

REVIEW

Are Wnt/ β -Catenin and PI3K/AKT/mTORC1 Distinct Pathways in Colorectal Cancer?Anna Prossomariti,^{1,2} Giulia Piazzi,^{1,2} Chiara Alquati,^{1,2} and Luigi Ricciardiello^{1,2}¹Department of Medical and Surgical Sciences, University of Bologna, Bologna, Italy; ²Center for Applied Biomedical Research, S. Orsola Hospital, University of Bologna, Bologna, Italy

SUMMARY

This article recapitulates the evidence on the interaction between Wnt/ β -catenin and phosphatidylinositol-3-kinase/protein kinase B/mammalian target of rapamycin complex 1 pathways in cancer, with a primary focus on intestinal tumorigenesis, and describes the main molecular mechanisms underlying this crosstalk and impact on the resistance to colorectal cancer target therapies.

Wnt/ β -catenin and phosphatidylinositol-3-kinase/protein kinase B/mammalian target of rapamycin complex 1 (PI3K/AKT/mTORC1) pathways both are critically involved in colorectal cancer (CRC) development, although they are implicated in the modulation of distinct oncogenic mechanisms. In homeostatic and pathologic conditions, these pathways show a fine regulation based mainly on feedback mechanisms, and are connected at multiple levels involving both upstream and downstream common effectors. The ability of the Wnt/ β -catenin and PI3K/AKT/mTORC1 pathways to reciprocally control themselves represents one of the main resistance mechanisms to selective inhibitors in CRC, leading to the hypothesis that in specific settings, particularly in cancer driven by genetic alterations in Wnt/ β -catenin signaling, the relationship between Wnt/ β -catenin and PI3K/AKT/mTORC1 pathways could be so close that they should be considered as a unique therapeutic target. This review provides an update on the Wnt/ β -catenin and PI3K/AKT/mTORC1 pathway interconnections in CRC, describing the main molecular players and the potential implications of combined inhibitors as an approach for CRC chemoprevention and treatment. (*Cell Mol Gastroenterol Hepatol* 2020;10:491–506; <https://doi.org/10.1016/j.jcmgh.2020.04.007>)

Keywords: Wnt/ β -Catenin; PI3K/AKT/mTORC1; Colorectal Cancer; Crosstalk; Resistance.

Colorectal cancer (CRC) is the third most common malignancy in terms of both incidence and mortality worldwide.¹ Although surgery combined with standard chemotherapy is effective for early stages, metastatic CRC often is resistant to conventional treatments.

The Wnt/ β -catenin pathway and the phosphatidylinositol-3-kinase (PI3K)/protein kinase B (AKT)/mammalian target of rapamycin (mTOR) axis frequently are deregulated

in CRC, therefore representing an attractive target for chemoprevention and treatment.^{2,3}

The Wnt/ β -catenin pathway, also known as the canonical Wnt pathway, controls the self-renewal of intestinal stem cells and is crucial for preserving intestinal homeostasis.^{4,5} However, sustained Wnt/ β -catenin signaling activation triggers hyperproliferation and oncogenic transformation of intestinal epithelial cells, leading to CRC onset.⁴

The PI3K/AKT/mTOR pathway regulates multiple cellular events including cell growth, proliferation, metabolism, protein and lipid synthesis, and autophagy.⁶ Moreover, the aberrant activation of the PI3K/AKT/mTOR pathway often has been reported in cancer settings.⁶

A close connection between Wnt/ β -catenin and PI3K/AKT/mTOR signaling has been described in CRC. Indeed, these pathways share common effectors and are able to mutually regulate each other.

Over the years, numerous inhibitors of Wnt/ β -catenin and PI3K/mTOR complex 1 (mTORC1) pathways have been developed and tested against CRC. These targeted therapies have shown clinical effectiveness in the treatment of advanced CRC, although the long-term effects frequently fail owing to the acquisition of resistance mechanisms.^{7,8} In particular, Wnt/ β -catenin pathway inhibition has been associated with the up-regulation of the PI3K/AKT/mTORC1 pathway and, similarly, blocking the PI3K/AKT/mTORC1 cascade results in Wnt/ β -catenin signaling hyperactivation as a compensatory mechanism.

Abbreviations used in this manuscript: AKT, protein kinase B; APC, adenomatous polyposis coli; CRC, colorectal cancer; DEPTOR, DEP domain-containing mTOR-interacting protein; DVL, Dishevelled; eEF2K, elongation factor 2 kinase; EGFR, epidermal growth factor receptor; eIF4E, eukaryotic translation initiation factor 4E; FAP, familial adenomatous polyposis; FOXO3A, Forkhead box O3A; FZD, frizzled; GSK3, glycogen synthase kinase 3; GTPase, guanosine triphosphatase; LRP, low-density lipoprotein receptors 5 and 6; MEK, Mitogen-activated protein kinase kinase; MNK, Mitogen-activated Protein kinase interacting kinases; mTOR, mammalian target of rapamycin; mTORC1, mammalian target of rapamycin complex 1; PI3K, phosphatidylinositol-3-kinase; PORCN, Porcupine; RAS, Rat Sarcoma; Rheb, ras homolog enriched in brain; RNF43, ring finger protein 43; S6K, S6 Kinase; TNKS, tankyrase; TNKSi, tankyrase inhibitors; TSC, tuberous sclerosis; YAP, Yes-associated protein; ZNRF3, zinc/ring finger 3; 4E-BP1, 4E binding protein 1.



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This review comprehensively discusses the literature concerning the mechanisms linking the Wnt/ β -catenin and PI3K/AKT/mTORC1 pathways in CRC development and elucidates the biological processes and components leading to pharmacologic resistance to selective inhibitors.

Role of Wnt/ β -Catenin Signaling in Colorectal Cancer

β -Catenin Turnover Regulation

Since the critical role of Wnt/ β -catenin signaling in the etiology of CRC has been established, many studies have been conducted to identify key molecular players that could represent concrete targets for CRC chemoprevention and therapy.

