# Wnt signaling and cancer

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The regulation of cell growth and survival can be subverted by a variety of genetic defects that alter transcriptional programs normally responsible for controlling cell number. High throughput analysis of these gene expression patterns should ultimately lead to the identification of minimal expression profiles that will serve as common denominators in assigning a cancer to a given category. In the course of defining the common denominators, though, we should not be too surprised to find that cancers within a single category may nevertheless exhibit seemingly disparate genetic defects. The wnt pathway has already provided an outstanding example of this. We now know of three regulatory genes in this pathway that are mutated in primary human cancers and several others that promote experimental cancers in rodents (Fig. 1). In all of these cases the common denominator is the activation of gene transcription by β-catenin. The resulting gene expression profile should provide us with a signature common to those cancers carrying defects in the wnt pathway. In this review, the wnt pathway will be covered from the perspective of cancer, with emphasis placed on molecular defects known to promote neoplastic transformation in humans and in animal models.

#### The wnt signaling mechanism

The model illustrated in Figure 2 is a proposed mechanism for wnt signaling and is based on the following literature. Signaling is initiated by the secreted wnt proteins, which bind to a class of seven-pass transmembrane receptors encoded by the frizzled genes (Bhanot et al. 1996; Yang-Snyder et al. 1996; He et al. 1997). Activation of the receptor leads to the phosphorylation of the dishevelled protein which, through its association with axin, prevents glycogen synthase kinase 3ß (GSK3ß) from phosphorylating critical substrates (Itoh et al. 1998; Kishida et al. 1999; Lee et al. 1999; Peters et al. 1999; Smalley et al. 1999). In vertebrates, the inactivation of GSK3ß might result from its interaction with Frat-1 (Thomas et al. 1999; Yost et al. 1998; Li et al. 1999a; Salic et al. 2000). The GSK3β substrates include the negative regulators axin and APC, as well as β-catenin itself (Rubinfeld et al. 1996; Yost et al. 1996; Yamamoto et al. 1999). Unphosphorylated β-catenin escapes recognition by β-TRCP, a component of an E3 ubiquitin ligase, and translocates to the nucleus where it engages transcrip-

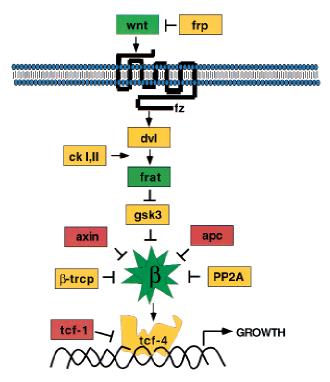
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tion factors such as TCF and LEF (Behrens et al. 1996; Molenaar et al. 1996; Hart et al. 1999). Additional components in the pathway include casein kinases I and II, both of which have been proposed to phosphorylate dishevelled (Sakanaka et al. 1999; Willert et al. 1997; Peters et al. 1999). The serine/threonine phosphatase PP2A associates with axin and APC, although its functional role in the pathway remains obscure (Hsu et al. 1999; Seeling et al. 1999). Also obscure is the manner by which the wnt receptors communicate with dishevelled.

# Receptors, ligands, and related proteins

The proto-oncogenic effects of wnt were discovered over 18 years ago inciting intense investigation into the role of wnt genes in human cancer (Nusse and Varmus 1982). The subsequent discovery of wingless, the fly homolog of wnt-1, paved the way for assembling a signaling pathway subsequently found to contain cancer causing genes (Cabrera et al. 1987; Rijsewijk et al. 1987). Although wnt was the prototypical oncogene in this pathway, no formal proof for its involvement in human cancer has ever been documented. There have been numerous reports on the overexpression, and sometimes underexpression, of wnt genes in human cancers, but mRNA expression levels are merely correlative. More compelling evidence, such as amplification, rearrangement, or mutation of genes encoding wnt ligands or receptors has not been forthcoming. In lieu of these sorts of findings, we are left to speculate on the consequences of epigenetic events implicating these genes in human cancer. In doing so we can use animal and cell culture models to guide our interpretation.

The wnt ligands, of which there are at least 16 members in vertebrates, are secreted glycoproteins that can be loosely categorized according to their ability to promote neoplastic transformation (for review, see Wodarz and Nusse 1998). For example, the activation of wnt-1, wnt-3, or wnt-10b by retroviral insertion in the mammary gland will promote tumor formation in mice (Lee et al. 1995; Nusse and Varmus 1982; Roelink et al. 1990). Oncogenic potential can also be assessed in cultured mammalian cells, such as C57MG and CH310T1/2, where expression of the proto-oncogenic wnts results in morphological transformation (Bradbury et al. 1994; Wong et al. 1994). These cells are transformed by wnt-1, wnt-2, wnt3a but not by wnt-4, wnt-5a, and wnt-6. The transforming wnt genes also promote the accumulation of β-catenin in some cultured mammalian cells (Shimizu et



**Figure 1.** Oncogenes and tumor suppressors in the wnt signaling pathway. Lines ending with arrows or bars indicate activating or inhibitory effects, respectively. Green and red indicate proto-oncogenic and tumor suppressive activity, respectively, in human cancer or transgenic animals. Definition of the genes and the basis for their activities are described in the text.

al. 1997). Some aspects of the wnt cancer pathway are also recapitulated in *Xenopus* development, where injection of transforming wnts into early embryos results in duplication of the dorsal axis (Wodarz and Nusse 1998). A caveat here is that the lack of specific receptors for certain wnts might also explain their inactivity in some of these assays (He et al. 1997). Nevertheless, identifying those wnts capable of neoplastic transformation will aid the interpretation of epigenetic evidence implicating wnts in cancer. For example, expression of the *wnt-16* gene is activated by the E2A–Pbx1 fusion product in acute lymphoblastoid leukemia (McWhirter et al. 1999), but the oncogenic potential of wnt-16 is unknown.

