

# Similarities and Differences Between the Wnt and Reelin Pathways in the Forming Brain

*Orly Reiner\* and Tamar Sapir*

*Department of Molecular Genetics, The Weizmann Institute of Science, Rehovot, Israel*

## Abstract

One of the key features in development is the reutilization of successful signaling pathways. Here, we emphasize the involvement of the Wnt pathway, one of the five kinds of signal transduction pathway predominating early embryonic development of all animals, in regulating the formation of brain structure. We discuss the interrelationships between the Wnt and reelin pathways in the regulation of cortical layering. We summarize data emphasizing key molecules, which, when mutated, result in abnormal brain development. This integrated view, which is based on conservation of pathways, reveals the relative position of participants in the pathway, points to control mechanisms, and allows raising testable working hypotheses. Nevertheless, although signaling pathways are highly conserved from flies to humans, the overall morphology is not. We propose that future studies directed at understanding of diversification will provide fruitful insights on mammalian brain formation.

**Index Entries:** Wnt; dishevelled; Presenilin; cdk5; Par-1;  $\beta$ -catenin; APP; lissencephaly; DCX; LIS1; JIP-1; JNK; reelin; ApoER2; phosphorylation; neuronal migration; brain development.

## Introduction

### *Brain Development*

Conservation and diversification, two seemingly contradictory actions, play a fundamental role in evolution. Signaling pathways are con-

served throughout metazoa and it has been estimated that 17 kinds operate in all animals (1). Our focus of interest is to identify and to understand the different signaling pathways that participate in the complex process of neocortical development and how they interact with each other. The functional complexity of the vertebrate cerebral cortex is facilitated by an intricate structural organization. In humans, formation of the brain occurs over months of prenatal development. Brain morphogenesis involves multiple steps, including cell proliferation, cell

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\* Author to whom all correspondence and reprint requests should be addressed. E-mail: orly.reiner@weizmann.ac.il

fate identity, cell migration, and circuit formation following growth of axons and dendrites. The migratory pathway of individual neurons can be extremely long, especially in primates (reviewed in ref. 2). Neurons in the neocortex are organized into six layers that share characteristic dendritic morphologies, axonal connections, and physiological properties (reviewed in refs. 3 and 4). The neocortex is also regionalized into areas characterized by distinctive cytoarchitectonic features (5) that house specific cognitive, sensory, or motor functions (6). The axonal connections of neurons in different areas reflect their functional specificity. The six layers of the neocortex are formed during development mainly by inward-to-outward migration of neurons (7) born in the ventricular zone to the cortical plate (8,9).

### **Abnormal Brain Development**

The most common disturbances of brain development affecting up to 4% of children cause functional deficits, leading, for instance, to epilepsy, mental retardation, behavioral disturbances, and functional psychosis (10). In addition, morphological abnormalities of the cortex account for a substantial fraction (5–15%) of epilepsy in adults (11–13). It has been estimated that harmful prenatal environmental events play a central role in the pathogenesis of neuronal migration defects in humans (14–16). Nevertheless, a portion of cortical malformations in humans are genetic in origin (reviews in refs. 17 and 18). Abnormalities in the migration of neurons into the embryonic cortex lead in extreme cases to loss of normal convolutions of the cortex in humans, known as lissencephaly (“smooth brain”). There are two types of lissencephaly: type I or “classical lissencephaly,” where four layers of abnormally positioned neurons are observed in the neocortex, and type II or “cobblestone” lissencephaly, where the cortex is unlayered (19). Mutations in two different genes might result in type I lissencephaly: *LIS1*, an autosomal gene located on chromosome 17p13.3 (20), and *doublecortin*, an X-

linked gene (21,22). The most studied neuronal signaling pathway involved in neocortical layering is the reelin pathway (reviews in refs. 23 and 24). In humans, reelin mutation is the cause of autosomal recessive lissencephaly with cerebellar hypoplasia (25).

Nevertheless, our information regarding this pathway is quite rudimentary. Therefore, the finding of similar and/or common components existing both in the reelin and Wnt (discussed next) pathways paved the route to outline these analogies in a more detailed fashion. As will be shown, there are multiple possibilities for crosstalk between the initially parallel pathways, and both play a significant role in brain development. Recent findings have allowed further strengthening of the proposed links.

### **The Reelin Pathway, Introductory Notes**

The “basic” reelin pathway includes the large extracellular ligand reelin (26–28), two receptors belonging to the family of lipoprotein receptors (VLDLR and ApoER2) (29–31), and an intracellular molecule known as Dab1 (25,32–34), which needs to be phosphorylated (35,36) in order to properly propagate the reelin signal (for review, see ref. 24). Mutations in the ligand, receptors, or the intracellular adaptor protein result in an indistinguishable phenotype known as the mouse “reeler” phenotype. Additional gene products have been implicated in this pathway and some of them will be discussed in this article. Reeler mice have multiple abnormal cell positioning in different areas of the central nervous system (CNS) (reviews in refs. 18 and 24). In the cerebral cortex, the typical layered organization is not observed, and neurons born relatively late during corticogenesis reside in deep layers beneath the older neurons, thus inverted in comparison with the normal organization (37,38). Furthermore, the splitting of the preplate, which occurs when waves of newly born neurons migrate through the first-born generation of neurons, does not occur. So far, a direct ortholog of reelin has not been detected in

*Drosophila* or *C. elegans*. However, multiple members of the lipoprotein receptors and Dab1 exist both in fruit flies and worms (review in ref. 39).

