

Signal transduction pathways participating in homeostasis and malignant transformation of the intestinal tissue

Minireview**

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Intestinal homeostasis is a complex and tightly regulated process governed by a variety of signalling pathways that balance cell proliferation and differentiation. As revealed by extensive use of defined mouse models, perturbations within the signalling circuitry trigger initial expansion of premalignant cells. In this review, we attempt to summarise recent advances in the knowledge of the cellular signalling mechanisms that drive tumorigenesis in the human and mouse intestine.

Key words: colorectal cancer, epithelium, gut, intestine, mouse models, stem cells

Carcinoma of colon and rectum [colorectal cancer (CRC)] represents the third most common human malignancy worldwide. It is estimated that more than one million patients are clinically diagnosed each year; up to one third of the cases constitute metastatic settings resulting in a disease-related mortality rate exceeding 30% [1]. Development of colorectal neoplasia is characterised by progression through histologically defined stages that include hyperplastic and dysplastic lesions, adenoma and adenocarcinoma [2]. This stepwise evolution towards more advanced stages is driven by genomic alterations and epigenetic changes. Colorectal cancers are characterised

by a complex genomic “landscape”; individual tumors harbour nine rearranged loci on average [3] and a median of 76 non-silent mutations [4]. However, only a fraction of these changes is considered to be causative in tumor initiation and progression. For example, several recent studies based on high-throughput sequencing of tumor DNA indicate that only a small portion of mutations are “driver” mutations affecting genes essential for tumor development [4, 5]. Nevertheless, the contributions of seemingly harmless “passenger” mutations should not be underestimated as these can substantially underpin the known tumorigenic pathways [6].

The single-layer epithelia of the small intestine and colon represent the most rapidly self-renewing adult tissue that completely regenerates approximately every five days [7, 8]. The long-lived stem cells located at the bottom positions of microscopic invaginations called *crypts* feed an upward compartment of transit-amplifying cells. On migrating up, cells terminally differentiate towards secretory (goblet and enteroendocrine cells) or absorptive (enterocytes) lineages that fulfil physiological roles of the tissue. When the differentiated cells arrive at the top of the villus – villi are finger-like

Abbreviations: *Ascl2* – achaete-scute complex homolog 2; *Apc* – adenomatous polyposis coli; *bHLH* – basic helix-loop-helix; *BMP* – bone morphogenetic protein; *BRAF* – v-raf murine sarcoma viral oncogene homolog B1; *CBC* – crypt base columnar; *CRC* – colorectal cancer; *EphB* – ephrin type-B receptor; *EGFR* – epidermal growth factor receptor; *Fz* – frizzled; *Hes* – hairy and enhancer of split; *Hh* – hedgehog; *KRAS* – v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog; *Lgr5* – leucine-rich-repeat containing G-protein coupled receptor 5; *Lkb1* – liver kinase B1; *MSI* – microsatellite instability; *NICD* – notch intracellular domain; *PI3K* – phosphatidylinositol 3-kinase; *Smo* – smoothened