As might be expected from the plethora of wnt genes, there are also numerous wnt receptors. At least 11 vertebrate frizzled genes have been identified, but how they differ in function and ligand specificity is far from clear. The analysis of mere binding specificity may not be sufficient to sort out the appropriate combinations of functional receptor-ligand interactions. Wnt-3a and wnt-5a both bind to Human frizzled 1 (Hfz1), yet only wnt-3a mediates TCF-dependent transcription (Gazit et al. 1999). This suggests that the activation of TCF/LEF-dependent transcription is a good correlate to neoplastic transformation. Implementation of this assay, along with a second assay involving the translocation of PKC to the cell membrane, resulted in the categorization of murine wnt receptors into two exclusive groups (Sheldahl et al. 1999). Human FzE3 fell into the TCF/LEF activation group, consistent with previous work showing that its overexpression resulted in nuclear localization of  $\beta$ -catenin (Tanaka et al. 1998). This receptor was also expressed in numerous human esophageal cancers, but not in matched normal tissue (Tanaka et al. 1998).

In addition to the frizzled receptors, there exists a family of secreted proteins bearing homology to the extracellular cysteine-rich domain of frizzled. The so-called secreted frizzled-related proteins (sFRP) bind to the wnt ligands, thereby exerting antagonistic activity when overexpressed in wnt signaling assays (Leyns et al. 1997; Wang et al. 1997). The vertebrate sFRPs, like the frizzled proteins, exhibit functional specificity with respect to the various wnts. In Xenopus assays, the prototypical frizzled related protein frzb, now known as sFRP-3, inhibited wnt-1 and wnt-8, but not wnt-5a (Leyns et al. 1997; Lin et al. 1997; Wang et al. 1997). Assays in mammalian cells showed that FrzA, now termed sFRP-1, inhibited wnt-1-induced accumulation of β-catenin (Dennis et al. 1999; Melkonyan et al. 1997). Again, binding specificity may not relate to functional specificity, as wnt-5a associated with sFRP-3 but was unable to inhibit its activity (Lin et al. 1997). Even the significance of specific functional interactions might be suspect based on recent titration experiments with purified soluble sFRP-1. At low concentrations sFRP-1 enhanced signaling activity by soluble wingless protein, whereas at higher concentrations it was inhibitory (Uren et al. 2000). The authors proposed high and low states of binding affinity that involved the carboxy-terminal heparin binding domain and the amino-terminal cysteine-rich domain of sFRP-1, respectively. Binding to the cysteine-rich domain might confer inhibition while binding to the carboxy-terminal region could facilitate presentation of active ligand to receptor. The potential for some sFRPs to activate wnt signaling is consistent with a previous study in which sFRP-2, then known as SARP-1, increased the intracellular concentration of \( \beta \)-catenin and conferred anti-apoptotic properties to cultured MCF-7 cells (Melkonyan et al. 1997). Functional studies are further complicated by the binding of a sFRP to the putative human receptor frizzled-6, underscoring additional possible modes of regulation (Bafico et al. 1999). The sFRPs have not been directly linked to cancer, but one could speculate that the anti-apoptotic activity observed with the SARP-1 could contribute to tumor progression. Alternatively, the identification of sFRP-2 as a target of the hedgehog signaling pathway might be relevant to human basal cell cancers (Lee et al. 2000). Additional structurally distinct secreted inhibitors of wnt signaling include the recently discovered dickopft-1 and wif-1 proteins (Fedi et al. 1999; Glinka et al. 1998; Hsieh et al. 1999).

#### GSK3B

The serine/threonine kinase GSK3β binds to and phosphorylates several proteins in the wnt pathway and is instrumental to the down regulation of β-catenin (Dominguez et al. 1995; He et al. 1995; Hedgepeth et al. 1999b; Ikeda et al. 1998; Itoh et al. 1998; Li et al. 1999a; Nakamura et al. 1998b; Rubinfeld et al. 1996; Yamamoto

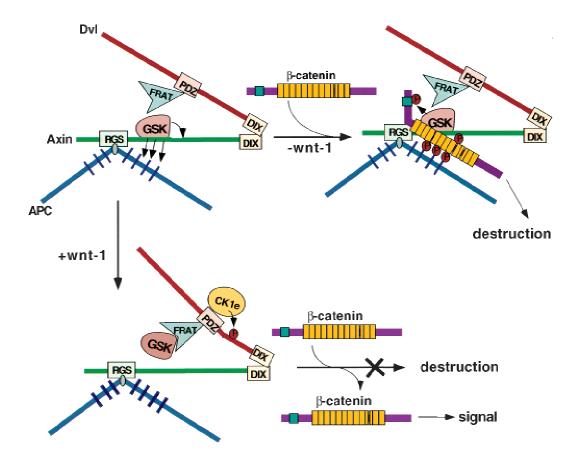


Figure 2. Proposed mechanism for the transmission of wnt signals. In the absence of wnt -wnt) GSK3β phosphorylates APC and axin, increasing their binding affinities for β-catenin, which too is phosphorylated by GSK3β, marking it for destruction. In the presence of wnt (+wnt) FRAT prevents GSK3β from phosphorylating its substrates, and β-catenin is stabilized. Casein kinaselε (CK1ε) binds to and phosphorylates dishevelled (dvl) modulating the FRAT1/GSK3β interaction. RGS, PDZ, and DIX are protein interaction domains.