### **The Wnt Pathway, Introductory Notes**

The Wnt pathway is highly conserved in evolution. Detailed analysis of components of this pathway revealed its function in numerous developmental roles. This includes roles as diverse as embryonic segmentation and patterning, gut patterning, nervous system development, formation and patterning of appendages, and stem cell proliferation. Most of the current information involves Wnt signaling through stabilization of  $\beta$ -catenin, which, in turn, enters the nucleus and controls gene expression (review in ref. 40). Components of the Wnt signaling pathway are also regulated by other signals as well; thus, the realization of how different information from signaling pathways can be incorporated. A comprehensive "canonical Wnt/ $\beta$ -catenin pathway" including information from *Drosophila*, *Xenopus*, and *C. elegans*, has been composed (<http://stke.sciencemag.org/cgi/cm/stkecm;CMP5533>). Nevertheless, an increasing amount of data has been accumulated for the non- $\beta$ -catenin Wnt signaling "noncanonical Wnt pathway" (review in ref. 41), where the best existing example is control of gastrulation movements. There are also indications for the participation of this pathway in processes as remote as cochlear hair cell morphology, heart induction, dorsoventral patterning, tissue separation, neuronal migration, and cancer. Potential signaling of the noncanonical Wnt pathway includes calcium flux, JNK (c-jun terminal kinase), and both small and heterotrimeric G proteins.

### **Ligands and Receptors**

Wnt has been nominated as one of the five kinds of signal transduction pathway that predominate early embryonic development of all animals (1). Wnts compose a large group of secreted glycoproteins, including the wingless

(wg) gene in *Drosophila* and numerous homologs across the phylogenetic tree (19 genes in human or mouse; <http://www.stanford.edu/~rnusse/wntwindow.html>), which serve as ligands, and their binding to membrane-coupled receptors initiate several signal transduction pathways. Wnt pathways are involved in the control of gene expression, cell behavior, cell adhesion, and cell polarity. In addition, they often operate in combination with other signaling pathways (reviews in refs. 42–44). Multiple Wnt ligands are expressed in distinct patterns in the developing mouse (45) and human (46) brain. Loss-of-function mutations in individual Wnts cause deletions or malformations of distinct brain regions (46–48). In addition to the large repertoire of Wnt proteins, there are multiple extracellular proteins that participate in Wnt regulation as antagonists. The Wnts bind to Frizzled (Fz) seven-transmembrane-span receptors (for a schematic presentation of most of the molecules appearing in this section, see Fig. 1). Many of Wnt antagonists contain structural similarities to the receptor (review in ref. 49). They can be generally divided into two different groups. The first group of proteins bind to Wnts and includes members of the sFRP (secreted Fz-related protein) family of proteins, WIF (Wnt inhibitory factor)-1, and Cer (Cerberus). The second group includes members of the Dkk (Dickkopf) family of proteins that binds to one subunit of the Wnt receptor complex. Both Dkk (50) and Cer (51) can inhibit brain formation in *Xenopus*; however, in the mouse Dkk (52) but not Cer (53,54) mutations inhibit normal head structures. Brain formation requires the simultaneous activity of additional secreted factors as bone morphogenetic proteins (BMPs) (51,55,56). In addition to Fz, LRP5/6 act as coreceptors of Wnt (57,58). In *Drosophila*, a mutation in the ortholog of LRP5/6 (the arrow gene) is phenotypically and molecularly indistinguishable from the wingless phenotype (59). The necessity of these coreceptors were demonstrated in the mouse, where deletion of a necessary chaperone for LRP5/6 resulted in disruption of embryonic polarity and mesoderm

differentiation (60). In addition, insertional mutagenesis of the mouse LRP6 locus resulted in developmental defects that were a striking composite of those caused by mutations in individual Wnt genes (61). Closer investigation of the brains of LRP6 mutants revealed reduced production of dentate granule neurons and abnormalities of the radial glial scaffolding (along which neurons migrate radially) in the forming dentate gyrus (62). LRP5/6 belong to the low-density lipoprotein receptor (LDLR) family of genes, whose products share a characteristic set of structural domains (review in ref. 57). Interestingly, a related family member, LRP1, was shown to interact with the human Fz-1 (HFz1) and to downregulate the best studied (canonical) Wnt signaling pathway (63). Two additional family members, the VLDLR and ApoER2, have not been shown to have a direct connection with the Wnt signaling pathway; nevertheless, our working hypothesis is that these pathways converge downstream. As mentioned earlier, mutations in both of these receptors (29–31), in their ligand reelin (26–28), or in the intracellular signaling molecule Dab1, which binds to these receptors, result in abnormal lamination in mice and humans (25,32–34). Receptor clustering followed by Dab1 dimerization is essential for proper signaling (64). Because Dab1 not only binds to the intracellular domains of the VLDLR and apoER2 but also to those of LDLR, LRP, and LRP-2 (31), it could serve as a link between several signaling pathways.

