Bmi1 regulates murine intestinal stem cell proliferation and self-renewal downstream of Notch

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ABSTRACT

Genetic data indicate that abrogation of Notch-Rbpj or Wnt-β-catenin pathways results in the loss of the intestinal stem cells (ISCs). However, whether the effect of Notch is direct or due to the aberrant differentiation of the transit-amplifying cells into post-mitotic goblet cells is unknown. To address this issue, we have generated composite tamoxifen-inducible intestine-specific genetic mouse models and analyzed the expression of intestinal differentiation markers. Importantly, we found that activation of β-catenin partially rescues the differentiation phenotype of Rbpj deletion mutants, but not the loss of the ISC compartment. Moreover, we identified Bmi1, which is expressed in the ISC and progenitor compartments, as a gene that is co-regulated by Notch and β-catenin. Loss of Bmi1 resulted in reduced proliferation in the ISC compartment accompanied by p16INK4a and p19ARF (splice variants of Cdkn2a) accumulation, and increased differentiation to the post-mitotic goblet cell lineage that partially mimics Notch loss-of-function defects. Finally, we provide evidence that Bmi1 contributes to ISC self-renewal.

KEY WORDS: Notch, β-catenin, Intestinal stem cells, Bmi1, Self-renewal

INTRODUCTION

The intestinal epithelium constitutes an excellent system for studying stem cell function. Intestinal stem cells (ISCs) reside at the bottom of intestinal crypts, where they are maintained in a multipotent and self-renewing state. ISCs are the source of a transit-amplifying compartment, which undergoes ~4-5 rounds of rapid cell division (Marshman et al., 2002) before achieving the terminally differentiated state. Then, the resulting differentiated enterocytes, goblet cells and enteroendocrine cells move towards the tip of the villi in a process that takes around 2-4 days, whereas a fourth differentiated cell type, the Paneth cells, migrate downwards to the crypt base where they reside for 6-8 weeks (van der Flier et al., 2009). Long-term lineage tracing has identified Lgr5, Bmi1, Tert and Hopx (Barker et al., 2007; Montgomery et al., 2011; Sangiorgi and Capecci, 2008; Schepers et al., 2011; Takeda et al., 2011; Tian et al., 2011) as ISC markers. However, it is plausible that different levels of these markers identify specific ISC subpopulations (Itzkovitz et al., 2012).

Notch and Wnt-β-catenin pathways are essential regulators of normal stem cells in multiple tissues, including the intestine (Ireland et al., 2004; Korinek et al., 1998; Pellegrinet et al., 2011; Riccio et al., 2008), and several examples of co-regulatory crosstalk have been described (Espinosa et al., 2003; Estrach et al., 2006; Hayward et al., 2005; Kwon et al., 2011; Rodilla et al., 2009). Notch signaling is activated by specific ligands that are present in neighboring cells, whereas β-catenin activation relies on the presence of soluble Wnt ligands (reviewed in Bigas et al., 2013). By using lineage-tracing analysis, it has recently been proven that Notch1 and Notch2 are specifically expressed (Fre et al., 2011) and required (Riccio et al., 2008) to maintain homeostasis in the intestinal crypt, with the Paneth cells being responsible for producing Wnt and Notch signals (Sato et al., 2011). Complete inhibition of Notch signaling in the intestinal epithelium results in the loss of the proliferative crypt compartment and the loss of the conversion of crypt progenitors into the post-mitotic secretory lineages (van Es et al., 2005), partially overlapping with the phenotype that is obtained after deletion of the Notch target gene Hes1 (Jensen et al., 2000). The molecular basis for the differentiation-associated defects is the overexpression of Math1, a master regulator of the absorptive intestinal lineage, which is repressed by Hes1. Nevertheless, genetic inactivation of Hes1 or knockout (KO) of Hes1, Hes3 and Hes5 simultaneously in the adult mouse intestine leads to reduced cell proliferation and increased secretory cell formation but does not affect ISC integrity (Ueo et al., 2012).