In the inactive state, β -catenin levels are kept stably low through the dynamic activity of a protein complex known as the destruction complex or degradosome.⁹ This complex includes casein kinase 1 α , glycogen synthase kinase 3 (GSK3), Axis inhibition protein 1, adenomatous polyposis coli (APC), protein phosphatase 2A, and the E3-ubiquitin ligase β -transducin repeats-containing protein.^{9–13} APC and Axis inhibition protein 1 function as scaffold proteins in the destruction complex, while casein kinase 1 α and GSK3 are the main serine/threonine kinases involved in β -catenin phosphorylation.¹⁴ β -transducin repeats-containing protein mediates the ubiquitination of phosphorylated β -catenin and targets it for degradation by the proteasome machinery.^{15,16} It is noteworthy that Axis inhibition protein 1 has been proposed as the rate-limiting factor for the degradosome assembly because its endogenous levels are finely regulated and kept low in the absence of Wnt stimulation.¹⁷

Wnt ligands are active molecules that bind the 7-transmembrane receptor frizzled (FZD) family and the coreceptors low-density lipoprotein receptors 5 and 6 (LRP5/6).^{18–21} The formation of the ligand-receptor complex Wnt-FZD-LRP5/6 and the recruitment of the adaptor dishevelled (DVL) by FZD lead to LRP6 phosphorylation, Axis inhibition protein 1 translocation to the plasma membrane, its association with LRP6, and the dissociation of GSK3 from Axis inhibition protein 1 and APC with consequent dephosphorylation and stabilization of β -catenin.^{22,23} These events cause the assembly of the signalosome, a multiprotein complex able of transducing Wnt signals, as well as the degradosome disassembly with consequent cytosolic β -catenin accumulation and nuclear translocation. Finally, nuclear β -catenin acts as a transcriptional coactivator interacting with T-cell transcription factor,²⁴ or lymphoid enhancer factor,²⁵ and inducing the transcription of target genes, including *AXIN2*,²⁶ *c-MYC*,²⁷ *CCND1*,^{28,29} thus promoting cell proliferation and activation of oncogenic mechanisms.

Two main critical steps have been proposed to be responsible for the impairment of β -catenin degradation on Wnt stimulation, attributable to the inhibition of β -catenin phosphorylation or ubiquitination, respectively. Despite inhibition of β -catenin ubiquitination showing effects on the prevention of β -catenin degradation,³⁰ most of the evidence supports the concept that the inhibition of β -catenin

phosphorylation and the disassembly of the β -catenin destruction complex represent the crucial event for Wnt/ β -catenin pathway activation. In particular, by studying the kinetics of β -catenin turnover at the steady-state level, Hernández et al³¹ showed that in the early phases after Wnt stimulation, the reduced levels of GSK3 β -mediated β -catenin phosphorylation are responsible for β -catenin degradation inhibition, while a subsequent recovery of β -catenin phosphorylation would restore its degradation. Thus, according to this model, inhibition of β -catenin phosphorylation leads to β -catenin accumulation during Wnt stimulation.

Moreover, in the early phases after Wnt stimulation, Axis inhibition protein 1 protein stability is increased, thus enhancing the signalosome assembly and Wnt/ β -catenin signaling initiation.³² On the other hand, on long-term Wnt stimulation, adenosine diphosphate-ribosylation by poly (adenosine diphosphate-ribose) polymerase enzyme tankyrase (TNKS) triggers Axis inhibition protein 1 proteolysis and degradation, resulting in the dissociation of the β -catenin destruction complex and sustained Wnt/ β -catenin signaling activation.³² Thus, Axis inhibition protein 1 also functions as a fundamental switch for controlling both Wnt/ β -catenin cascade activation and inhibition.

More comprehensive results about the mechanisms underlying Wnt/ β -catenin signaling regulation and the dynamics of the β -catenin destruction complexes under the presence of Wnt signals have been described recently.³³ Indeed, under Wnt stimulation, a fraction of the β -catenin destruction complexes is disassembled with a consequent initial accumulation of cytosolic β -catenin. At the same time, a portion of functional complexes do persist, capable of progressively restoring β -catenin phosphorylation and degradation rates.³³

Moreover, emerging evidence has shown that ring finger protein 43 (RNF43), the transmembrane E3 ubiquitin ligase zinc and ring finger 3 (ZNRNF3) and DVL play a critical role in controlling extrinsic Wnt/ β -catenin pathway activation by regulating the levels of Wnt receptors on the cellular membrane. Indeed, RNF43 and ZNRNF3, promoting the internalization and the subsequent degradation of Wnt receptors FZD and LRP6, act as crucial negative regulators of the signaling.^{34,35} Importantly, recent data have shown that DVL is required not only for Wnt/ β -catenin signaling initiation but also for RNF43 and ZNRNF3-mediated degradation of FZD and LRP6.³⁶ In contrast, R-spondin, by inhibiting ZNRNF3, operates as a Wnt/ β -catenin signaling enhancer.³⁵

In addition, an interaction between Hippo and the Wnt/ β -catenin signaling pathway has been described. However, the literature evidence still is quite controversial and the mechanisms underlying this crosstalk are under investigation. Indeed, although some studies described the Hippo signaling transducers Yes-associated protein (YAP) and Transcriptional coactivator with PDZ-binding motif as components of the degradosome and transcriptional coactivators of β -catenin,³⁷ other reports have indicated a possible involvement of the Hippo cascade in noncanonical Wnt signaling, showing that it acts as an inhibitor of the canonical Wnt signaling.^{38,39} Moreover, APC has been

described as a dual upstream regulator of both Hippo YAP and β -catenin pathways, which independently contribute to the intestinal tumorigenesis in the absence of functional APC,⁴⁰ although another study showed that Wnt/ β -catenin signaling directly regulates YAP expression through the β -catenin/T-cell transcription factor 4 transcriptional complex.⁴¹

Overall, these extensive findings suggest that the regulation of this pathway is more complex than previously thought, and probably many mechanisms still need to be clarified.

Mutations in Wnt/ β -Catenin Signaling Components

Genetic alterations in the Wnt/ β -catenin pathway components, frequently observed in CRC, lead to the intrinsic aberrant canonical Wnt/ β -catenin signaling activation. Inactivating germ-line mutations in the *APC* gene, encoding for the core scaffold element of the β -catenin destruction complex, are causative for the development of the rare hereditary CRC-predisposing syndrome familial adenomatous polyposis (FAP),^{42,43} while somatic mutations in the *APC* gene constitute the most frequent initiating event in sporadic CRC (approximately 80%–90% of cases).⁴⁴ Recent data have shown that APC regulates β -catenin levels, also acting as a modulator of the Wnt receptor LRP6.^{45,46} Indeed, genetic alterations in the *APC* gene induce an autoassembly of the signalosome in the absence of Wnt ligands, thus resulting in uncontrolled pathway activation. Importantly, these new relevant data have raised the possibility of counteracting the functional effects induced by APC loss through the modulation of the upstream receptors.