## Intracellular Signal Transduction

### *The Canonical Pathway and Beyond*

The Wnt signaling is transmitted to the Dishevelled (Dsh) protein (review in refs. 44 and 65). Dsh is an intriguing family of proteins (three Dsh-related genes in human and mouse) by virtue of the fact that it participates in at least three signaling pathways but yet is activated by similar Fz receptors. Within the cell, the Wnt pathway has several branches; the

canonical Wnt/ $\beta$ -catenin pathway (review in ref. 42), the planar cell polarity pathway (PCP) (66–70), and the Wnt/ $\text{Ca}^{2+}$  pathway (71) (for reviews, see refs. 41 and 72). The best understood Wnt pathway is the “canonical” one. The Wnt-induced signaling leads to the activation of Dsh, which is regulated by several means. For example, the naked cuticle (nkd) gene attenuates Wnt signaling through a negative feedback loop mechanism (see Fig. 1) first discovered in *Drosophila* (73,74) and then in vertebrates (75–77). Fly and vertebrate Nkd proteins contain a putative calcium-binding motif, which interacts with Dsh (74,76,78). Dapper is an additional regulator of this pathway, acting at the level of Dsh. Depletion of maternal Dapper RNA from *Xenopus* embryos resulted in loss of notochord and head structures (79).

### *$\beta$ -Catenin Stability*

Dsh can suppress degradation of the  $\beta$ -catenin protein, enabling it to accumulate in the nucleus (Fig. 1). The suppression of degradation is through the inhibition of the so-called  $\beta$ -catenin destruction complex, a complex of proteins including APC, Axin, and GSK-3 that otherwise phosphorylates  $\beta$ -catenin, targeting it for destruction by the ubiquitin–proteasome pathway. These and other mechanisms allow Wnt ligands to both stabilize  $\beta$ -catenin and promote its entry into the nucleus where it recruits transactivators to HMG box DNA-binding proteins of the LEF/TCF family. Mice mutated for different components in this pathway exhibit different brain phenotypes. As mentioned previously, LRP6 mutants had obvious abnormalities in the hippocampus. These defects were more severe with the addition of a single Lef1 null allele (LRP6 $^{-/-}$  Lef1 $^{-/+}$  mice) (62). Lef1 $^{-/-}$  mice completely lack dentate gyrus hippocampal cells (80).

### *$\beta$ -Catenin and the Brain*

$\beta$ -Catenin has two important cellular functions in a wide variety of tissues: (1) As a key component of the Wnt signaling pathway in embryonic development, it regulates gene tran-



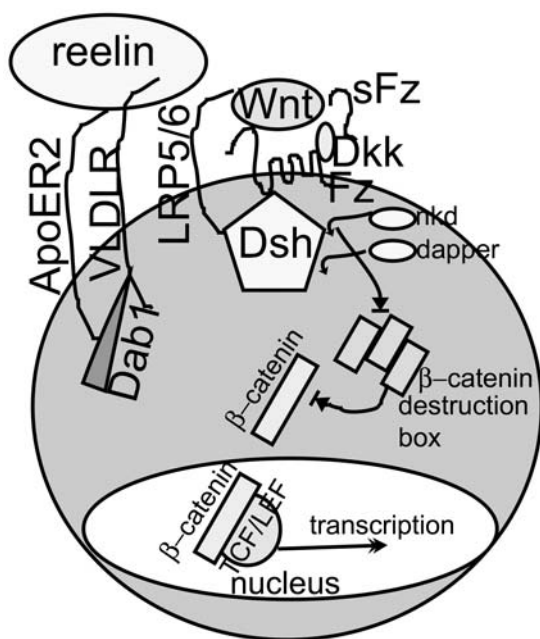


Fig. 1. Schematic presentation of the canonical Wnt pathway and the reelin pathway. The reelin signal is transmitted through binding to two receptors (ApoER2, VLDLR), that are structurally related to LRP5/6, one of the co-receptors to Wnt. Reelin signal mediates Dab1 dimerization and tyrosine phosphorylation. Wnt binds to frizzled (Fz) and LRP5/6. Secreted molecules as secreted frizzled (sFz) and Dickkopf (Dkk) can inhibit the Wnt pathway. Wnt signaling activates Dishevelled (Dsh), which can be modulated by naked cuticle (nkd), or dapper. Activation of Dsh suppresses the activity of the  $\beta$ -catenin destruction box, thus allowing the entry of  $\beta$ -catenin into the nucleus and TCF/LEF mediated transcription is initiated.