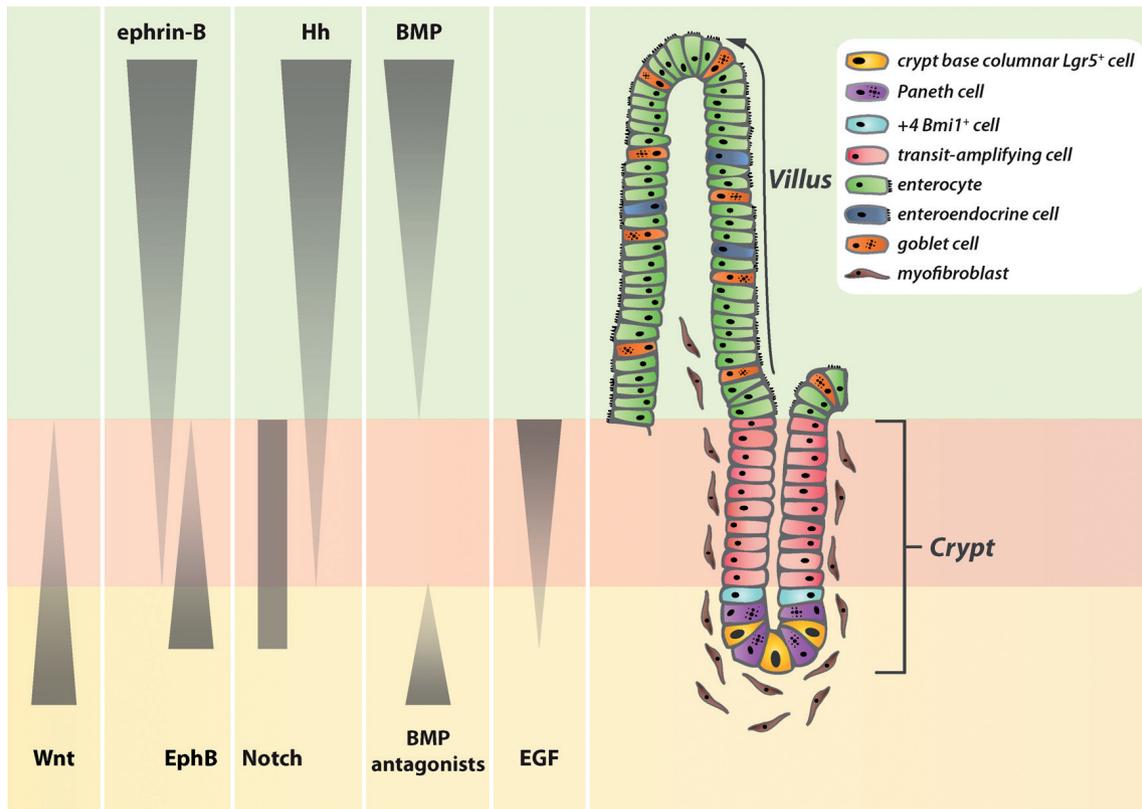


Figure 1. Architecture of the small intestine epithelium and pathways governing its fate

A population of actively cycling, crypt base columnar (CBC) stem cells positive for *Lgr5* resides at the bottom of the crypt intermingled with Paneth cells. In contrast, more quiescent stem cells expressing *Bmi1* are present above the Paneth cells at the +4 position from the crypt base. Cell divisions in the CBC compartment give rise to transit-amplifying (i.e. committed progenitor) cells that terminally differentiate towards all intestinal lineages as they move up the villus (arrow). Once reaching its top, the cells undergo apoptosis and are shed to the intestinal lumen. The only exceptions are long-lived postmitotic Paneth cells which stay at the bottom of the crypt. The proper homeostasis of the intestinal epithelium is regulated by an interconnected network of principal signalling pathways that govern the balance between proliferation and lineage specification. Synergism of the Wnt and Notch pathways sustains undifferentiated and proliferative stem and progenitor cells; moreover, both cascades are essential for adopting a specific lineage commitment. A descending Wnt signal generates an opposing gradient of repulsive EphB/ephrin-B interactions that facilitate spatial segregation of distinct cellular compartments within the crypt. Paracrine Hedgehog and BMP signalling in the upper part of the crypt and on the villus promote differentiation while restraining cell proliferation. The pro-differentiation activity of the BMP pathway is, at the bottom of the crypt, locally counteracted by secreted mesenchyme-derived BMP antagonists. Notably, the amplitude of mitotic signalling downstream of EGF is, at the crypt base, suppressed to restrict the expansion of the stem cell compartment.

projections of epithelium found only in the small intestine – or to the luminal surface of the large intestine, they undergo apoptosis and are shed to the intestinal lumen. Paneth cells of the small intestine are the only exception to this scheme. These antibacterial agent-producing cells stay at the crypt base where they persist for approximately three to six weeks. In addition, M-cells [9], brush cells [10] and tuft cells [11] represent further minor mucosal populations.