Activating point mutations of the β -catenin encoding gene *CTNNB1* have been observed in a small percentage of CRC cases with wild-type *APC*,⁴⁷ while somatic mutations in *AXIN2* mainly have been associated with mismatch repair-deficient CRC cases.⁴⁸ Somatic *AXIN1* mutations, resulting in loss of function, also are found at low frequency in colorectal adenomas and CRC.^{49,50} Finally, further causative alterations have been described in *RNF43*, *ZNRF3*, and *TCF4* genes.^{35,51,52}

The mTOR Pathway in CRC

PI3K/AKT/mTORC1 Axis

mTOR is a serine/threonine protein kinase made of 2 multiprotein complexes: mTORC1 and mTORC2.⁵³ Mammalian lethal with SEC13 protein 8 (mLST8) (also known as G Protein beta Subunit-like),⁵⁴ DEP domain-containing mTOR-interacting protein (DEPTOR),⁵⁵ and the Tel-2 interacting protein 1/Telomere maintenance 2 factors⁵⁶ are common to both protein complexes. Regulatory-associated protein of mTOR⁵⁷ and Proline-Rich AKT Substrate of 40 kDa⁵⁸ are distinctive of the mTORC1 complex, while Rapamycin-insensitive companion of mTOR,⁵⁹ mammalian Stress-activated protein kinase-interacting protein 1,⁶⁰ and Protein observed with RICTOR 1/2⁶¹ belong to the mTORC2 complex. The 2 complexes act through different mechanisms and show a distinct sensitivity to stimuli, in particular to

rapamycin, which is higher for mTORC1.⁶² Although the mTORC2 function still is not completely characterized, mTORC1 has been largely described.⁶ mTORC1 is activated on different stimuli, such as growth factors, nutrients, cellular stress, hypoxia, and DNA damage.⁶ The heterodimer complex constituted by tuberous sclerosis (TSC)1 and TSC2 plays a key role in the upstream regulation of the pathway and functions as a bridge to flow activating signals and molecules onto mTORC1. The TSC1/TSC2 complex works as a guanosine triphosphatase (GTPase) activating protein for Ras homolog enriched in brain (Rheb), a GTPase belonging to the Ras family.⁶³ Rheb-GTP functions as a potent inducer of mTORC1 kinase activity. The TSC1/TSC2 complex, promoting the conversion from Rheb-GTP to Rheb-guanosine diphosphate, acts as a negative regulator of mTORC1 signaling.⁶⁴

Although the mTORC1 cascade is induced through different mechanisms, the main activation route in response to mitogenic stimuli involves the upstream regulators PI3K and AKT.⁶⁵ PI3K induces AKT by promoting the conversion of phosphatidylinositol (3,4)-bisphosphate to phosphatidylinositol (3,4,5)-trisphosphate, and triggering AKT phosphorylation at Thr308 via 3'phosphoinositide-dependent kinase 1.⁶⁶ This event leads to mTORC1 activation by AKT-mediated phosphorylation and the consequent inactivation of Proline-Rich AKT Substrate of 40 kDa (PRAS40)⁵⁸ and TSC2.^{67,68} Moreover, AKT also acts through mTORC1 phosphorylation at Ser2448.⁶⁹ Once activated, mTORC1 mediates the phosphorylation of 2 main downstream targets: eukaryotic translation initiation factor 4E (eIF4E) binding protein 1 (4E-BP1), and p70S6 ribosomal kinase 1 (S6 Kinase 1 [S6K1] or p70S6 ribosomal kinase 1). Phosphorylated 4E-BP1 dissociates from the cap-binding protein eIF4E, thus promoting messenger RNA translation.^{70,71} In addition, activation of S6K1 protein leads to ribosomal protein S6 phosphorylation and consequent induction of translation initiation and elongation.⁷²

Genetic Alterations in the PI3K/AKT/mTORC1 Pathway

The involvement of the mTORC1 pathway in cancer onset and promotion has been widely described. The aberrant activation of this pathway frequently depends on genetic alterations in upstream regulators rather than in *mTOR* genes. Gain-of-function mutations in the *PIK3CA* gene have been described in 12%–32% of CRC patients and have been associated with proximal CRC.^{73–79} Moreover, somatic mutations in components of the PI3K/AKT/mTORC1 pathway have been observed frequently in Lynch syndrome cases.⁸⁰ Inactivating mutations or loss of heterozygosity in the *PTEN* gene, a negative regulator of PI3K activity, also have been found, particularly in tumors with microsatellite instability.^{79,81–86} *PTEN* epigenetic silencing represents an additional mechanism for PI3K activity regulation in CRC.⁸⁷ Furthermore, somatic mutations in the *STK11/LKB1* gene, which encode for an mTORC1 repressor,⁸⁸ have been observed in a small percentage of sporadic CRC cases.^{89,90} Finally, *AKT* mutations are a rare occurrence in CRC.⁹¹

PI3K/AKT/mTORC1 Signaling in Intestinal Tumorigenesis Driven by *Apc* Loss

The involvement of PI3K/AKT/mTORC1 signaling in the progression of *Apc*-driven CRC has been shown largely in murine models. Treatment with the mTORC1 inhibitor everolimus was found to reduce tumor burden in the *Apc*^{D716} mouse model of FAP that showed induced mTORC1 signaling in the intestinal polyps.⁹² Similar findings have been obtained in the *Apc*^{Min/+} mouse model of FAP,^{93,94} and in the *Apc* conditional knock-out mouse model with treatment with rapamycin.⁹⁵ It should be noted that both β -catenin-dependent and β -catenin-independent mechanisms have been described to explain mTORC1 induction with Wnt pathway activation.^{92,96}

Subsequent studies further clarified the involvement of mTORC1 signaling upon *Apc* inactivation. Indeed, although mTORC1 activation is crucial to ensure the survival and proliferation of murine enterocytes upon *Apc* gene deletion, its inhibition has no relevant effects on the intestines of *Apc* wild-type mice.⁹⁷ This study described important mechanisms linking mTORC1 activation to the intestinal tumorigenesis driven by *Apc* loss. Upon *Apc* gene deletion, activated mTORC1 enhances the elongation translation rate by inhibiting the elongation factor 2 kinase (eEF2K) via S6K and activating the eEF2. Importantly, this mechanism involving the mTORC1-S6K-eEF2K-eEF2 axis seems crucial to sustain the growth and expansion of *Apc*-deficient enterocytes.⁹⁷ Furthermore, the synergic effect of the Wnt/ β -catenin and PI3K/AKT/mTORC1 pathways on the development of colonic lesions was shown in another study by crossing the *Apc*^{Min/+} and FC PIK3ca* mice. In this model, characterized by a germline mutation in the *Apc* gene and constitutive activation of PI3K in the intestine, the simultaneous activation of both pathways boosted tumor initiation and promotion.⁹⁸