scription and (2) as a component of the cadherin/catenin complex, it helps to stabilize the actin cytoskeleton and to mediate cell adhesion (reviews in refs. 81–83). There are numerous examples for the importance of  $\beta$ -catenin in the developing and adult brain. Most of the genetic loss-of-function studies of  $\beta$ -catenin (84) and gain-of-function (85,86) dramatically affect brain formation. Inactivation of  $\beta$ -catenin in the hippocampus and the cortex resulted in abnormalities in the hippocampus similar to those

described in *Lef1*<sup>-/-</sup> mice and in severe abnormalities in the organization of the neuroepithelium of the cortex. This included disrupted interkinetic nuclear migration (movement of neurons within the ventricular zone, which is correlated with cell cycle), loss of adherens junctions, impaired radial migration of neurons toward superficial layers, and decreased cell proliferation after E15.5. At the newborn stage, a premature disassembly of the radial glial scaffold and increased numbers of astrocytes were found in the cortex (87). Furthermore, a function for  $\beta$ -catenin was demonstrated later in neuronal development in individual cells, where it regulated dendritic arborization (88). In hippocampal primary neurons lacking  $\beta$ -Catenin, abnormal synapse vesicle organization was observed (89).  $\beta$ -catenin is controlled by multiple molecules, which are not part of the canonical pathway (e.g., presenilin-1 [PS1]). The Alzheimer's disease-linked gene product PS1 is better known for its functions related to intramembrane proteolysis of amyloid precursor protein (APP) and Notch (review in ref. 90). There are several examples of the intersection between the Notch and the Wnt pathways (91–93). PS1 interacts with  $\beta$ -catenin (94–96), thus acting as a scaffold, which negatively regulates  $\beta$ -catenin phosphorylation (97–100). This activity was found to be conserved from *Drosophila* (101). PS1 deficiency resulted in increased  $\beta$ -catenin stability in vitro and in vivo (the position of PS1 in the pathway is indicated in Fig. 2). In addition, PS1 was found to regulate the transcriptional activity of  $\beta$ -catenin, thus controlling  $\beta$ -catenin at two different levels (102,103). Interestingly, PS1<sup>-/-</sup> mice show brain abnormalities, with a phenotype resembling lissencephaly type II (104–107). The phenotype observed is probably the result of a combination of depletion of the neural progenitor cells with premature differentiation and migration to inappropriate targets. We raise the hypothesis that PS1 affects the Wnt/ $\text{Ca}^{2+}$  pathway as well as the canonical pathway, because it has been shown to have a role in the refilling mechanism for depleted intracellular calcium stores (108,109).

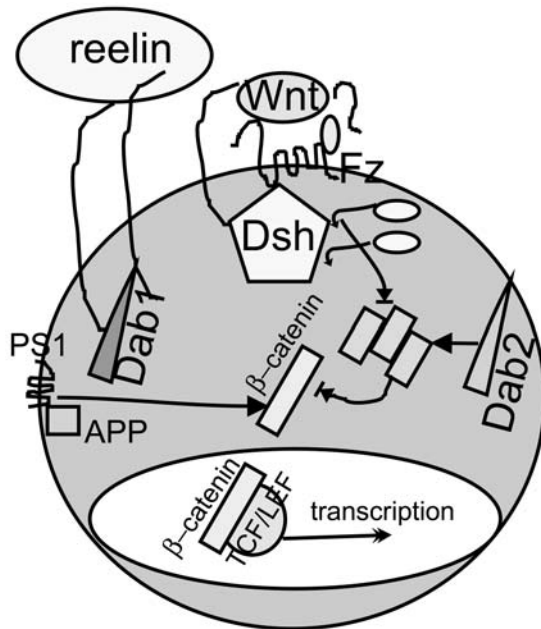


Fig. 2. The Wnt pathway is modulated by additional proteins, including Dab2, APP, and PS1. Dab2, which is similar to Dab1, can stabilize the  $\beta$ -catenin destruction box and inhibit Wnt signaling. Both Dab1 and Dab2 interact with APP, the processing of which is regulated by PS1. PS1 may also interact with  $\beta$ -catenin and negatively regulate its phosphorylation.