Two types of intestinal stem cells have been described based on their markers and location in the crypt. Fast-cycling crypt base columnar (CBC) stem cells are found interspersed among the Paneth cells and are positive for leucine-rich-repeat containing G-protein coupled receptor (*Lgr*) 5 [12]. The intestine also contains slowly dividing stem cells that reside several cell diameters from the bottom of the crypt. These

cells express polycomb group protein *Bmi1* and represent the reserve stem cell population [13, 14]. The niche for the stem cells is possibly constituted by pericryptal myofibroblasts closely lining the crypt base basal lamina [15]. Recently, Sato and colleagues reported that the tissue niche for CBC cells is generated mainly by Paneth cells [16]. However, since the *Lgr5*-positive CBC cells retain their proliferative and clonogenic capacity even upon complete ablation of Paneth cells, the contribution of Paneth cells to the stem cell niche remains questionable [17].

The proper maintenance of epithelial architecture is controlled by various signalling pathways that regulate the balance between the opposing processes of proliferation and differentiation [18]. Importantly, the majority of these pathways is deregulated in CRC, including Wnt/ β -catenin,

Hedgehog and Notch signalling, the ephrin type-B receptor (EphB)/ephrin-B cell communication system, the bone morphogenetic protein (BMP) signal transduction pathway and signalling downstream of the epidermal growth factor receptor [(EGFR); Figure 1]. Here, we present recent findings regarding the role of these principal pathways in both the healthy or diseased gut tissue. Moreover, particular types of CRC, both sporadic and hereditary, can be recapitulated in genetically engineered mice [19]. Employment of the mouse models brings new insights about the signalling mechanisms functioning in the gut tissue and in addition provides valuable clues for the establishment of stratification criteria for patients with CRC [20].

Wnt/ β -catenin and EphB/ephrin-B signalling. Wnt proteins are secreted ligands that bind to the Wnt receptor complex composed of a seven-span transmembrane receptor of the Frizzled (Fz) family and a lipoprotein-related co-receptor (Lrp5/6). The central feature of canonical Wnt signalling is the post-transcriptional control of β -catenin protein stability [21]. In the absence of a Wnt ligand, the intracellular level of β -catenin is kept constantly low due to the activity of its degradation complex, consisting of scaffolding proteins axis inhibition protein (Axin) and adenomatous polyposis coli (Apc), and kinases casein kinase 1 alpha (Ck1 α) and glycogen synthase kinase-3 beta (Gsk-3 β). The recruited β -catenin is phosphorylated and subsequently destroyed in the ubiquitin-proteasome pathway. Wnt signalling leads to the membrane sequestration of Axin followed by disruption of the β -catenin degradation complex and the accumulation of the protein in the cytoplasm and nucleus. Nuclear β -catenin associates with transcription factors of the lymphoid enhancer-binding (Lef)/T-cell factor (Tcf) family (afterwards referred to as Tcfs). These high mobility group (HMG) box-containing effectors of the Wnt pathway function in an unstimulated cell as transcriptional repressors. However, since β -catenin contains a strong transactivation domain, Tcf/ β -catenin heterocomplexes activate transcription of specific Wnt-responsive genes such *c-Myc* [22], *Cyclin D1* [23, 24], *CD44* [25] and *Axin2* [26]. For a more comprehensive survey on Wnt signalling, refer to the Wnt signalling home page at <http://www.stanford.edu/group/nusselab/cgi-bin/wnt/>.