Recently, Brandt et al⁹⁹ showed that although mTORC1 inhibition could represent an effective preventive strategy against *Apc* mutant CRC, it could promote carcinogenesis in long-standing inflammatory bowel diseases. Indeed, in a setting of chronic inflammation, mTORC1 signaling plays a critical protective role by promoting intestinal regeneration upon injury. Interestingly, given the existing link between protein intake and mTORC1 activation, the investigators have proposed that it would be possible to affect colonic tumor progression by adjusting the dietary protein intake, depending on the underlying mechanisms of CRC development (ie, low-protein intake in Wnt-sustained tumors or high-protein intake in a condition of persistent inflammation).⁹⁹ This evidence suggests a new possible scenario in the prevention of CRC, coupling a pharmacologic approach with dietary strategies that could increase the effectiveness of targeted drugs substantially.

Common Effectors and Linking Elements Between Wnt/ β -Catenin and PI3K/AKT/mTORC1 Pathways

GSK3 β

Wnt/ β -catenin and PI3K/AKT/mTORC1 pathways share some effectors critically involved in both signaling

pathways. GSK3 β represents a common key element, which independently participates in both signaling cascades regulating different cellular processes. GSK3 kinase is constitutively active and is regulated negatively through different mechanisms. Distinct intracellular pools of GSK3 β have been implicated in the regulation of Wnt/ β -catenin and PI3K/AKT/mTORC1.¹⁰⁰ The activation of both signaling pathways results in the inhibition of GSK3 β activity, although via different upstream events. The regulation of GSK3 β activity during Wnt signaling occurs mainly through protein-protein interactions and intracellular sequestration.¹⁰⁰ In the Wnt/ β -catenin pathway, a fraction of AXIN-bound GSK3 β has an important role in controlling β -catenin degradation, through the regulation of β -catenin phosphorylation.¹⁰¹ In particular, the GSK3 β interaction with the scaffolding protein AXIN is crucial to allow an efficient GSK3 β -mediated phosphorylation of β -catenin.¹⁰ Importantly, APC also regulates GSK3 β . Indeed, the APC dissociation from AXIN, which is induced rapidly on Wnt stimulation, weakens GSK3 β activity, with consequent β -catenin stabilization.¹⁰² In addition, the GSK3 β -mediated LRP6 phosphorylation, which occurs on Wnt stimulation, leads to GSK3 β inhibition.¹⁰³

GSK3 β also interacts with the PI3K/AKT/mTORC1 pathway through different mechanisms.^{96,102,104} Upon PI3K activation, phosphorylated AKT is able to inhibit GSK3 β kinase activity by inducing its phosphorylation at Ser9.^{105,106} In addition, in specific circumstances, such as reduced AKT activation, GSK3 β can be phosphorylated and inactivated by S6K.¹⁰⁷ Importantly, much evidence has shown that GSK3 β inhibition (induced upon Wnt stimulation) does not occur through AKT-mediated phosphorylation at Ser9.¹⁰⁸ Thus, AKT activation has no direct effects on the Wnt/ β -catenin pathway.^{109,110} However, as suggested by Ding et al,¹⁰⁹ it is possible that in conditions of AKT hyperactivation and active canonical Wnt signaling, the simultaneous inhibition of GSK3 β activity induced by the 2 signaling pathways may result in enhanced β -catenin accumulation. Moreover, APC loss, leading to GSK3 β dysregulation and reduction of its kinasic activity, has been associated with mTORC1 activation with a mechanism independent from β -catenin accumulation.¹⁰² Thus, APC inhibition represents a critical event for the simultaneous induction of both β -catenin and mTORC1 signaling through independent downstream mechanisms sharing the upstream inhibition of GSK3 β .¹⁰²

mTORC1 inhibition promotes GSK3 β nuclear translocation,¹¹¹ and, importantly, GSK3 β expression seems crucial for cancer cell responsiveness to mTOR inhibitors.¹¹² A new mechanism explaining the relationship between GSK3 β and mTORC1 has been proposed recently.^{113,114} The investigators showed that GSK3 β nuclear translocation induced by rapamycin was associated with increased phosphorylation of the nuclear proteins Forkhead Box K1 and General Transcription Factor IIF Subunit 1, slowing down cell proliferation.^{113,114}

Although the role of the PI3K/AKT/mTORC1 pathway in the modulation of translation is widely described,¹¹⁵ the involvement of Wnt/ β -catenin signaling in this process is poorly characterized. Preclinical studies have shown that