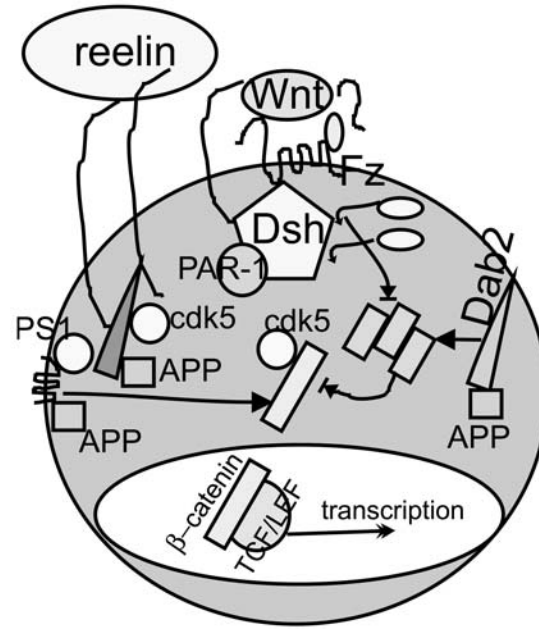


Fig. 3. Cdk5 and Par-1 phosphorylate multiple substrates found in the reelin and the Wnt pathway. Cdk5 interacts with and phosphorylates both PS1 and  $\beta$ -catenin. In addition, it phosphorylates Dab1. Par-1 is a kinase with activity important for cell polarity, regulates the Wnt pathway. Par-1 associates with Dsh, and is a positive regulator of the Wnt/ $\beta$ -catenin pathway.

### $\beta$ -Catenin Intracellular Localization

$\beta$ -Catenin is regulated not only by transcription and degradation, but its intracellular localization is important to conduct its numerous functions. Recently, mutations in the gene ADP-ribosylation factor guanine nucleotide-exchange factor-2 (ARFGEF2) were implicated in microcephaly and periventricular heterotopia in humans (122). These mutations caused abnormal intracellular localization of  $\beta$ -catenin among many other proteins. It is indeed unclear whether this abnormal localization is causative for the observed brain phenotypes, but it might be a target of future investigations. Indeed, brain abnormalities as a result of expression of  $\beta$ -catenin gain of function (85,86) might be interpreted in part as abnormal intracellular localization of the protein.

### Cdk5: A Kinase With Multiple Functions

An additional protein that has the potential of linking the Wnt/ $\beta$ -catenin and reelin pathways is cyclin-dependent kinase 5 (Cdk5). It has been shown to interact with and phosphorylate both PS1 and  $\beta$ -catenin (108), thus regulating the interaction between these two proteins (position indicated in Fig. 3). The activity of this enzyme links multiple components of cytoskeletal, membrane, and adhesion systems (reviewed in ref. 110). Furthermore, Cdk5 activity is of great importance in the developing brain. Evidence of the involvement of Cdk5 in neuronal positioning came from analysis of mice with homozygous deletions in the genes encoding Cdk5 (111) or its neuronal activator p35 (112); these mice suffer from abnormal cortical layering. Cdk5 phosphory-

lates Dab1 independent of the reelin signaling pathway (113,114). In addition, Cdk5 phosphorylated NudeL (115) and DCX (116), both are LIS1 interacting proteins (described later), which interacts with reelin-induced phosphorylated Dab1 (117).

### *Dab2*

Another modulator of the Wnt/ $\beta$ -catenin is Dab2, which has been proposed to function as a negative regulator of canonical Wnt signaling by stabilizing the  $\beta$ -catenin degradation complex (118). Dab2 is not only structurally similar to Dab1 (119), but they also interact with a common set of proteins including a GTPase activating protein (120) and APP (119,121). Therefore, Dab2 can serve as an additional link between the reelin and the Wnt pathway.

### *Par-1: An Additional Kinase That Might Link the Wnt and the Reelin Pathways*

Phosphorylation and dephosphorylation are classical ways to control transient signaling pathways. Indeed, both kinases (as mentioned, cdk5) and phosphatases as PP2A (123–128) play an important role in control mechanisms of the Wnt pathway. An additional kinase that has been found to control the Wnt pathway in is Par-1 (129). Par-1 was associated with Dsh (indicated in Fig. 3), and its activity increased with the Wnt signal. Treating cells with Wnt increased endogenous Par-1 activity coincident with Dsh phosphorylation. Suppressing endogenous Par-1 function inhibited Wnt signaling through  $\beta$ -catenin in mammalian cells and *Xenopus* and *Drosophila* embryos. According to the results, Par-1 is a positive regulator of the Wnt/ $\beta$ -catenin pathway (canonical) and an inhibitor of the Wnt/JNK (noncanonical) pathway (129).

Par-1 is important for determination of cell polarity, first identified in *C. elegans* (130), then both in *Drosophila* (131) and mammalian cells (132–134). The mammalian homologs of Par-1, MARK, phosphorylated several microtubule-associated proteins (MAPs) (132) and probably participates in the initial polarity decisions of a

differentiating neuron. Recently, DCX, a MAP (135–137), has been shown to be phosphorylated by MARK/Par-1 (138), by cdk5 (116) (Fig. 4), and by JNK (139) (Fig. 6).