In the adult mouse intestine, crypt-restricted expression of *Wnt3*, *Wnt6*, *Wnt9b* and their cognate receptor *Fz5* was observed, indicating that proper epithelial turnover is maintained by a descending gradient of Wnt signalling along the crypt-villus axis [27, 28]. The activity of the Wnt pathway is essential for preservation of undifferentiated and proliferative stem and progenitor cells as revealed by disruption or conditional ablation of the genes encoding HMG box family member *Tcf4* [29, 30, 31] or β -catenin [32, 33]. Importantly, sustainment of the progenitor phenotype is dependent on the direct repression of cell cycle inhibitor *p21^{Cip1/Waf1}* which is mediated by the Tcf4 target gene *c-Myc* [34]. Inhibition of the pathway results in a robust G1 arrest and consequently halts cell proliferation [35]. A similar phenotype was observed upon

blocking the signalling via ectopic expression of dickkopf 1 (*Dkk1*), a secreted Wnt inhibitor [36, 37].

The pathway controls self-renewal of CBC stem cells via activity of its responsive genes encoding the basic helix-loop-helix (bHLH) transcription factor achaete-scute complex homolog 2 (*Ascl2*) [38] and *Lgr5*. Targeted deletion of either *Ascl2* [38] or *Lgr5* [39] leads to the elimination of CBC stem cells. In contrast to CBC cells, *Bmi1*-positive intestinal stem cells are Wnt signalling independent [14]. Interestingly, *Lgr5* and its related receptors *Lgr4* and *Lgr6* bind extracellular Wnt signalling agonists R-Spondins (RSpos) and association of RSpos with the receptors mediates enhancement of the Wnt signal [39, 40, 41]. The Wnt signalling pathway in CBC cells is possibly activated by the *Wnt3* ligand secreted from neighbouring Paneth cells [42]. Nevertheless, as described above, CBC cells maintain their "stemness" even in the absence of Paneth cells. Therefore, the cellular source of the Wnt signal in the intestinal crypts remains unknown. Some controversies also prevail about a possible role of *Ascl2* and *Lgr5* in gut tumorigenesis. While *Ascl2* expression in transgenic mice induced crypt hyperplasia, ectopic *Ascl2* did not promote intestinal neoplasia [38, 43]. In addition, several research teams described elevated expression of *ASCL2* or *LGR5* in human sporadic cancer [44, 45, 46, 47]; however, these observations have not been confirmed by parallel studies [48, 49].

Injection of human RSPO1 into mice induced a rapid onset of proliferation of crypt cells [50]. Similarly, homozygous inactivation of the *Apc* gene in the mouse intestine drives hyperproliferation of the crypt compartments followed by formation of adenomatous intestinal polyps displaying increased levels of β -catenin [51]. In humans, germinal mutations of the *APC* gene are causative in development of the Familial adenomatous polyposis (FAP) syndrome, an autosomal dominant disorder characterised by multiple colorectal polyps and a variety of extraintestinal manifestations [52]. Moreover, inactivating mutations of both alleles of *APC* are detected in approximately one third of all sporadic CRC cases [53]. Mutations inactivating other negative regulators of Wnt signalling, *AXIN1* or *AXIN2*, are rare and observed in CRC cases displaying microsatellite instability (MSI) [54]. Similarly to *AXIN1/2*-deficient neoplasia, oncogenic mutations in the β -CATENIN gene have low frequency and are found mainly in tumors with MSI [53]. These mutations affect the regions encoding regulatory N-terminal serine or threonine residues phosphorylated in the wild-type protein by CK1 α or GSK-3 β kinases. Consequently, a mutated form of β -catenin accumulates in the affected cell and triggers aberrant Wnt signalling [55]. The oncogenic activation of β -catenin was successfully recapitulated in mice by cre-mediated "in-frame" deletion of exon 3 (encoding regulatory serines and threonines) of the β -catenin gene in the intestine [56, 57]. All this data supports the notion that non-physiological Wnt signalling is associated with cancer development. Unexpectedly, one recent study indicated that silencing of the Wnt-responsive genes such as *ASCL2*, *AXIN2* and *LGR5* by selective promoter methylation

identifies patients with a risk of recurrence [58]. Importantly, re-expression of these genes was associated with reduced tumor growth *in vitro* and *in vivo*. Therefore, the activity status of the selected Wnt signalling target genes can be used as one of the patient stratification criteria.