et al. 1999; Yost et al. 1996). As a negative regulator of wnt signaling, GSK3β would qualify as a potential tumor suppressor. However, mutations or deletions in the gene coding for GSK3B were not been detect ed in a survey of colorectal tumors (Sparks et al. 1998). Perhaps GSK3B can compensate for the loss of GSK3ß and the biallelic inactivation of both these genes is unlikely in tumor progression. Alternatively, the utilization of GSK3β by pathways independent of wnt could make its overall ablation incompatible with cell viability. Nevertheless, inactivation of GSK3B can still be achieved by a means other than genetic ablation and can occur in a manner that uniquely affects wnt signaling. This mode of inactivation involves the association of GSK3ß with Frat-1. Frat-1 was identified by insertional mutagenesis in a screen for genes that enhanced the progression of transplanted T-cell lymphomas in mice (Jonkers et al. 1997). Subsequent transgenic expression of Frat-1 alone did not induce spontaneous lymphomas, but greatly enhanced lymphomagenesis initiated either by leukemia virus M-MuLV or expression of the *Pim1* oncogene (Jonkers et al. 1999). A connection to GSK3β was realized by the discovery of the Frat-1 Xenopus homolog GBP, a GSK3B binding protein inhibitory to wnt signaling when expressed in *Xenopus* embryos (Yost et al. 1998). Frat-1 is also antagonistic to wnt signaling in mammalian cells, presumably because it competes with axin for binding to GSK3 $\beta$  (Li et al. 1999a; Thomas et al. 1999). GBP also inhibited the phosphorylation and degradation of  $\beta$ -catenin in vitro when added to *Xenopus* extracts (Salic et al. 2000). Although Frat-1 contributes to cancer progression in a transgenic mouse model, its contribution to human cancer has not been documented.

#### Dishevelled

The genetic analysis of dishevelled in developmental systems has defined it as a positive mediator of wnt signaling positioned downstream of the receptor and upstream of  $\beta$ -catenin (Noordermeer et al. 1994). Overexpression or constitutive activation of dishevelled would be expected to promote neoplastic transformation, but its involvement in human cancers has not been reported. This might reflect the dual function of dishevelled, one that transduces wnt signals for the stabilization of  $\beta$ -catenin and a second that relays signals for the activation of jun kinases (Li et al. 1999b; Moriguchi et al. 1999). Although these two functions are housed in physi-

cally separable regions of the protein, dysregulation of one function, without impacting the other, could place severe constraints on selection for potential oncogenic mutations. A possible connection of dishevelled to cancer is through casein kinase II, which binds to and phosphorylates dishevelled and also promotes the formation of lymphomas when expressed in transgenic mice (Seldin and Leder 1995; Song et al. 2000; Willert et al. 1997).

#### **B**-catenin

Mutations in the β-catenin gene (CTNNb1) affecting the amino-terminal region of the protein make it refractory to regulation by APC (Morin et al. 1997; Rubinfeld et al. 1997). These mutations affect specific serine and threonine residues, and amino acids adjacent to them, that are essential for the targeted degradation of β-catenin (for review, see Polakis 1999). The mutations abrogate the phosphorylation dependent interaction of β-catenin with β-TRCP, a component of an E3 ubiquitin ligase that makes direct contact with amino terminal sequence in β-catenin (Hart et al. 1999). This regulatory sequence in B-catenin is mutated in a wide variety of human cancers as well as in chemically and genetically induced animal tumors. Importantly, β-catenin mutations in tumors are exclusive to those that inactivate APC. This is particularly apparent in colorectal cancer where the vast majority of these tumors contain APC mutations and the overall frequency of β-catenin mutations is quite low (Samowitz et al. 1999; Sparks et al. 1998; Kitaeva et al. 1997) (Table 1). When colorectal tumors lacking APC mutations were analyzed separately, the likelihood of finding a CTNNb1 mutation was greatly increased (Iwao et al. 1998; Sparks et al. 1998). The exclusivity of CTNNb1 and APC mutations in colorectal cancer was also evident from the analysis of replication error-positive tumors identified by microsatellite instability. Both the hereditary and sporadic forms of replication errorpositive colorectal cancers had a relatively high frequency of β-catenin mutations, whereas APC mutations were relatively rare (Mirabelli-Primdahl et al. 1999; Miyaki et al. 1999) (Table 1). Interestingly, this correlation between microsatellite instability and CTNNb1 mutations was not apparent in endometrial cancers (Mirabelli-Primdahl et al. 1999).

Aggressive fibromatosis, otherwise known as desmoid tumor, is a locally invasive fibrocytic growth that occurs with increased incidence in patients with familial adenomatous polyposis coli (FAP). FAP individuals carry APC mutations in their germline and present with multiple intestinal adenomas at an early age. Desmoids also occur sporadically and, with the exception of colorectal cancer, represent a rare example of biallelic inactivation of APC in individuals without a pre-existing germline mutation in APC (Alman et al. 1997). Not surprisingly, mutations