### *Lissencephaly Associated Genes: The Reelin and Wnt Pathways*

Mutations in *doublecortin* (DCX) cause X-linked lissencephaly and double cortex syndrome in humans (21,22). One of the sites phosphorylated in DCX by MARK/Par-1, the S47 residue, has been mutated in several lissencephaly patients (21,22,138), and overexpression of the mutated protein (S47R) abolished neurite outgrowth in PC12 cells (140). Interestingly, RNA interference (RNAi) of DCX has been shown to cause migrating neurons to adopt multipolar morphologies (141), suggesting that DCX plays a role in neuronal polarity. A large number of normal migrating neurons in the developing brain exhibit multipolar morphology, which might constitute a type of normal migration (142,143); therefore, the significance of these findings await further investigation. Nevertheless, these neurons do not migrate to their proper position. DCX localization at the neurite tips is maintained by phosphatase activity (138). Indeed, when neurons were treated with okadaic acid, which mainly inhibits the activity of PP2A, DCX was lost from most tips of the neurons. At present, it is unclear which sites are dephosphorylated by PP2A. As mentioned previously, PP2A plays a role also in the regulation of the Wnt pathway (123–128). DCX physically interacts with LIS1 (Fig. 4), as demonstrated using different biochemical assays (144). Moreover, genetic interactions between these two genes have been suggested. Mutations in LIS1 (20), or mutations in X-linked DCX (21,22) result in lissencephaly in human. In the mouse, DCX mutants exhibit a lamination defect in the hippocampus (145) identical to that described in *Lis1*<sup>-/+</sup> mice (146), suggesting that the two gene products participate in the same pathway. Furthermore, recently a link between LIS1 and the reelin pathway has been suggested (117), and LIS1 has been shown to interact with

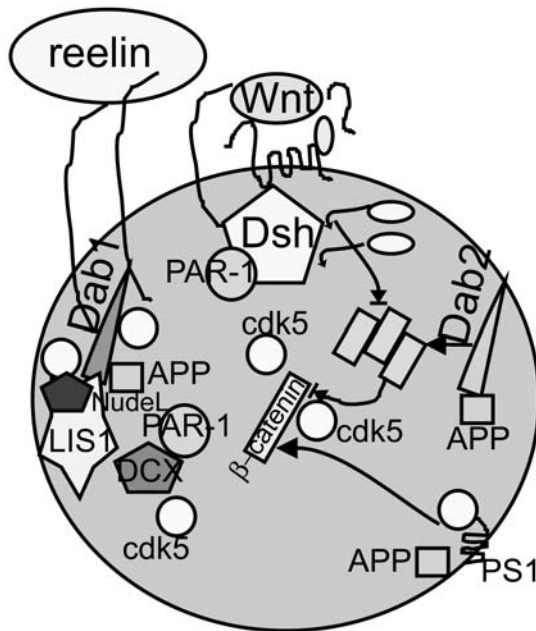


Fig. 4. Par-1 and Cdk5 both phosphorylate DCX, a microtubule-associated protein (MAP). Cdk5 also phosphorylates Nudel, a LIS1-interacting protein. In addition to Nudel, LIS1 interacts with DCX, and in a phospho-specific manner with Dab1, which is part of the reelin pathway.

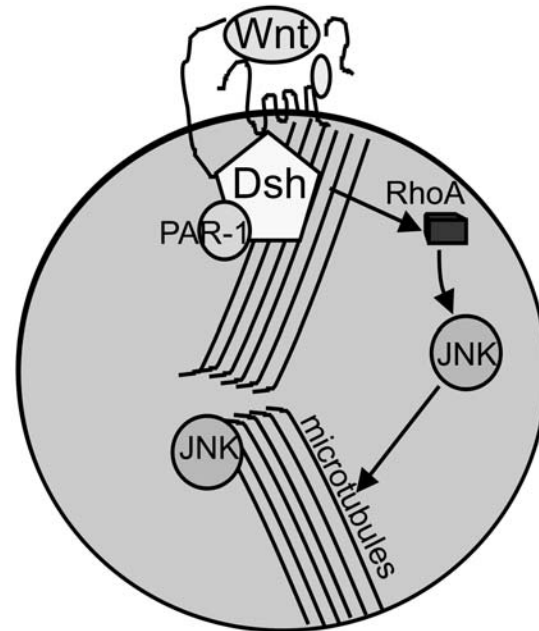


Fig. 5. The noncanonical JNK/Wnt pathway. In this pathway, Dsh is activated by Wnt at the membrane, it then activates downstream RhoA, which affects the cytoskeleton, and activates JNK, which phosphorylates additional downstream targets.

phosphorylated Dab1. LIS1 also interacts with Nudel and a similar protein mNude (115,147–152). Nudel (115) and DCX (116) are both cdk5 substrates. Phosphorylation of DCX by cdk5 affected neuronal migration (116). Overexpression of DCX in cerebellar neurons resulted in faster migration, whereas a point mutation in S297 (the site phosphorylated by cdk5) or pharmacological inhibition of cdk5 abolished this effect.