Wnt signalling is also implicated in the proper commitment and morphological maturation of the Paneth cell lineage. A homeostatic threshold of active Wnt/ β -catenin signalling is required for terminal differentiation towards the Paneth cells fate, as this is otherwise severely impaired [27, 59]. In the lower parts of the intestinal crypts, high levels of Wnt signalling induce expression of the cell-sorting receptors EphB2 and EphB3 with concomitant transcriptional repression of their repulsive ephrin-B1 ligand [60]. As progenitor cells leave the crypt bottom, the decline in Wnt cues results in the de-repression of the repulsive ephrin-B1 ligand [60, 61]. The decrease of Wnt signalling along the crypt-villus axis is therefore involved not only in proper epithelial turnover but also controls correct positioning of cells by opposing gradient of transmembrane EphB2/B3-ephrin-B1 signalling. Paneth cells that exclusively express EphB3 escape the upward flow and drift towards the crypt bottom [60]. The importance of EphB3 in the positioning of Paneth cells was gleaned from studies using EphB3 null mice. In the EphB3^{-/-} small intestine, Paneth cells do not follow their correct migratory path but are scattered along the villi [60]. A similar phenotype was observed in Fz5^{-/-} mice [27] or upon conditional deletion of the gene encoding ephrin-B1 ligand [62]. Paneth cells fail to correctly specify upon conditional ablation of the Wnt target genes sex determining region Y (SRY)-box 9 (Sox9) [63, 64] and SAM pointed domain containing the ets transcription factor (Spdef) [65]. Expectedly, aberrant Wnt signalling induces de novo production of Paneth cells [27, 59, 66]. Inappropriate expression of Paneth cell-specific genes [e.g. matrix metalloproteinase 7 (Mmp7), EphB3] was frequently observed in gastrointestinal cancer with aberrant Wnt signalling [27, 67]. Interestingly, the increased expression of EphB is often silenced during cancerous growth possibly to overcome spatial restraints imposed by surrounding healthy tissue expressing ephrin-B1 [62, 68]. In general, abrogation of EphB-ephrin-B1 interactions in CRC coincides with acquisition of the malignant phenotype [62] and the degree of EPHB2 down regulation parallels a poor prognosis [69, 70].

Hedgehog signalling. The twelve-pass transmembrane proteins patched (Ptch) 1 and 2 are receptors for secreted ligands of the Hedgehog (Hh) family which consists of three identified members in vertebrates designated as sonic hedgehog (Shh), Indian hedgehog (Ihh), and desert hedgehog (Dhh). In its “off-state”, Ptch prevents the entry of an otherwise constitutively active receptor *smoothened* (Smo) to the primary cilium. Under these circumstances, the zinc-finger transcription factors glioma-associated oncogene (Gli) 2 and Gli3, major effectors of the Hedgehog pathway, are cleaved by proteasome into repressive forms. Conversely, upon Hh binding, de-repression of Smo results in a cascade of downstream events that ultimately

lead to Gli-dependent transcriptional activation of Hedgehog signalling target genes (reviewed in [71]).

Hedgehog signalling in gut homeostasis mediates reciprocal cross-talk between the epithelium and the adjacent mesenchyme. Shh and Ihh ligands secreted by transit-amplifying cells interact with Ptch receptors localised on mesenchymal cells to induce Bmp production [72, 73]. Paracrine Bmp signalling promotes enterocyte commitment and inhibits formation of additional crypts [72, 74]. The constitutive activation of the Hedgehog pathway – upon deletion of the *Ptch1* gene – leads to increased Bmp signalling with concomitant depletion of the proliferating progenitors [74]. In contrast, reduction in the levels of Hedgehog signalling enhances the Wnt pathway activity resulting in impaired intestinal differentiation and crypt hyperplasia [72, 75, 76]. Additionally, the Hedgehog pathway controls proper maintenance of intestinal smooth muscle populations [74, 76, 77].