ns ın	human	cancers
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tissue	freq.	S29	Y30	L31	D32	S33	G34	135	H36	S37	G38	A39	T40	T41	T42	A 4 3	P44	S45	L46	S47	G48	K49	Δ	reference
colorectal	9/202		-				1							3				5				-	0	Samowitz 1999
colorectal	2/92	<del>                                     </del>	_		<b></b>		i –	<u> </u>						1				1					<u> </u>	Kitaeva 1997
colorectal-w/o APC mutation		<b> </b>			<b>-</b>			-			_			·									7	Iwao 1998
colorectal-w/o APC mutation		<b></b>		$\overline{}$		2	1							3				5					1	Sparks 1998
colorectal HNPCC	12/28	<b>-</b>	<b></b>		2		2			1				2				5					<u> </u>	Miyaki 1999
colorectal w/ MSI	13/53	<b> </b>	l		<u> </u>													6						Mirabelli-primdahl 1999
colorectal w/o MSI	0/27	<b></b>			<b>-</b>																			Mirabelli-primdahl 1999
desmoid, sporadic	1/1													1									0	Shitoh 1999
desmoid, sporadic	22/42	<b>†</b>			<b> </b>									10				12						Tejpar 1999
endometrial w/ MSI	3/9	<b>-</b>			2	1																		Mirabelli-primdahl 1999
endometrial w/o MSI	10/20				3	1	2			3				1										Mirabelli-primdahl 1999
gastric, Intestinal-type	7/26	2			5																			Park 1999
gastric, diffuse-type	0/17	<u> </u>																						Park 1999
hepatocellular w/HCV	9/22				3	1				3				1				2						Huang 1999
hepatocellular	12/35				1	1	2	1	1				1	2				2		1			2	Van Nhieu 1999
hepatocellular	6/26		T		2		1			1								1					1	de la Coste 1998
hepatocellular	14/75				5	1	1							1				4					2	Miyoshi 1998
hepatocellular	21/119				3	3	1	1		2				4				8					2	Legoix 1999
hepatoblastoma, sporadic	8/9						2			1								1					4	Jeng 2000
hepatoblastoma, sporadic	27/52				2		3			1				5									16	Koch 1999
hepatoblastoma	12/18				2		1							1				1					7	Wei 2000
kidney, Wilm's tumor	6/40													1				2					3	Koesters 1999
medulloblastoma, sporaic	3/67					2				1														Zurawel 1998
melanoma	1/65																	1						Garcia-Rostan 1999
ovarian, endometriod	7/13				3	1				2				1									0	Gamallo 1999
ovarian, endometriod	3/11									2				1										Palacios 1998
ovarian, endometriod	10/63					2	2			6														Wright 1999
pancreatic tumors	0/111																							Gerdes 1999
pilomatricoma	12/16				2	4	3			2				1										Chan 1999
prostate cancer	5/104				1	2								1				1						Voeller 1998
thyroid, anaplastic	19/31					1			1	3	1		8	2	1	1	4	2	1	2		9	0	Garcia-rostan 1999
uterine endometrium	10/76					1				2				4				3						Fukuchi 1998

Amino acids affected by mutations in CTNNb1 gene are indicated for sequence located between serine-29 (S29) and lysine-49 (K49). The overall frequency (freq.) of mutations in each tumor type is represented as the number of tumors with mutations/total number of tumors analyzed. The amino acid affected by the mutation and the number of mutations at each position are listed across columns. Interstitial deletions affecting one or more amino acids in the sequence are indicated as  $\Delta$ . In some cases, more than one mutation was found in a single tumor and therefore the sum of all mutations exceeds the number of tumors with mutations.

in CTNNb1 have also been detected in sporadic desmoid tumors (Shitoh et al. 1999; Tejpar et al. 1999). The  $\beta$ -catenin mutations were found in over half of the 42 desmoids analyzed, while inactivating mutations in APC were detected in nine and, again, there was no overlap between APC and  $\beta$ -catenin mutations (Tejpar et al. 1999). The  $\beta$ -catenin mutations were all of the missense variety and were confined to codons 41 and 45. Some of the desmoids lacked mutations in either  $\beta$ -catenin or APC, but all displayed increased expression of  $\beta$ -catenin, implying that yet unidentified defects in  $\beta$ -catenin regulation exist in some of these tumors.

There appears to be a low probability of accruing biallelic inactivating mutations in APC in most sporadic cancers, despite increased cancer incidence at numerous extracolonic sites in FAP patients. This suggests that the stabilization of β-catenin can promote cancer in many tissue types, but the biallelic inactivation of APC is an unlikely means to this end. Components in the wnt pathway other than APC, such as β-catenin, might make easier targets for oncogenic mutations. Indeed, several mutations in CTNNb1 were recently identified in gastric cancers, which occur with increased incidence in FAP patients (Park et al. 1999). In this study, 27% of intestinal type gastric cancers harbored mutations in  $\beta$ -catenin. Hepatoblastoma also occurs with increased incidence in FAP individuals (Hughes and Michels 1992; Giardiello et al. 1996; Cetta et al. 1997), but biallelic inactivation of APC is uncommon in the sporadic forms of these tumors. In three separate studies, mutations in  $\beta$ -catenin were identified at high frequency in hepatoblastoma, while no APC mutations were found (Koch et al. 1999; Jeng et al. 2000; Wei et al. 2000). Hepatoblastoma is also associated with Beckwidth-Wiedemann syndrome (BWS), however, a direct link between wnt signaling and the genetic defects underlying BWS are unlikely as a tumor from one of these patients also contained a somatic mutation in β-catenin (Wei et al. 2000). By contrast, a subset of patients with Turcot's syndrome harbor germline mutations in APC and are at increased risk of medulloblastoma (Hamilton et al. 1995; Lasser et al. 1994). Although inactivating mutations in APC have not been detected in the sporadic forms of medulloblastoma, CTNNb1 mutations were found in a small percentage (Zurawel et al. 1998).

Hepatocellular carcinoma (HCC) has become one of the most common tumors harboring mutations in the wnt pathway. Based on five separate studies, the frequency of CTNNb1 mutations in hepatocellular carcinoma (HCC) was ~20% overall and perhaps higher still for HCCs associated with hepatitis C virus (de La Coste et al. 1998; Miyoshi et al. 1998; Huang et al. 1999; Legoix et al. 1999; Van Nhieu et al. 1999) (Table 1). Preliminary data indicated a poorer prognosis associated with nuclear accumulation of β-catenin in HCC and histological data indicated enhanced nuclear staining in the invasive and intravascular compartments of the tumors (Huang et al. 1999; Van Nhieu et al. 1999). In one of these studies an inverse correlation between β-catenin mutations and loss of heterozygosity in the genome was noted (Legoix

et al. 1999). This suggests that chromosomal instability and mutations in *CTNNb1* represent alternative modes of tumor progression in HCC.