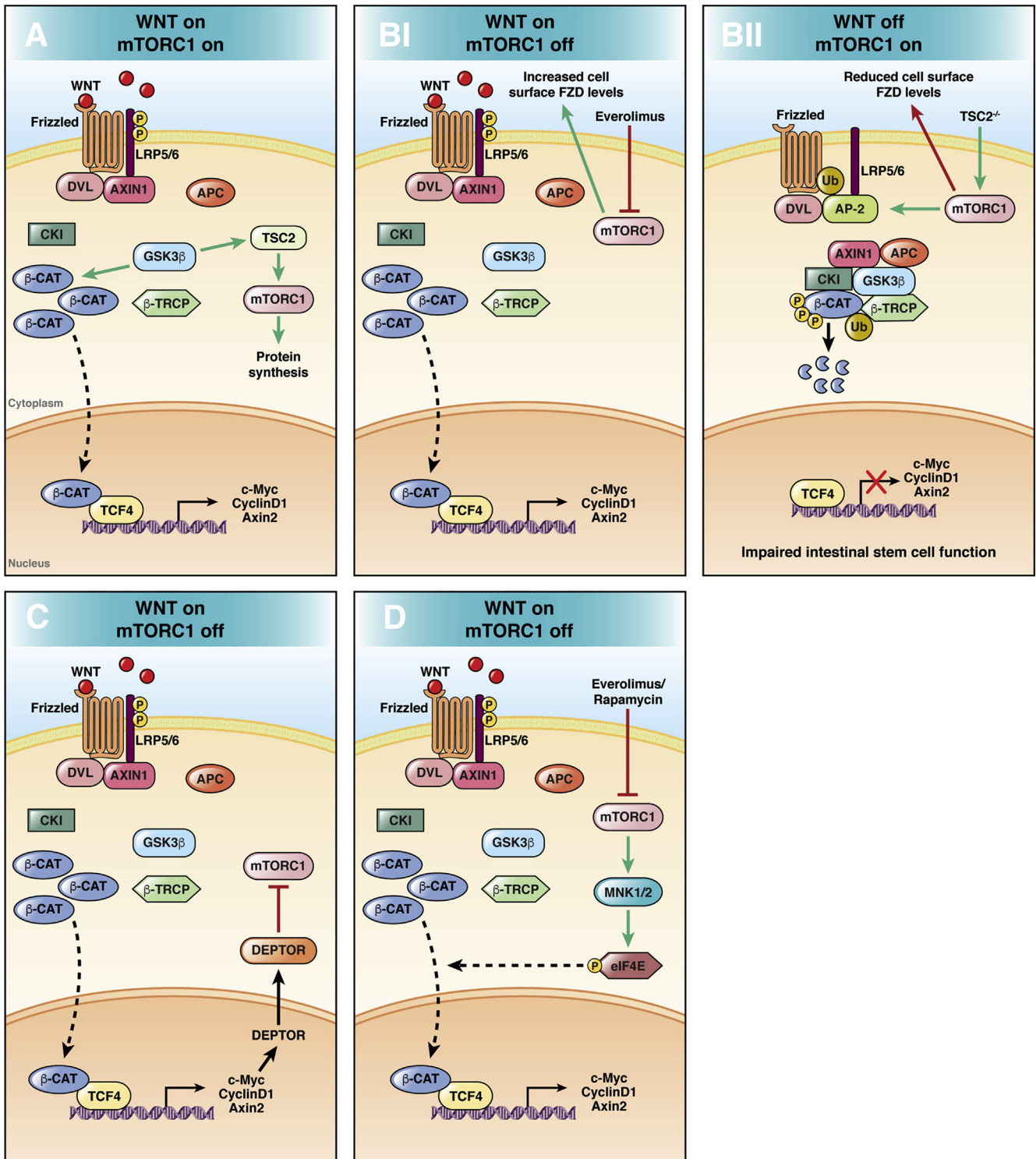


Figure 1. Main mechanisms of Wnt/ β -catenin and PI3K/AKT/mTORC1 pathway interconnections. (A) The Wnt/ β -catenin pathway modulates transcription through β -catenin and translation via mTORC1 regulating GSK3 β activity.⁹⁶ (B*i*) mTORC1 inhibition by the rapalog everolimus induces Wnt/ β -catenin signaling activation by increasing the expression of FZD receptor levels with a mechanism dependent on DVL. (B*ii*) Activated mTORC1 promotes the association between DVL and the clathrin Adaptor protein 2 (AP-2) adaptor with a consequent reduction of FZD expression levels, with a negative regulation of Wnt/ β -catenin signaling.¹¹⁶ (C) Wnt/ β -catenin signaling switches off the mTORC1 cascade by inducing its negative regulator DEPTOR.¹¹⁷ (D) Inhibited PI3K/AKT/mTORC1 pathway leads to increased eIF4E phosphorylation via MNK.¹²⁴ Phosphorylated eIF4E is associated with β -catenin nuclear translocation and signaling activation.¹²⁷ β -CAT, β -catenin; β -TRCP, Beta-transducin repeat containing E3 ubiquitin protein ligase.

both intrinsic and extrinsic Wnt pathway activation, leading to S6K and 4E-BP1 phosphorylation, may affect the protein synthesis turning on the mTORC1 cascade. Importantly, the Wnt-driven mTORC1 signaling activation seems to be independent from β -catenin and mediated by an axis involving APC-AXIN-GSK3 β and TSC2 (Figure 1A).⁹⁶

FZD, DVL, and Deptor

Recently, Zeng et al¹¹⁶ showed that mTORC1 negatively regulates Wnt/ β -catenin signaling by modulating the extrinsic Wnt response both *ex vivo* and *in vivo*, and showed that mTORC1 would affect the expression of the Wnt receptor FZD with a mechanism dependent on the Wnt-positive regulator DVL (Figure 1B). Importantly, the mTORC1-driven inhibition of Wnt/ β -catenin signaling resulted in a compromised stem cell function in intestinal organoids, highlighting the importance of mutual regulation for intestinal homeostasis maintenance.¹¹⁶ The role of DVL in the regulation of Wnt receptors LRP6 and FZD has been shown previously *in vitro* through a genome editing approach. Although DVL is critically involved in the signalosome assembly, it also modulates the cellular turnover of Wnt receptors, being implicated in a negative feedback loop controlled by ZNRF3 and RNF43.³⁶

Wang et al¹¹⁷ recently described a mechanism linking the Wnt/ β -catenin and mTORC1 pathways, showing that Wnt/ β -catenin signaling induction, up-regulating the mTORC1-negative regulator DEPTOR, leads to DEPTOR-mediated mTORC1 suppression (Figure 1C).

eIF4E

An additional connection between the 2 signaling pathways involves the translation initiation factor eIF4E.¹¹⁸ The up-regulation of eIF4E has been described in multiple cancers,¹¹⁹ including CRC.^{120,121} The main oncogenic mechanism attributed to eIF4E is related to promoting the translation of genes critically involved in the malignant transformation of epithelial cells.¹²² The oncogenic activity of eIF4E is enhanced through its phosphorylation at Ser209, promoted by Mitogen-activated Protein kinase (MAPK) interacting kinases (MNK) 1 and MNK2.¹²³ It is known that mTORC1 inhibition by rapamycin leads to increased eIF4E phosphorylation and activation via a MNK1- and PI3K-dependent mechanism in different types of cancer cells, including CRC cell lines.¹²⁴ It should be noted that this feedback mechanism could be counteracted by using PI3K inhibitors, as shown in human lung cancer cells.¹²⁵ Importantly, eIF4E phosphorylation also has been associated with Wnt/ β -catenin signaling activation by promoting β -catenin nuclear translocation in different cancer settings (Figure 1D).^{126,127}

Wnt/ β -Catenin and PI3K/AKT/mTORC1 Pathways as Drivers of CRC Resistance to Treatment

Target cancer therapy resistance generally is driven by the development of additional mutations in downstream