Several types of sporadic and hereditary cancers are dependent on Hedgehog signalling and/or carry genetic changes in the components of the Hedgehog pathway. *SHH* and *IHH* expression is significantly increased in a subset of human CRC and CRC-derived cell lines [78, 79, 80]; however, the contribution of the pathway to CRC is somewhat controversial [81]. In concordance with the role for Hedgehog signalling in healthy tissue, Hh proteins produced in tumor cells likely activate the signalling in the tumor-associated stroma. This was confirmed in experiments utilising human tumor xenografts. Yauch and colleagues showed that inhibition of the pathway by either small molecule inhibitors of Smo, neutralising anti-Hh antibody, or genetic ablation of the *Smo* gene substantially reduced size of the tumor implants growing in mice [80]. Contrary to these results, Varnat and colleagues described ligand-driven autocrine Hedgehog signalling loops promoting the growth of tumor cells [79]. Despite these rather contradictory data, inhibition of the Hedgehog pathway is considered to be promising for treatment of Hh-dependent tumors [81].

Notch signalling. The mammalian Notch family comprises four single transmembrane Notch1–4 receptors and five transmembrane Delta/Serrate/Lag2 (DSL) ligands, jagged (Jag) 1, Jag2, delta-like (Dll) 1, Dll3 and Dll4. Ligand-receptor engagement on neighbouring cells triggers a cascade of proteolytic cleavage of the Notch receptor liberating its notch intracellular domain (NICD). NICD then shuttles to the nucleus, where it binds to the recombination signal binding protein for immunoglobulin kappa J region (RBPj) core transcription factor. Heterocomplex NICD-RBPj activates expression of target genes, such as bHLH transcription repressors *achaete-scute* and *hairy and enhancer of split (Hes)* [82].

The Notch pathway governs the intestinal binary cell fate decision between the secretory versus absorptive cell lineages. Progenitor cells receiving a Notch signal are stimulated to express Hes1, which in turn antagonises the effector bHLH transcriptional factor atonal homolog 1 (Atoh1, also called Math1) [83]. Subsequent differentiation towards enterocytes is under the control of the Hes1/E74-like factor 3 (Elf3)/trans-

forming growth factor beta (TGF β) signalling cascade [84, 85]. Consistently, blocking the pathway using pharmacological inhibition of the Notch receptor-cleaving protease γ -secretase [86], genetic ablation of *RBPj* [86], *Hes1* [83], *Elf3* [87] or simultaneous deletion of both *Notch1* and *Notch2* genes [88] is phenotypically associated with an excess of secretory cells at the expense of enterocytes. Production of secretory lineages from the cells expressing Notch ligands depends on the function of *Atoh1*, since inactivation of the *Atoh1* gene results in depletion of goblet, Paneth and enteroendocrine cells [89, 90, 91]. Moreover, cell commitment to the secretory lineages is blocked in transgenic mice expressing the intestine-specific NICD protein [92]. Of note, Notch activity promotes terminal differentiation of goblet cells via suppression of zinc-finger transcription factor *Krüppel-like factor 4* (*Klf4*) [93, 94].