It is noteworthy that c-myc and cyclin D genes are amplified in a subset of HCCs and both these genes are downstream targets of β-catenin (He et al. 1998; Nishida et al. 1994; Peng et al. 1993; Shtutman et al. 1999; Tetsu and McCormick 1999). It would be of interest to determine whether any overlap exists between their amplification and CTNNb1mutations in HCC. Animal models of HCC have provided some clues toward understanding the relationship between these genes in cancer. HCCs induced by transgenic expression of SV40 T antigen in murine liver did not contain mutations in CTNNb1 (Umeda 2000). As T antigen activates cyclin D kinase by sequestration of Rb, the activation of the cyclin D gene by mutant β-catenin may no longer be required. By contrast, activating mutations in CTNNb1 were identified in half of the HCCs generated by transgenic expression of c-myc in murine liver (de La Coste et al. 1998). This animal model suggests that β-catenin mutations occur as a second "hit" in HCC tumor progression in cooperation with a distinct cancer pathway initiated by c-myc. That CTNNb1 mutations can occur subsequent to other oncogenic defects is also evident from their occurrence in Wilm's tumor. Mutations in β-catenin were detected in 15% of these pediatric kidney cancers and in two of these cases they were concomitant with mutations in the Wilm's tumor gene WT1 (Koesters et al. 1999). One of these cases was associated with Denys-Drash syndrome, a familial disorder attributable to germline mutations in WT1.

It makes sense that extracolonic tumors associated with FAP, such as desmoids, medulloblastoma, and HCC, would contain CTNNb1 mutations in their sporadic forms. Thyroid cancers also occur with increased incidence in FAP and, not surprisingly, a high frequency of CTNNb1 mutations was recently reported for anaplastic thyroid cancers (Cetta et al. 2000; Garcia-Rostan et al. 1999). Although many of these mutations affected amino acids known to influence the regulation of \( \beta \)-catenin, many of them affected residues for which the consequence of their mutation is unknown (Garcia-Rostan et al. 1999). In particular, the substitution K49R was detected nine times. This mutation was frequently detected in the context of independent CTNNb1 mutations in the same thyroid tumor, and up to four independent CTNNb1 mutations were found in some tumors. The occurrence of multiple independent CTNNb1 mutations was also noted in some HCCs and might reflect the multifocal origin of some cancers (Huang et al. 1999; Legoix et al. 1999; Van Nhieu et al. 1999). In one HCC study, examination of different tumor areas from the same patient revealed distinct CTTNb1 mutations in two independent cases (Huang et al. 1999).

Some cancers, such as endometrial ovarian tumors, do not occur with increased incidence in patients with FAP, yet they contain activating mutations in *CTNNb1* (Palacios and Gamallo 1998; Gamallo et al. 1999; Wright et al. 1999). Perhaps inactivation of the remaining wild-

type APC allele in FAP individuals is unlikely in this tissue, or the expression of an alternative APC gene compensates for its loss. The CTNNb1 mutations associated with ovarian cancer appeared to be confined to the endometrioid subtype. In this tissue, cancers with activated β-catenin signaling were reported to be less aggressive than their nonactivated counterparts. In one report, a more favorable prognosis was associated with cancers exhibiting enhanced nuclear staining of \( \beta \)-catenin and another indicated higher frequency of CTNNb1 mutations in lower grade tumors (Palacios and Gamallo 1998; Wright et al. 1999). A similar inverse correlation between tumor grade and occurrence of CTNNb1 mutations was also reported for uterine endometrial cancers (Fukuchi et al. 1998). The overlap between mutations in CTNNb1 and other gene defects in ovarian cancers has not been explored in detail, although one study noted coexisting mutations in the PTEN tumor suppressor and CTNNb1 in endometrioid tumors (Wright et al. 1999).

Additional types of cancers with CTNNb1 mutations, albeit at low frequency, include melanoma and prostate. Although only one of sixty-five melanomas contained detectable mutations, nuclear localization of the protein was seen in one-third (Rimm et al. 1999). Thus, additional mechanisms for β-catenin activation likely occur in these tumors. Possibly the highest percentage of CTNNb1 mutations occurs in a common skin tumor known as pilomatricomas (Chan et al. 1999). That these tumors might contain CTNNb1 mutations was surmised from the genesis of similar tumors in transgenic mice expressing mutant  $\beta$ -catenin in the skin (Gat et al. 1998). The tumors appeared to originate from the hair follicle, which is consistent with the lack of hair in mice homozygous for mutations in LEF, a transcription factor responsive to β-catenin (van Genderen et al. 1994).

#### Axin

Axin was originally identified as an inhibitor of wnt signaling in Xenopus embryos and was subsequently shown to bind directly to APC, β-catenin, GSK3β and dishevelled (for review, see Peifer and Polakis 2000). A plethora of in vitro and in vivo studies in Xenopus, Drosophila, and cultured mammalian cells has demonstrated that axin is central to the down regulation of β-catenin (Zeng et al. 1997; Behrens et al. 1998; Hart et al. 1998; Ikeda et al. 1998; Nakamura et al. 1998a; Sakanaka et al. 1998; Fagotto et al. 1999; Hedgepeth et al. 1999a; Li et al. 1999a; Willert et al. 1999a; Farr et al. 2000). It is not entirely clear how axin functions, but it has been proposed to facilitate the phosphorylation of β-catenin and APC by GSK3β (Hart et al. 1998; Ikeda et al. 1998). Thus axin would be viewed as a tumor suppressor based on its ability to downregulate signaling, and this has now been verified by documentation of its biallelic inactivation in human hepatocellular cancers and cell lines (Satoh et al. 2000). Importantly, these mutations were identified in those HCCs that lacked activating mutations in CTNNb1. All of the mutations were predicted to truncate the axin protein in a manner that eliminated the β-catenin binding sites. Axin, which should now be regarded as a tumor suppressor, constitutes the third genetic defect in the wnt pathway that contributes to human cancer. There also exists a close homolog of axin termed conductin, which exhibits of all the binding and regulatory functions of axin (Behrens et al. 1998). That this apparent redundancy did not suppress axin mutations in HCC suggests conductin is either not functionally equivalent to axin or not expressed at levels sufficient to compensate for its loss in HCCs.