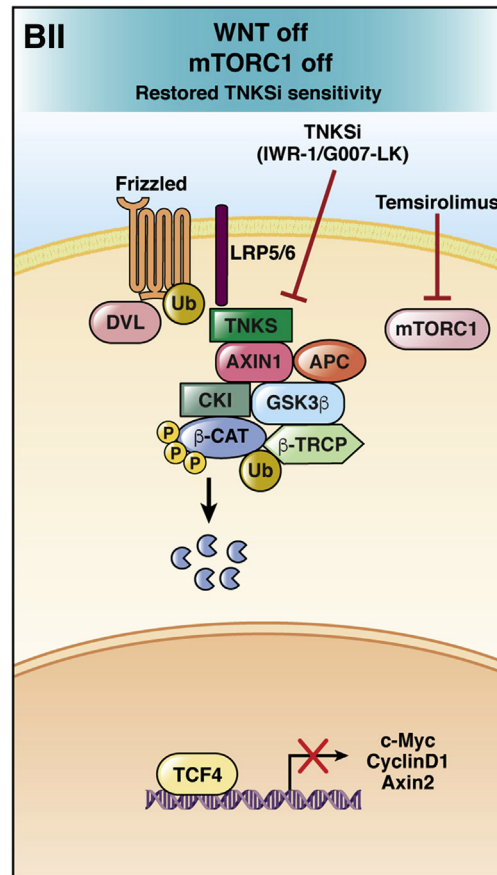
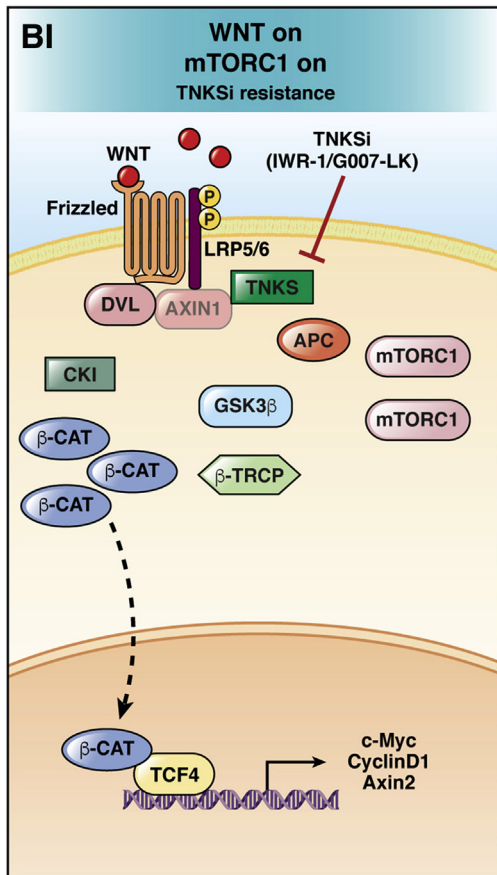
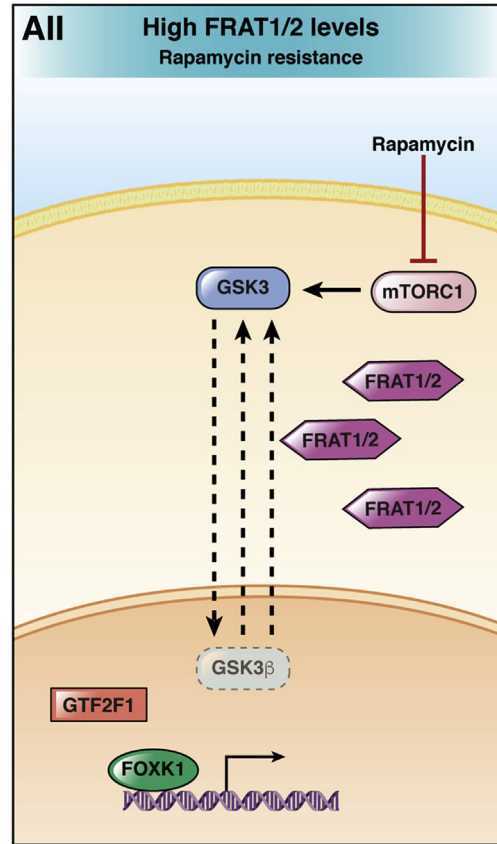
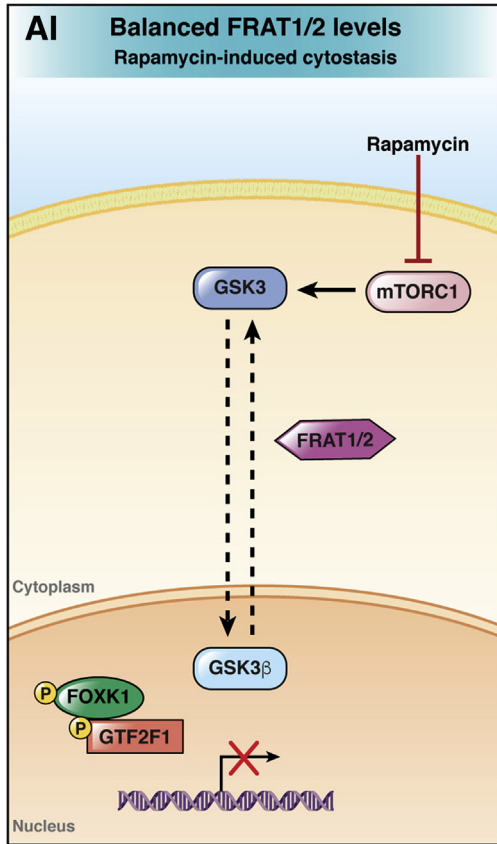
effectors of the same targeted pathway or activation of alternative signaling pathways as compensatory mechanisms.⁷

Rapalogs and Dual PI3K/mTOR Inhibitors

Everolimus and temsirolimus are 2 mTORC1 inhibitors whose efficacy have been evaluated in phase II clinical trials in metastatic CRC patients.^{128,129} However, a small retrospective analysis of tumors with activating *PIK3CA* mutations showed that treatment with the mTORC1 inhibitor everolimus had no relevant effect.¹³⁰ In addition, it has been shown that mTORC1/2 inhibition could restore sensitivity to everolimus in *PIK3CA* mutant CRC in preclinical models.¹³⁰ PKI-587,¹³¹ XL765,¹³² BEZ235,¹³³ and LY3023414¹³⁴ are dual PI3K/mTOR inhibitors that have completed phase I clinical trials in patients with advanced solid tumors, including CRC. It has been shown that the Wnt/ β -catenin pathway activation induces resistance to dual PI3K/mTOR inhibitor PKI-587 in *PIK3CA* mutant CRC cells, while GSK3 β inactivation restored the sensitivity to PKI-587.¹³⁵ However, these counterintuitive results are not in agreement with the general view supporting the negative regulator role of GSK3 β in the Wnt/ β -catenin pathway, and contradict robust literature data showing that GSK3 β inhibitors activate Wnt/ β -catenin signaling. Importantly, endogenous levels of GSK3 β are crucial in determining the sensitivity to mTORC1 inhibitors in CRC. Indeed, GSK3 β down-regulation has been associated with mTORC1 inhibitor resistance.¹³⁶ Moreover, high levels of the GSK3 β nuclear exporter Frequently rearranged in advanced T-cell lymphomas 1/2, which interferes with the cytostatic effects of rapamycin, might be relevant to predict the response to rapalogs as shown in lung and breast cancer cell lines (Figure 2A).¹¹⁴ Recently, Foley et al¹³⁷ showed that turning off both PI3K and mTOR by using the inhibitors BEZ235 and LY3023414 may represent an effective therapeutic strategy in CRC carrying concomitant *APC* and *PIK3CA* mutations.