Although the contribution of Paneth cells to the niche for CBC cells remains to be confirmed (see previous text), the involvement of Notch signalling in the maintenance of intestinal stem cells has been well-established. In the mouse, Notch1 and Notch2 represent the predominant receptors produced on the surface of CBC cells [95], with their ligands Dll1 and Dll4 being expressed on neighbouring Paneth cells [16]. Furthermore, sustained proliferation of crypt cells is mediated through direct transcriptional repression of cyclin-dependent kinase (CDK) inhibitors p27^{Kip1} and p57^{Kip2} by the Notch-responsive gene *Hes1* [88]. In agreement with these data, Dll1/4 double deficient mice displayed premature differentiation of stem cells [96]. In CRC with perturbed Wnt signalling, β -catenin-driven aberrant expression of the Notch ligand JAG1 was observed, indicating synergism of both pathways. It has been proposed that while Wnt signalling enhances proliferation, the Notch-dependent contribution to tumorigenesis includes a block of differentiation and promotion of vasculogenesis [97].

The BMP pathway. BMPs belong to the TGF β superfamily of extracellular signalling molecules. Upon binding of a BMP ligand to a membrane heterocomplex of BMP type I (*Bmpr1*) and BMP type II (*Bmpr2*) receptor, the signal is further transduced through receptor-mediated phosphorylation of Smad1/5/8 transcription factors [alternatively named, *mothers against decapentaplegic homolog* (*Madh*)]. Phosphorylated Smads associate with the core mediator Smad4 and enter the nucleus to regulate expression of target genes such as the *Msx* homeobox genes or proto-oncogene *JunB* [98]. Extracellular antagonists, such as noggin, follistatin or gremlin, sequester Bmp ligands, thereby abrogating their interaction with the receptors [99].

In the intestine, the BMP pathway is implicated in restraining cell proliferation. The signalling is activated in the epithelial cells by BMPs produced in the mesenchyme [15, 100]. Bmp signalling is restricted to epithelial compartments containing differentiated cells as the activity of the pathway in the crypt is locally counteracted by expression of the Bmp antagonists [15, 101, 102, 103]. Inhibition of the Bmp pathway in the mouse intestine using transgenic expression of noggin [104] or conditional ablation of the *Bmpr1a* receptor [101]

was associated with development of hamartomatous polyps morphologically corresponding to lesions found in the human Juvenile polyposis syndrome [101]. The formation of benign intestinal hamartomas represents an initiator event in carcinoma development in affected individuals carrying inactivating mutations in the *BMPRIA* or *SMAD4* genes [105]. Interestingly, in sporadic CRC, epigenetic silencing of *BMPR2* or deletion of *SMAD4* promotes transition from adenoma to carcinoma, i.e. a late event in the tumor progression cascade [99, 106]. In the mouse, conditional inactivation of *Bmpr2* in stromal cells of the colon initiated epithelial hyperplasia and formation of hamartomatous polyps. Strikingly, the polyps formed in these mutant animals showed increased proliferation not only of epithelial but also mesenchymal cells, especially myofibroblasts [107].

EGF signalling. Binding of EGF or related ligands to their cognate receptors, members of the ErbB/HER/Neu family of receptor tyrosine kinases, activates several major cellular pro-survival and proliferation-inducing pathways that include the Ras-Raf-mitogen activated protein kinase (MAPK) cascade, phosphatidylinositol 3-kinase (PI3K)/Akt, and phospholipase C pathways [108]. EGF signalling is required for proliferation and maintenance of the intestinal CBC stem cell compartments [16]; however, its output is tightly controlled by leucine-rich repeats and immunoglobulin-like domains (*Lrig*) 1 produced in the stem cell niche [109, 110].

As many as 30% of sporadic CRC cases carry mutations in the *KRAS* gene that compromise inactivating hydrolysis of Ras-bound GTP to GDP, thus rendering the mitogenic downstream signalling constitutively activated [53]. Oncogenic *Kras* is considered to be involved in later stages of CRC, where it synergises with the changes initiated by the loss of *Apc* [111, 112]. This stage-specific function of *Kras* in CRC was supported by studies in the mouse showing that oncogenic activation of *Kras* induced premalignant epithelial hyperplasia [113] which, however, did not progress to malignancy [114]. Interestingly, perturbed Wnt signalling promotes stabilisation of the Ras protein and, consequently, stimulates activity of the MAPK pathway [115].

