may not be limited to neuronal fate determination and neuroblast proliferation. Several recent *in vitro* studies have provided evidence that Wnt signaling can enhance the proliferation of neural stem cells derived from the early postnatal and adult central nervous system (Das et al. 2006; Yu et al. 2006; Hirsch et al. 2007). Moreover, analysis of the activity pattern of the Wnt/ β -catenin pathway in the adult brain reveals that the pathway is not only active in the subgranular zone, i.e., the region where neural stem cells and newly generated immature neurons reside, but also strongly active in the granule cell layer (Maretto et al. 2003; Lie et al. 2005), i.e., the region where new neurons integrate into the hippocampal circuit. This activity pattern raises the possibility that Wnt/ β -catenin signaling may also be involved in later events of hippocampal neurogenesis such as maturation and integration of newborn neurons.

Neurotransmitter-regulated signaling has been demonstrated to be another potent and physiological regulator of hippocampal neurogenesis (Gould et al. 1994; Cameron et al. 1995; Arvidsson et al. 2001; Tozuka et al. 2005; Wang et al. 2005; Ge et al. 2006; Overstreet-Wadiche et al. 2006; Tashiro et al. 2006). It remains to be determined if and how Wnts are cooperating with neurotransmitters in the control of hippocampal neural stem cell behavior (Jagasia et al. 2006). Complex stimuli such as exposure to an enriched environment, running, learning, and seizures, increase the rate of adult hippocampal neurogenesis [for review see (Ming and Song 2005)]. At present, it is unknown whether Wnt signaling as a central regulatory pathway in adult hippocampal neurogenesis is modulated by such stimuli and mediates the enhancement of hippocampal neurogenesis. However, it is interesting to note that two recent studies reported neuronal activity-induced expression of Wnt proteins in the hippocampus (Chen et al. 2006; Wayman et al. 2006). It will be interesting to investigate in the future whether such activity-dependent modulation of Wnt expression may mediate the neurogenic effect of behavioral stimuli.

Conclusion

In the past few years, fascinating discoveries have revealed an increasingly complex Wnt-signaling network. This remarkable Wnt web can be regulated and modulated at multiple nodes ranging from the level of ligand-receptor interaction to the level of the diversity of downstream transcriptional complexes and of the mRNA as well as protein turnover of Wnt-signaling components. The past few years have also firmly established Wnts as essential

regulators for neural stem cells and neural development. What is less clear is the question of how Wnts achieve a precise control of the multitude of biological decisions with which neural stem cells are confronted during developmental and adult neurogenesis. Incorporating the growing knowledge of the complex Wnt-signaling network into neural stem cell biology will greatly promote our understanding of how Wnts regulate neural stem cell behavior and will ultimately promote the development of novel stem cell based strategies for diseases of the nervous system.

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