### **The Noncanonical JNK/Wnt Pathway and More**

The noncanonical JNK/Wnt pathway (Fig. 5) is best known for its involvement in changes of cell morphology and cell movement. It plays an essential role in the regulation of convergent extension movements in developing

embryos (66,67,70), which is related to planar cell polarity in flies (reviews in refs. 41,153, and 154). The exact details of this alternative pathway are still controversial (41). In this pathway, the positioning of Dsh to the cell membrane is essential for its activity. In *Xenopus*, it is transported along microtubules, probably by a kinesin molecular motor (155). In *Drosophila*, it has been shown that Dsh activates downstream RhoA (156–159), which might affect the actin cytoskeleton, and activates JNK, which might phosphorylate additional downstream targets as MAPs and transcription factors in the nucleus. The same has been demonstrated in human cells and during *Xenopus* embryogenesis and also that RhoA activation requires a formin-domain protein, Daam1 (160). Inhibition or depletion of Daam1 prevents Wnt/Fz activation of Rho and of *Xenopus* gastrulation,



but not of  $\beta$ -catenin signaling. Formin homology (FH) proteins have been implicated in cell polarity from yeast to human (161). Furthermore, additional proteins, which are part of the pathway but are difficult to place within the cascade, are involved in neuronal migration. For instance, zebrafish *Stbm* (161) and *Prickle1* (66,162) are required for the correct migration of hindbrain facial motor neurons from rhombomere 4 to rhombomeres 6 and 7.

### The Importance of Scaffold Proteins

In processes involving cell polarity, the precise intracellular localization is crucial for proper function. To achieve this, spatial regulation protein kinases (as JNK) that form MAPK signaling modules might be organized into signaling complexes by binding to a common scaffold protein. The scaffold protein interacts with the proteins that compose the signaling module (review in ref. 163). We detected an interaction between DCX and JNK Interacting Proteins, JIP1, or JIP2 (139) (Fig. 6). These proteins serve as scaffold JNK module and bind both activating and inhibitory components of this signaling pathway. Therefore, it is likely that proteins belonging to the noncanonical JNK/Wnt pathway will interact with JIP1/2 as well. JIP1/2 bind, among their multiple interacting proteins, JNK, MKK7, and members of the mixed-lineage kinase (MLK) group of MAP3K (164,165). Furthermore, both can bind the MAPK phosphatase MKP7 (166). The C-terminal region of JIP1/2 provides a link with a molecular motor, as its last 11 amino acids are essential for interaction with the microtubule-associated motor kinesin (167), and as mentioned earlier, Dsh is likely to be transported along microtubules by a kinesin (155). The interaction between the scaffold protein (known as Sunday driver) and the kinesin molecular motor is conserved and found in *Drosophila* and *C. elegans* as well (168,169). We demonstrated that the distribution of DCX to the proximal parts of neurites is dependent on its interaction with JIP1/2 and of the later with

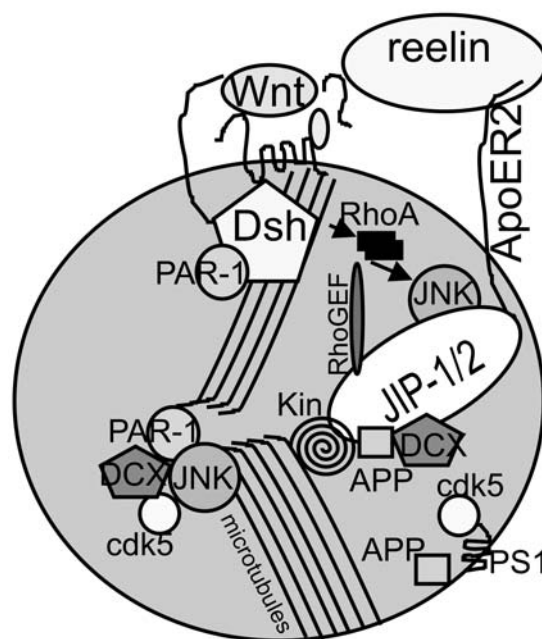


Fig. 6. JIP1/2 are scaffold proteins, which interact with the JNK signaling module and additional components. JIP1/2 interacts with ApoER2, one of reelin receptors. In addition, it interacts with RhoGEF, which belongs to the guanine nucleotide exchange factors family (GEF) active on Rho GTPases. It interacts with DCX, and in the same region, it interacts with APP. The C-terminal region of JIP1/2 is important for its interaction with the microtubule-dependent molecular motor kinesin (Kin).

kinesin (139) (review in ref. 170). JIP1/2 are structurally similar and contain a SH3 domain and a PID (protein-interacting domain) domain in the C-terminal region (164,165, 171–173). The PID domain interacts with p190 RhoGEF (174), with APP (175–177) (which, in addition, interacts with Dab1, Dab2, and PS1), and with members of the LRP family, ApoER2 and Megalin (known also as LRP2) (121,178). ApoER2 as one of the receptors for reelin is of particular interest because it provides a link between DCX and the JNK pathway with the reelin pathway. As mentioned earlier, the same cortical layering phenotype is observed in cases of mutations in the extracellular protein