## PP2A

The dependence upon serine/threonine kinases for the regulation of β-catenin implies that phosphatases are also involved. Indeed, the rapid dephosphorylation of the axin protein is a consequence of wnt signaling and has been proposed to both destabilize axin and reduce its affinity for β-catenin (Willert et al. 1999b; Yamamoto et al. 1999). Although axin binds directly to the PP2A catalytic subunit, the phosphatase affecting axin in response to wnt signaling has not been identified (Hsu et al. 1999). If PP2A is this phosphatase, it would be viewed as protooncogenic because it downregulates the tumor suppressor axin. On the contrary, expression of the PP2A regulatory subunit B56 in human colon cancer cells results in the downregulation of β-catenin, consistent with a tumor suppressive function in the wnt pathway (Seeling et al. 1999). Moreover, the beta isoform of the PP2A A subunit is deleted in some human colon tumors, again implying tumor suppression (Wang et al. 1998). Also, disruption of twins, a Drosophila gene coding for a PP2A subunit, complemented the overexpression and underexpression of the β-catenin homolog armadillo, in a manner consistent with negative regulation of wnt signaling (Greaves et al. 1999). By all accounts, PP2A plays a role in wnt signaling, but its potential role as proto-oncogene or tumor suppressor might be dependent upon the precise nature of the defect.

#### APC

Genetic analysis of FAP families led to the identification of the APC gene, and subsequent studies demonstrating an interaction with  $\beta$ -catenin placed it tentatively in the wnt pathway (Groden et al. 1991; Kinzler et al. 1991; Munemitsu et al. 1995; Rubinfeld et al. 1993; Su et al. 1993). Experiments in Drosophila ultimately revealed that genetic ablation of APC indeed resulted in upregulation of β-catenin signaling (Ahmed et al. 1998). In some systems, such as Xenopus and Caenorhabditis elegans, a positive role for APC in the wnt pathway has been proposed, but the former study suffers from potential overexpression artifacts and the latter from a lack of relatedness to the vertebrate APC protein (Rocheleau et al. 1997; Vleminckx et al. 1997). In any case, APC is a tumor suppressor in human cancers and its mutation relates strongly to the regulation of  $\beta$ -catenin. The spectrum of APC mutations, which typically truncate the protein, suggest selection against β-catenin regulatory domains,

albeit not necessarily against β-catenin binding (for review, see Polakis 1999). The selective pressure might be directed against the presence of Axin binding sites, of which there are three, dispersed across the central region of the APC protein (Behrens et al. 1998). The presence of axin binding sites are critical to APC in the regulation of β-catenin levels and signaling in cultured cells (Kawahara et al. 2000). Moreover, mice lacking wild-type APC but expressing a truncated mutant APC retaining a single axin binding site are viable and do not develop intestinal neoplasia (Smits et al. 1999). This has not been the case for mice with more extensive truncations in APC (Oshima et al. 1995a; Su et al. 1992). Also, milder forms of colorectal polyposis, as well as familial infiltrative fibromatosis (desmoid tumors), have been associated with germline mutations in the 3' region of the APC open reading frame. These mutations predict truncated proteins that retain only one or two of the three axin binding sites in APC (Walon et al. 1997; Kartheuser et al. 1999; Scott et al. 1996; van der Luijt et al. 1996). A recent study has also demonstrated that the expression of just the central region of APC, which contains all of the axin and β-catenin binding sites, was sufficient to elicit cellular growth suppression (Shih et al. 2000). This effect is consistent with previous work showing that a like fragment of APC was sufficient to downregulate  $\beta$ -catenin levels in cancer cells (Munemitsu et al. 1995).

Although both copies of the APC gene are typically inactivated in colorectal cancers, it remains possible that a mutant truncated APC could contribute to cancer progression. This was tested by transgenic expression of two different APC mutants in a wild-type intestinal background (Oshima et al. 1995b). This did not result in cancer-prone mice, despite high levels of expression of mutant proteins and, therefore, argues against a dominant negative effect by these particular mutants. However, it does not rule out an additive contribution to tumor progression by mutant APC protein in a background lacking wildtype APC. In fact, genetic evidence argues in favor of selection for a somewhat specific mutant APC protein. The mutation cluster region (MCR) in APC, roughly defined by codons 1250-1500, is not only consistent with selection against specific sequence, but also retention of an APC molecule that extends into the MCR (Fig. 3.). A correlation between the presence of a germline mutation in the MCR and the severity of polyposis has been noted (Ficari et al. 2000; Nagase et al. 1992; Wu et al. 1998). The enhanced severity of polyposis suggests there should

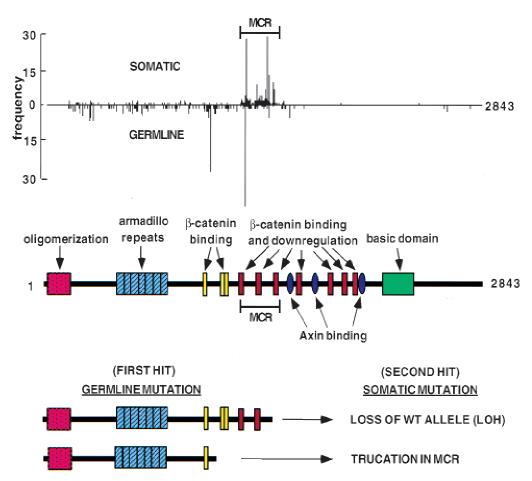


Figure 3. Mutations in APC. A compilation of germline and somatic mutations in APC illustrates selection for mutations in the mutation cluster region (MCR). MCR mutations result in truncated proteins retaining  $\beta$ -catenin binding but not regulatory activity. Somatic MCR mutations are more frequently selected for in FAP patients with germline mutations outside of the MCR.