Bmi1 is a member of the Polycomb group of transcriptional repressors, the function of which in the intestine is unknown. Bmi1 is an essential regulator of hematopoietic, neural and lung epithelial stem cells, mainly through repression of the cell cycle regulators p16INK4a and p19ARF (splice variants encoded by Cdkn2a) (reviewed in Bigas et al., 2013). By using lineage-tracing analysis, it has recently been proven that Notch1 and Notch2 are specifically expressed (Fre et al., 2011) and required (Riccio et al., 2008) to maintain homeostasis in the intestinal crypt, with the Paneth cells being responsible for producing Wnt and Notch signals (Sato et al., 2011). Complete inhibition of Notch signaling in the intestinal epithelium results in the loss of the proliferative crypt compartment and the loss of the conversion of crypt progenitors into the post-mitotic secretory lineages (van Es et al., 2005), partially overlapping with the phenotype that is obtained after deletion of the Notch target gene Hes1 (Jensen et al., 2000). The molecular basis for the differentiation-associated defects is the overexpression of Math1, a master regulator of the absorptive intestinal lineage, which is repressed by Hes1. Nevertheless, genetic inactivation of Hes1 or knockout (KO) of Hes1, Hes3 and Hes5 simultaneously in the adult mouse intestine leads to reduced cell proliferation and increased secretory cell formation but does not affect ISC integrity (Ueo et al., 2012).

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demonstrate that Bmi1 expression is unrestricted throughout the crypt compartment, similar to that of other proposed stem cell markers, such as Hopx and Tert.

We find here that Bmi1 is a downstream effector of Notch in the ISC and progenitor compartment and that Bmi1 is involved in ISC self-renewal.

RESULTS
Notch and Wnt pathways are simultaneously required to maintain the intestinal stem cell compartment in vivo

We first investigated the relative contribution of Notch to the ISC compartment using a combination of gain- and loss-of-function (GOF and LOF, respectively) mutants that had been previously developed. Specifically, we used a tamoxifen-inducible Cre recombinase driven by the villin promoter (Villin-CreER-T2) to conditionally delete Rbpj in the intestinal epithelium, which we combined with the active form of β-catenin (Ctnnb1lox(ex3)). We have previously demonstrated that genetic depletion of Notch signaling results in the complete loss of ISC markers and the intestinal stem cell function (Pellegrinet et al., 2011; Riccio et al., 2008). We have now confirmed this Notch-dependent ISC phenotype and found that it was not rescued by ectopic activation of the β-catenin pathway using Rbpjlox.Ctnnb1lox(ex3) mice (Fig. 1A,B; supplementary material Fig. S1). Consequently, all single and double mutants died around day 5-6 after the first tamoxifen injection. As a control, constitutive activation of β-catenin alone led to the expansion of the undifferentiated crypt compartment, which was accompanied by ectopic expression of Olfm4, Lgr5 and Ascl2. Immunohistochemistry (IHC) analysis of these mice further confirmed that post-mitotic goblet cells (Fig. 1C) accumulate in the intestinal crypts of Rbpj-depleted mice, which was associated with a profound reduction of the proliferative compartment, as shown by the small number of Ki67-positive cells. Interestingly, in the intestinal crypts of the composite Rbpjlox.Ctnnb1lox(ex3) mutants, both the differentiation to goblet cells imposed by Rbpj (Notch) LOF,
the reduction in the number of proliferating ISCs and progenitor cells were significantly rescued, leading to values comparable to those of the wild-type (WT) intestine, although reduced compared with the single β-catenin GOF (Fig. 1C-E).

These results indicate that β-catenin activation partially compensates the effect of Rbpj (Notch) LOF in goblet cell differentiation without rescuing the loss of the ISC compartment.