Non-physiological activation of the EGF cascade may also occur through changes affecting *EGFR*, *PI3K*, or RAS downstream effector *BRAF* (full name: *v-raf murine sarcoma viral oncogene homolog B1*) [116]. *EGFR* itself can be hyperactivated by overexpression and mutations in the kinase domain or by gene amplification [117]. The p110 catalytic subunit alpha of PI3K (encoded by the *PIK3CA* gene) is found mutated in 15-18 % of CRC [118]; however, the clinical relevance of distinct mutations found in *PIK3CA* remains to be elucidated [119]. Additionally, loss of *phosphatase and tensin homolog* (*PTEN*), a tumor suppressor gene encoding dual phosphatase regulating the levels of phosphatidylinositol-3,4,5-trisphosphate, is involved in the process of bowel tumorigenesis. Notably, germline mutations in *PTEN* underlie the Cowden syndrome, a disease characterised by development of hamartomatous polyps [120]. A phenotype similar to the Cowden syndrome

was recapitulated in *Pten* heterozygous mice [121], supporting the role of PTEN in human cancer. In sporadic CRC, loss of heterozygosity (LOH) in the *PTEN* locus is common but presumably represents an additional “hit” during later stages of malignant progression [122]. Approximately 12–19% of colorectal carcinomas harbour an oncogenic mutation activating kinase *BRAF* [123, 124]. These mutations occur in a mutually exclusive manner with activation of *KRAS* [125]. Strikingly, whereas *BRAF* changes are associated with colorectal cancers with a so-called *serrated morphology* displaying CpG island methylator phenotype (CIMP) or MSI, *KRAS* mutations are linked predominantly to tumors characterised by chromosomal instability (CIN) [126]. The “druggable” properties of EGFR led to clinical usage of EGFR antagonists, e.g. receptor-specific monoclonal antibodies cetuximab and panitumumab or small molecule tyrosine kinase inhibitors gefitinib and erlotinib [127]. Moreover, the presence of mutant *KRAS* or *BRAF* has been established as a predictive marker of “non-response” to EGFR-targeting treatment [128].

Other signalisations involved in intestinal homeostasis and CRC development. Several other cellular signalling systems have been demonstrated to regulate proper maintenance of the intestinal epithelium. Abrogation of the interaction between epithelial platelet-derived growth factor (Pdgf) ligand A with its cognate mesenchymal Pdgf receptors (Pdgfr) results in misshaping of villi and loss of the pericryptal stroma [129]. Furthermore, liver kinase B1 (Lkb1) [also known as serine/threonine kinase (Stk) 11] regulates epithelial cell polarity and metabolism [130, 131]. *LKB1* acts as a tumor suppressor and its germline mutations cause the Peutz-Jeghers syndrome, a predominantly inherited disease characterised by development of gastrointestinal hamartomatous polyps [132]. The Peutz-Jeghers syndrome is phenocopied in *Lkb1*^{-/-} mice [133]. Interestingly, polyp development can also be initiated by a mesenchymal-specific deletion of the *Lkb1* gene [134]. In summary, results obtained in mouse models of the Juvenile polyposis, Cowden and Peutz-Jeghers syndromes support the notion that the initiating event in the development of some CRC likely occurs in mesenchymal tissue adjacent to the epithelia.

Conclusion

A wealth of genetic studies have provided invaluable insights into the signalling networks that govern homeostasis of the gastrointestinal tissue and are at the same time “hijacked” to drive malignant conversion. A better understanding of the relationships and interconnectivity between tissue homeostatic signalling and distinct aspects of tumor initiation and progression can lead to the discovery of potential targets for therapeutic intervention. Concomitantly, mouse model systems can substantially contribute to the establishment of prognostic or predictive biomarkers that, upon translation and validation in human medicine, can be implemented to individualise anti-cancer treatment.

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