also be selective pressure for somatic mutations in the MCR, which indeed appears to be the case (Miyoshi et al. 1992). Selective pressure for an MCR mutant has also been proposed based on the occurrence of somatic mutations in the MCR relative to the position of the germline mutation in FAP (Lamlum et al. 1999). Tumors from FAP patients with a germline MCR mutation exhibited frequent inactivation of the remaining APC allele by LOH, while those without a germline MCR mutation had frequent somatic mutations in the MCR (Fig. 3). Therefore, a germline mutation in the MCR could relieve the constraint for a subsequent somatic MCR mutation, thereby increasing the likelihood of polyposis. This implies that a truncated MCR APC mutant has an interfering or gain of function property that enhances tumor progression beyond simple loss of APC function. An interfering function would probably not involve interaction with wild-type APC, as recently suggested, because the MCR mutant is still selected for in the absence of a wild-type APC gene copy (Dihlmann et al. 1999). Finally, some of the germline mutations in APC do not disrupt the open reading frame yet correlate with increased risk of colorectal cancer (Frayling et al. 1998; Gryfe et al. 1999; Laken et al. 1997). These mutations have been proposed to increase the occurrence of subsequent truncating mutations by enhancing the mutational susceptibility of the affected nucleotide tract.

## Transcription factors

Prior to discussing the potential role for LEF/TCF transcription factors in cancer, it is important to outline the mechanism by which they have been proposed to operate. Although LEF/TCFs bind directly to DNA through their HMG domains, they are incapable of independently activating gene transcription (Eastman and Grosschedl 1999; Roose and Clevers 1999). This has best been illustrated for LEF, which through its binding to the cofactor ALY, makes indirect contacts with a second transcription factor AML (Bruhn et al. 1997). The TCFs do not contain the ALY binding site, but like LEF they cannot activate test genes comprised of multimerized TCF/LEF binding sites and a minimal promotor sequence. However, these reporter genes are activated on coexpression of TCF with  $\beta$ -catenin, suggesting that  $\beta$ -catenin supplies additional cofactors required for transcriptional activation (Molenaar et al. 1996). This activity was localized to the carboxy-terminal region of the Drosophila β-catenin armadillo, which when fused directly to TCF resulted in β-catenin independent transcriptional activation (van de Wetering et al. 1997).

The simple interpretation is that the TCF/LEF- $\beta$ -catenin complex comprises a bipartite positive acting transcription factor in the wnt pathway. This interpretation agrees well with developmental studies in which the manipulation of LEF/TCF function results in phenotypes consistent with the genetic manipulation of wnt/ $\beta$ -catenin signaling (Behrens et al. 1996; Brunner et al. 1997; Huber et al. 1996; van de Wetering et al. 1997). For example, a zygotic homozygous null mutation in *Dro*-

sophila LEF results in a loss of naked cuticle in the larval epidermis, a phenotype typical of loss of function wingless mutations (Brunner et al. 1997). Moreover, the formation of excess naked cuticle by ectopic expression of armadillo in wild-type embryos does not occur in the LEF null mutants. Exactly how β-catenin contributes to transcriptional activation is unclear, but might involve additional proteins that bridge the TCF/β-catenin complex to the basal transcriptional machinery. The bridging function might be fulfilled by Pontin 52, a TATA-binding protein that was reported to bind to β-catenin (Bauer et al. 1998). Also, a mutant form of β-catenin incapable of binding LEF squelched LEF-dependent reporter gene activation, presumably by titration of an essential cofactor (Prieve and Waterman 1999). Finally, the carboxyterminal region of armadillo binds to the Zinc finger protein teashirt, a homeotic gene essential for a subset of wingless signaling outputs in Drosophila (Gallet et al. 1999).

The simple model of positive transcriptional activation by the TCF-β-catenin complex is not in accord with all experiments. Mutation of the TCF/LEF binding sites in the promotors of the wingless responsive gene ultrabithorax and the Wnt-responsive Xenopus gene Siamois enhanced their activities under conditions where the wingless/β-catenin signal input was weak (Brannon et al. 1999; Riese et al. 1997). The mammalian cyclin D gene was recently identified as a wnt target and, again, mutation of the corresponding TCF binding sites enhanced its basal activity (Tetsu and McCormick 1999). These results suggest TCF represses transcription of its target genes in unstimulated cells and the binding of β-catenin promotes derepression. Derepression cannot fully account for signaling activity, however, as mutations in the TCF binding sites compromise target gene activation under conditions of active wnt signaling (Brannon et al. 1999; Riese et al. 1997). Repression of gene expression by TCF is consistent with its direct physical interaction with at least three different gene products, the Groucho/TLE and CtBP corepressors, and the CREB binding protein CBP (Brannon et al. 1999; Cavallo et al. 1998; Levanon et al. 1998; Roose et al. 1998; Waltzer and Bienz 1998).

The groucho/TLE proteins bind to the central region of TCF/LEF at a site distinct from that of β-catenin binding and inhibit gene activation of TCF target genes (Levanon et al. 1998; Roose et al. 1998). By contrast, CtBP binds to two independent sites in the carboxy-terminal region of Xtcf-3, which when mutated abrogated the repressor function of this region of Xtcf-3 (Brannon et al. 1999). The binding sites for CtBP are not present in LEF, which might explain the ability of LEF, but not Xtcf-3, to induce axis duplication in *Xenopus* embryos. Finally, the Drosophila CREB binding protein CBP was reported to bind to the HMG domain of dTCF (Waltzer and Bienz 1998). Loss-of-function CBP mutants displayed some features of wingless over expression and also suppressed phenotypes resulting from loss of the β-catenin homolog armadillo. The genetics imply suppression of wingless by CBP, which is somewhat paradoxical when considering the role of CBP acetyltransferase activity in chromatin remodeling and gene activation. However, it was shown that CBP acetylates a lysine proximal to the armadillo binding site in TCF, thereby reducing its affinity for armadillo. Repression of  $\beta$ -catenin/TCF signaling by CBP does not occur in all settings, though, as two recent studies demonstrated activation of *Xenopus* TCF target genes by CBP (Hecht et al. 2000; Takemaru and Moon 2000). CBP directly associated with carboxy-terminal sequence in  $\beta$ -catenin and overexpression of E1A, which also directly binds CBP, reduced  $\beta$ -catenin dependent transactivation.