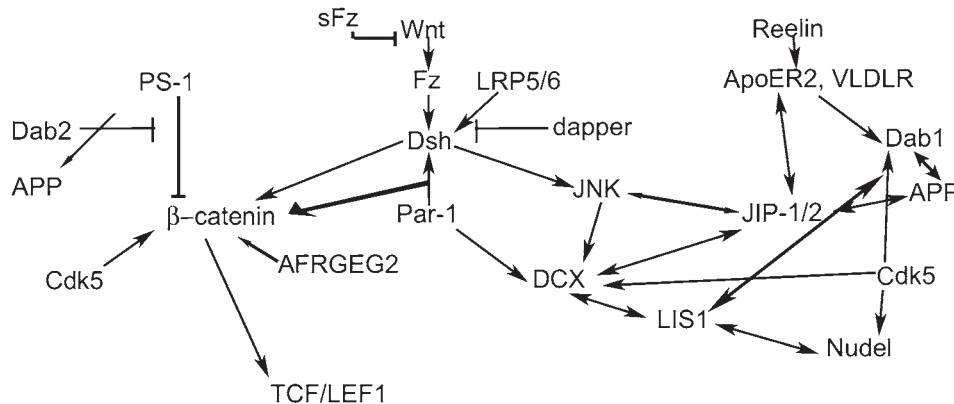


Fig. 7. Possible interrelationships among components of the  $\beta$ -catenin/Wnt pathway (left side), the JNK/Wnt pathway (middle), and the reelin pathway (right side). The extracellular bound proteins are located in the top of the scheme, followed by membrane-bound receptors and proteins. Intracellular components are drawn below and to the bottom nuclear proteins.

reelin (26–28), in two of its multiple receptors (ApoER2 and VLDLR) (29,30), or in the intracellular adaptor protein mDab1 (25). JIP1/2 also interacts with DCX in the PID, and the same point mutation in the PID previously reported to affect the interaction of JIP-1 with RhoGEF (174) affected the interaction with DCX (139). The JIP proteins also bind the Rac exchange factors Tiam1 and Ras-GRF1, although the interaction with JIP2 is significantly stronger than the interaction with JIP1 (179).

## Conclusions and Beyond

In this article, the overall similarities and possible crosstalks between the Wnt and the reelin pathways were highlighted (Fig. 7). In particular, the role of the different components of these pathways in brain development and neuronal migration were emphasized. The similarities are less obvious at the ligand levels. Structural similarities are observed at the receptor levels and LRP5/6, ApoER2, and VLDLR belong to the same gene family. Likewise, Dab1 and Dab2 are close homologs. The interconnectivity of these pathways is apparent downstream. Several of the proteins play a

role in both pathways. For example, Par-1, which has a significant role in regulation of the Wnt pathway, phosphorylates DCX. Cdk5 phosphorylates multiple substrates, which are part of both pathways. JIP-1/2 as a JNK scaffold protein and as a RhoGEF-binding protein is likely to take part in the JNK/Wnt pathway and to link it to the reelin pathway through interactions with ApoER2, DCX, and APP. A portion of the several possible crosstalk possibilities is shown in the general scheme (Fig. 7). Based on the fact that successful pathways are reutilized multiple times, it is evident that the Wnt pathway plays an important role not only during early developmental events but also in regulating the formation of the proper brain structure (*see also* reviews in refs. 43 and 180). Indeed, Wnt signaling has been shown to be important not only for synaptogenesis, axon, and dendrite development (88,181) but also for maintenance of the integrity of the nervous system (as exemplified in frizzled 4 mutant mice) (182).

We have emphasized the striking similarities in conservation of the relevant signaling pathways; nevertheless, the overall similarity between the “brain” of the fly and the human brain is minimal. This notion was already

raised by Darwin in his “principle of divergence” (183):

I have overlooked one problem of great importance; and it is astonishing to me how I could have overlooked it and its solution. This problem is the tendency in organic beings descended from the same stock to diverge in character as they become modified. That they have diverged greatly is obvious from the manner in which species of all kinds can be classed under genera, genera under families, families under sub-order and so forth... The solution occurred to me long after I had come to Down. The solution, as I believe, is that the modified offspring of all dominant and increasing forms tend to become adapted to many and highly diversified places in the economy of nature.

The understanding of the species diversification is still lacking, although possible driving forces taking part in this process were termed as evolvability (discussed briefly below) (184). Evolvability is an organism's capacity to generate heritable phenotypic variation. Core biological processes are highly conserved, probably the result of recurrent selection. The control mechanisms involved (mainly inhibitory) are usually subject to a high degree of variance, making this a flexible component. In addition, weak coupling of processes, such as signal transduction pathways, facilitates each component's accommodation to novelty. Furthermore, many biological systems are highly flexible and might lead to a wide repertoire of states, which might be stabilized in different modes. These systems are not only flexible but highly robust and, as such, are able to accommodate changes. An additional factor playing a role in evolvability is compartmentalization, at the gene expression level or the body axis level. Consequently, any specific change (or mutation) could be limited to a particular area, and not spread out throughout the whole animal. Thus, following the conservation and similarities, understanding of the dissimilarity might be an appealing and ample line of research.

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