### Transcriptional activation of the Bmi1 gene is downstream of Notch and β-catenin

To better understand the requirement for Notch in the ISC compartment, we explored a previously identified transcriptional gene signature that is simultaneously dependent on Notch and β-catenin in colorectal cancer cells (Rodilla et al., 2009). The ISC-related gene PCGF4/Bmi1 was included in this signature as it was downregulated following β-catenin or Notch inhibition, but failed to be induced by active Notch1 (intracellular fragment of Notch1, ICN1) in the absence of β-catenin signaling. By contrast, the canonical Notch target gene Hes1 was found to be strictly dependent on ICN1 in intestinal cancer cells (Fig. 2A). Using the Genomatix software, we identified several adjacent TCF- and Rbpj-binding consensus sequences in the regulatory region of the murine Bmi1 gene that were functionally validated in purified murine crypt cells by sequential chromatin immunoprecipitation (ChIP) assay. In particular, the recruitment of Notch and β-catenin proteins was detected in a predicted region close to the transcriptional start site that contained both consensus binding sequences (Fig. 2B, pp2 region; supplementary material Fig. S2A). Next, we tested whether Bmi1 transcription required Notch and β-catenin activities in the normal intestinal crypt cells. By using IHC, we found that Bmi1...
expression was mainly restricted to the intestinal epithelial crypt cells of WT mice (Fig. 2C), where activation of both pathways occurs (Sato et al., 2011). Importantly, specific Rpnb7 deletion resulted in the total loss of Bmi1 expression in these cells (data not shown) that was not recovered by the constitutive activation of the β-catenin pathway (Fig. 2C). However, β-catenin was also essential to maintain Bmi1 expression even in the presence of active Notch1 (Fig. 2C). By co-precipitation of protein extracts from purified intestinal crypts, we demonstrated that endogenous β-catenin and active Notch1 physically interact in this tissue (Fig. 2D), further supporting the notion of their functional interplay. Next, we generated a reporter construct carrying 2.5 kb of the proximal Bmi1 promoter, including the putative Rbpj and TCF consensus sites, fused to the luciferase gene (supplementary material Fig. S2B). We found that pharmacological inhibition of Notch or β-catenin pathways (by using DAPT or PKF115-584, respectively) (supplementary material Fig. S2C), or the ectopic expression of dominant-negative forms of RBPJ and TCF4 (supplementary material Fig. S2D), were sufficient to repress transcription driven by the Bmi1 promoter. Conversely, the Notch coactivator Mastermind (MaM) induced this construct in an RBPJ- and TCF4-dependent manner (Fig. 2E), although neither Notch nor β-catenin alone could induce Bmi1-driven transcription, suggesting that MaM was a limiting factor in these cells. By contrast, transcriptional repression through the specific Notch target Hes1 protein is a widely used mechanism for attenuating Notch-dependent transcription (Krejcí et al., 2009). We found several Hes consensus binding sites in the Bmi1 promoter (supplementary material Fig. S2B) that we functionally tested in the reporter experiments. Ectopic Hes1 expression totally abolished (supplementary material Fig. S2B) that we functionally tested in the (Fig. 2E), although neither Notch nor β-catenin-dependent reporter activity and facilitated its activation through ICN1, β-catenin and MaM (Fig. 2F). Our results indicate that Bmi1 transcription is positively regulated by Notch, β-catenin and the coactivator MaM, and is repressed by Hes1 (Fig. 2G), which fine-tunes Bmi1 levels in response to Notch activation (see Discussion).

By interrogating the whole human and mouse genomes for the frequency of contiguous Rpnb7- and TCF-binding consensus sequences, we found that both sequences were not randomly distributed but that they clustered in the promoter region of multiple genes close to their transcription start sites (supplementary material Fig. S2E). Rpnb7-binding consensus sites were significantly enriched at distances of 100-200 bp, 300-400 bp and 700-800 bp from the TCF-binding consensus (supplementary material Fig. S2F), compared with not only 1000 randomly permuted site distributions (P=0.001) but also with the 500 bp neighborhood of the observed data (P=0.001 for 100-200 bp and 300-400 bp; P=0.002 for 700-800 bp), indicative of a conserved mechanism for Notch and Wnt co-regulation.