Tankyrase Inhibitors

Tankyrase inhibitors (TNKSi) are small molecules that induce Axis inhibition protein 1/2 stabilization, abrogating Wnt/ β -catenin signaling.⁴ Several TNKSi, including XAV939,¹³⁸ IWR-1,¹³⁹ JW74,¹⁴⁰ and G007-LK,¹⁴¹ have been shown to impair Wnt/ β -catenin signaling *in vitro* or in mouse models of CRC. However, Wnt/ β -catenin inhibition induced by TNKSi has been associated with intestinal cytotoxicity and CRC cell lines have shown heterogeneous sensitivity to TNKSi.^{142,143} Mashima et al,¹⁴⁴ by using the TNKSi-resistant cell line 320-IWR, provided evidence of mTORC1 activation as a resistance mechanism to TNKSi IWR-1 and G007-LK. Interestingly, inhibition of mTORC1 by temsirolimus restored sensitivity to TNKSi (Figure 2B). These data further show that mTORC1 activation might represent a survival mechanism used by cancer cells upon Wnt/ β -catenin signaling inhibition. Recently, the combined effect of TNKSi inhibitor G007-LK, the PI3K inhibitor NVP-BKM120, and the epidermal growth factor receptor (EGFR) inhibitor erlotinib has been evaluated in CRC cell



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Table 1. Overview of Wnt/ β -Catenin, Rapalogs, and Dual PI3K/mTOR Inhibitors Discussed in This Review

Inhibitors	Target	Tested settings	Findings	References
Rapamycin	mTORC1	Murine model	Inhibition of intestinal neoplasia in <i>Apc</i> mutant models	93,95
Everolimus	mTORC1	Murine model	Reduced tumor burden in the <i>Apc</i> ^{d716} mouse model	92
Everolimus	mTORC1	CRC (phase II study)	Limited efficacy in metastatic CRC	128
Temsirolimus	mTORC1	CRC (phase II study)	Limited efficacy in <i>KRAS</i> mutant CRC	129
Temsirolimus	mTORC1	CRC cell lines	Reversed resistance to TNKSi	144
TAK228	mTORC1/2	Murine models and spheroids	Overcomes resistance to everolimus and induces response in <i>PIK3CA</i> mutant CRCs	130
PKI-587	PI3K/mTORC	Solid tumors (phase I study)	Antitumor activity in patients resistant to conventional therapies	131
PKI-587	PI3K/mTORC	CRC cell lines	Resistance to PKI-587 in <i>PIK3CA</i> mutant CRC cells	135
XL765	PI3K/mTORC	Solid tumors (phase I study)	Antitumor activity in patients resistant to conventional therapies	132
BEZ235	PI3K/mTORC	Solid tumors (phase I study)	No effect in patients with advanced solid tumors	133
LY3023414	PI3K/mTORC	Solid tumors (phase I study)	Efficacy in patients with advanced solid tumors	134
LY3023414	PI3K/mTORC	Murine models and spheroids	Potential treatment strategy in <i>PIK3CA</i> mutant CRCs	137
XAV939	TNKS	Cell lines, patient-derived cells, murine models	Reversed resistance in patient-derived primary cultures and in corresponding xenograft tumors in mice	147
JW74	TNKS	Cell lines and murine models	Decreased cell growth in CRC xenograft and reduced polyp formation in <i>Apc</i> ^{Min/+} mice	140
G007-LK	TNKS	Cell lines and murine models	Reduced CRC cell line growth; tumor growth inhibition in <i>Apc</i> mutant CRC xenograft and genetically engineered CRC models	141
G007-LK	TNKS	Cell lines and murine models	Enhanced effect of PI3K (BKM120) and EGFR (erlotinib) inhibition in CRC cells and reduced growth of CRC xenografts in vivo	145
NVP-TNKS656	TNKS	Cell lines, patient-derived cells, murine models	Overcomes resistance to PI3K or AKT inhibitors in CRC patient-derived sphere cultures and represses tumor growth in CRC-PDX models	148
NVP-TNKS656	TNKS	Cell lines and murine models	Overcomes resistance to MEK inhibitors in CRC with <i>KRAS</i> and <i>PIK3CA</i> mutations	151
ETC-159	PORCN	Murine models	Effective for treatment of <i>RSPO</i> translocation in CRC xenografts	156
LGK974	PORCN	Cell lines and murine models	Loss of AXIN1 mediates resistance to LGK974 in CRC cells carrying <i>RSPO3</i> fusions	158

AXIN1, Axis inhibition protein 1; PDX, Patient derived xenografts.

lines and xenografts. In both TNKSi-sensitive COLO320 DM and TNKSi-insensitive HCT-15 cell lines the combined inhibition of TNKSi, PI3K, and EGFR was able to reduce cell growth, as well as tumor size in vivo, by acting on multiple cancer-related pathways including Wnt/ β -catenin, AKT/

mTOR, EGFR, and Rat Sarcoma (RAS) signaling, with different effects depending on the genetic profile of the studied cell lines.¹⁴⁵

Forkhead box O3a (FOXO3a) is a transcription factor that acts as a tumor suppressor, inducing cell-cycle arrest and