Does the activation of TCF/LEF target genes by β-catenin cause cancer? Good evidence to this effect was provided by the expression of a chimeric protein consisting of the LEF DNA binding sequence fused to the transcriptional activation domain of either VP16 or the estrogen receptor (Aoki et al. 1999). Expression of these constructs in chicken embryo fibroblasts resulted in their neoplastic transformation. The proliferative potential of TCF was also apparent from the phenotype resulting from homozygous disruption of TCF-4 in the germline of mice. These animals were incapable of maintaining a proliferative stem cell compartment in the small intestine and died shortly after birth (Korinek et al. 1998). Whether the TCF/LEF genes are directly activated by mutations in cancer is unclear, but mutations in TCF-4 have been detected in a subset of colorectal tumors (Duval et al. 1999). The mutations all occur as single base deletions in an (A)9 nucleotide repeat within the 3' coding region of the gene. These deletions generate frame shifts predicted to effect the proportion of the long and short forms of TCF that normally result from alternative mRNA splicing. The mutations were also found in cancer cell lines, all of which possessed mutations in either APC or β-catenin. This indicates that the TCF mutations do not substitute for APC/β-catenin mutations but could act in an additive manner.

An additional mechanism by which TCFs could contribute to cancer was gleaned from the phenotype of mice homozygous for mutations in TCF-1 (Roose et al. 1999). Fifteen percent of these animals developed adenomatous intestinal polyps by one year of age, implicating TCF-1 as a tumor suppressor. The major isoforms of TCF-1 do not contain a β-catenin binding site and could therefore act in a dominant negative manner in wnt signaling. Crossing TCF-1 null mice with cancer-prone ApcMin/+ mice resulted in offspring with ten times the number of intestinal polyps relative to ApcMin/+ littermates. This experimental model suggests that the genetic ablation of TCF-1 could modify, or even independently contribute to cancer progression in humans. Additional potential mechanisms for cancer would include the inactivation of corepressors such as CtBP and TLE/ groucho.

#### Cross talk

Defects leading to activation of the wnt pathway could also occur in signaling systems that are seemingly unre-

lated to wnt signaling. One potential mode of cross talk includes the kinase TAK1, which can substitute for MAPK kinase kinase in the yeast pheromone pathway. TAK1 (TGF-β activated kinase) is activated by TGF-β in mammalian cells and has also been implicated in interleukin-1 activation of NFκB (Ninomiya-Tsuji et al. 1999; Yamaguchi et al. 1995). In c. elegans, the TAK1 homolog MOM-4 negatively regulates the TCF homolog POP-1 by activating another kinase LIT-1, which then phosphorylates POP-1 (Meneghini et al. 1999; Shin et al. 1999). LIT-1 is thought to gain access to POP-1 through its direct binding to the β-catenin homolog WRM-1 (Shin et al. 1999). Parallel interactions have been demonstrated for the mammalian counterparts of these proteins where the phosphorylation of TCF, by the LIT-1 homolog NLK, reduces its DNA binding affinity (Ishitani et al. 1999). Thus a MAPK-like signaling system might downregulate the wnt-1 pathway. A second opportunity for cross talk with wnt signaling was realized by a physical interaction between the β-catenin-TCF complex and SMAD4, a mediator of TGF-B signaling (Nishita et al. 2000). This interaction was proposed to be synergistic with respect to the activation of the Xenopus wnt target gene twin. How this relates to cancer is somewhat puzzling when considering that TGF-β signaling is typically compromised by genetic and epigenetic defects during tumor progres-

An additional mode of cross regulation was recently revealed by the discovery that retinoids inhibit β-catenin dependent gene transcription (Easwaran et al. 1999). β-catenin associated with a retinoic acid receptor (RAR) and cooperated with retinoids to enhance activation of a retinoic acid responsive promotor. Moreover, the identification of RAR-γ as a target of wnt signaling in *Xenopus* also points to an interaction between these signaling systems (McGrew et al. 1999). Signaling by β-catenin was also reported to be repressed by expression of sox3 and sox17 transcription factors, which associated directly with β-catenin (Zorn et al. 1999). Although inhibition of β-catenin signaling was clearly demonstrated, it is also possible that β-catenin drives gene activation independent of LEF/TCF, through its association with the sox proteins. Finally, the activation of the WISP genes by  $\beta$ -catenin is highly dependent upon the presence of a CREB binding site in the WISP promotor (Xu et al. 2000). This implies that cAMP-dependent protein kinase A feeds into wnt signaling and might cooperate with the activation of some wnt target genes. The binding of CBP to β-catenin is particularly relevant with respect to this proposal (Hecht et al. 2000; Takemaru and Moon 2000).

#### Conclusion

It is apparent that wnt signaling causes cancer and that tumor promotion by this pathway can proceed through a number of different genetic defects. Additional mechanisms by which defects in the regulation of wnt signaling contribute to tumor progression probably remain undiscovered. The manifestation of cancer by aberrant wnt signaling most likely results from inappropriate gene activation mediated by stabilized  $\beta\text{-catenin}$ . Target genes need not contain TCF/LEF binding sites in their promotors, though, as new potential modes of gene activation by  $\beta\text{-catenin}$  are becoming apparent. Several target genes of  $\beta\text{-catenin}$  signaling have now been identified and some of their functions are consistent with control of cellular growth, differentiation, and survival. For an excellent summary of wnt target genes, and a wealth of information on wnt signaling in general, I refer the reader to the Wnt Home Page posted by the Nusse lab (http://www.stanford.edu/rnusse/wntwindow.html).

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