Figure 2. (See previous page). Resistance mechanisms to rapamycin and TNKSi. (A*i*) mTORC1 inhibition promotes GSK3 β nuclear translocation. Nuclear GSK3 β mediates rapamycin-induced cytostasis by increasing the phosphorylation of Forkhead Box K1 and General Transcription Factor IIF Subunit 1. (A*ii*) In conditions of high cellular levels of the GSK3 β nuclear exporter Frequently rearranged in advanced T-cell lymphomas 1/2 (FRAT 1/2), upon mTORC1 inhibition, nuclear GSK3 β levels are not sufficient to induce cytostasis leading to rapamycin resistance.^{113,114} (B*i*) mTORC1 induction is associated with TNKSi resistance and persistent Wnt/ β -catenin signaling activation. (B*ii*) mTORC1 activity reduction by temsirolimus restores the sensitivity to TNKSi, leading to Wnt/ β -catenin down-regulation.¹⁴⁴ β -CAT, β -catenin; β -TRCP, Beta-transducin repeat containing E3 ubiquitin protein ligase; CKI, Casein Kinase I.

apoptosis.¹⁴⁶ Phosphorylation of FOXO3a by AKT induces its sequestration into the cytoplasm and inhibition of its transcriptional activity while PI3K or AKT inhibitors relocate FOXO3a into the nucleus, restoring its tumor-suppressor role. Importantly, high levels of nuclear β -catenin confer resistance to FOXO3a-induced apoptosis in metastatic CRC patient-derived cells treated with PI3K/AKT inhibitors.¹⁴⁷ Notably, TNKSi XAV-939 reverted this resistance, sensitizing cells to FOXO3a-induced apoptosis.¹⁴⁷ In addition, CRC patient-derived cells with high levels of nuclear β -catenin show reduced apoptosis upon treatment with the AKT or PI3K inhibitors API2 or NVP-BKM120.¹⁴⁸ As suggested by the investigators, these data support the concept that Wnt/ β -catenin hyperactivation leads to pharmacologic resistance to PI3K and AKT inhibitors in CRC. Importantly, the association of the TNKSi NVP-TNKS656 (a derivative of XAV939) with PI3K and AKT inhibitors improve the response to treatment both in vitro and in vivo, in particular in the presence of high nuclear β -catenin and FOXO3a levels.¹⁴⁸

Taken together, these findings indicate that a valid strategy to overcome resistance to PI3K/AKT/mTOR inhibitors could be combining these inhibitors with TNKSi to block the Wnt/ β -catenin pathway.

Targeting RAS/Rapidly Accelerated Fibrosarcoma/Mitogen-Activated Protein Kinase Kinase/Extracellular Regulated Kinase

EGFR is upstream of both mitogen-activated protein kinase and PI3K/AKT pathways. Much evidence has shown that, after the administration of the anti-EGFR therapies cetuximab or panitumumab, CRC acquires drug resistance through the activation of the downstream extracellular regulated kinase 1/2 signaling as a consequence of mutations in *KRAS*, *NRAS*, and Mitogen-activated protein kinase kinase (MAPKK or MEK) (MEK)1/2.¹⁴⁹ MEK is downstream of Kirsten rat sarcoma 2 viral oncogene homolog in the RAS/Rapidly Accelerated Fibrosarcoma/MEK/extracellular regulated kinase pathway and inhibition of MEK blocks signal transduction independently from the upstream mutation. Moreover, it is known that *PIK3CA* mutations confer resistance to MEK inhibitors in *KRAS* mutant cancers.¹⁵⁰ Recently, a study showed that β -catenin was responsible for the resistance of *PIK3CA* mutated tumors to MEK inhibitors.¹⁵¹ Notably, pharmacologic inhibition of β -catenin with TNKSi NVP-TNKS656 can resensitize *PIK3CA* mutant cells to MEK inhibitors.¹⁵¹

Porcupine Inhibitors

A further mechanism that turns off the Wnt/ β -catenin signaling is through the impairment of the enzymatic activity of Porcupine (PORCN), which mediates the palmitoylation and subsequent secretion of Wnt ligands.^{152–154} Various PORCN inhibitors have been tested in preclinical models as a strategy against Wnt-driven cancers, some of

which, including LGK974 or ETC-159, have been used in early phase clinical trials.^{155–157} However, as for the majority of Wnt inhibitors, PORCN inhibitors also impair intestinal homeostasis and are subjected to resistance.¹⁵⁷ Interestingly, Axis inhibition protein 1 suppression recently has been described as a driver of resistance to the PORCN inhibitor LGK974 in CRC cell lines, carrying genomic rearrangements in the *RSPO3* gene.¹⁵⁸ It should be noted that the combination of PORCN inhibitor ETC-159 with PI3K/mTOR inhibitors has shown a synergistic effect against tumor growth in pancreatic cancer cells with RNF43 mutations, as well as in vivo models, indicating that the dual blockage might be effective in CRC.¹⁵⁹

An overview of Wnt/ β -catenin, rapalogs, and dual PI3K/mTOR inhibitors tested in clinical and preclinical CRC settings is shown in Table 1.

Conclusions

The interconnection between the Wnt/ β -catenin and PI3K/AKT/mTORC1 pathways has been shown widely in different cancer settings, including CRC. Most of the studies elucidating the relationship between these pathways have been conducted in preclinical models. As discussed in this review, there are many connecting elements between these 2 pathways capable of interfering with key processes regulating the β -catenin turnover: (1) in particular, the regulation of β -catenin phosphorylation mediated by GSK3 β and the degradosome assembly/disassembly; (2) the modulation of the Wnt receptor levels (extrinsic Wnt activation) in which DVL has a crucial role; (3) mechanisms affecting the β -catenin nuclear translocation, which involves many components including eIF4E; and (4) the regulation of the downstream effectors of the PI3K/AKT/mTORC1 pathway mediated by GSK3 β . Moreover, clinical data in patients with advanced disease showed increased resistance to targeted therapies, highlighting the relevance of this interaction in predicting patient response. In this context, GSK3 β levels seem crucial for predicting the response to mTORC1 inhibitors. In addition, defined cancer and precancerous subsets could benefit from the combination of PI3K/mTORC1 inhibitors with TNKSi. In particular, simultaneous inhibition of both the Wnt/ β -catenin and PI3K/AKT/mTORC1 pathways may represent a valid chemopreventive strategy in FAP, in which the proliferative boost and oncogenic transformation of intestinal epithelial cells is supported by Wnt/ β -catenin signaling overactivation. In conclusion, it is important to note 2 relevant concepts for future studies: the interdependence, which characterizes these pathways, constitutes a critical factor, for developing new drugs against CRC progression; and the dynamics that characterize these 2 signaling pathways, in the context of colorectal carcinogenesis, should be evaluated, taking into account the response and the fine regulation processes that distinguish these pathways. Future studies on this topic in human beings will be indispensable to better define unsolved mechanisms in this challenging scenario and to establish the translational impact of these crosstalk mechanisms.

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Conflicts of interest

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