Bmi1-deficient mice display intestinal defects that resemble a Notch LOF phenotype

Bmi1 protein is detected in different intestinal crypt cells, including the long-term ISC population (Sangiorgi and Capecechi, 2008); however, the functional significance of Bmi1 in intestinal homeostasis has not been addressed. Bmi1-deficient mice are born at Mendelian ratios but die prematurely (around 2-3 months of age), presenting growth retardation and stem cell-associated defects (Bruggeman et al., 2005; Molofsky et al., 2005; Oguro et al., 2006). We analyzed the intestine of Bmi1 KO mice at 2-3 months of age and found that the small intestine was significantly shorter (35.88±2.3 cm in the WT and 28.33±2.5 cm in the KO, P<0.001) (Fig. 3A) and thinner (Fig. 3B) compared with that of WT littermates, and a similar length defect was found in the colon (7.05±1.0 cm in the WT and 5.5±1.2 cm in the KO, P=0.04) (Fig. 3A). Through IHC analysis of Ki67 expression and Alcian Blue staining (Fig. 3C,D), as well as the use of a 5-bromo-2′-deoxyuridine (BrdU) proliferation assay (supplementary material Fig. S3A), we observed that Bmi1 mutants display a significant reduction in the number of cycling crypt cells in both the small intestine and the colon. This observation was associated with a moderate but significant increase in goblet cell differentiation, partially resembling the phenotype obtained upon Rpnb7 (Notch) deficiency. Double staining for BrdU and the ISC marker Olfm4 demonstrated that proliferation defects involved both the ISC (3.1±2.2 BrdU and Olfm4 double-positive cells in the WT compared with 1.0±1.6 in the KO; P=0.001) and, to a minor extent, the transit-amplifying compartment (6.9±3.4 BrdU-positive cells in the WT compared with 6.3±3.6 in the KO, P=0.17) (Fig. 3E). Comparable results were obtained through the analysis of the cell cycle profile of intestinal crypt populations expressing different levels of the surface marker Ephb2; ISCs were included in the Ephb2high population, and most of the transit-amplifying cells were included in the Ephb2medium population (Jung et al., 2011) (Fig. 3F). The intestinal phenotype of Bmi1-deficient mice was not exclusive of adult animals, but it was already detectable at day 3 after birth (supplementary material Fig. S3B,C), indicating that it originates during development. Consistent with the alterations of the colonic tissue, Bmi1 protein was also detected in cells located at the bottom of the WT colonic crypts (supplementary material Fig. S3D), which has not been reported previously.

Next, we determined the expression levels of different stem cell markers in the intestinal crypts of Bmi1-deficient mice. Using IHC and quantitative reverse-transcriptase (qRT) PCR analyses, we did not find any significant change in the expression levels of the Lgr5, Olfm4, Ephb2, c-Myc, Hopx and Lrig1 genes in the Bmi1-deficient intestines (Fig. 3G,H). However, Tert, recently identified as a marker for slow-cycling intestinal stem cells in mice, was significantly downregulated in the Bmi1-deficient crypt cells (Fig. 3H), which could indicate altered long-term self-renewal.

Bmi1 or Notch deficiency results in increased expression of the cell cycle regulators p16INK4a and p19ARF

Because most of the stem cell defects that have been previously identified in the Bmi1 KO mice are associated with upregulation of p16INK4a and p19ARF, which are targets of Bmi1 repression, we next determined their levels in the intestinal crypts of our different mutant mice. By using IHC (Fig. 4A,C) and qRT-PCR (Fig. 4D) analyses, we found that p16INK4a and p19ARF levels were significantly increased in the absence of Bmi1, which might account for the observed decrease in ISC proliferation. Similarly, the number of intestinal p16INK4a-positive cells was significantly increased in the absence of Rpnb7, both in the single LOF and the composite β-catenin GOF and Rpnb7 LOF mutants (Fig. 4B,C). By contrast, the highly proliferative Cimbb1lox/lox transgenic intestines did not show any increase in p16INK4a expression. These results strongly suggest that Bmi1, downstream of Notch and β-catenin, contributes to the regulation of ISC and progenitor proliferation either directly or through p16INK4a and p19ARF.

Because Bmi1 protein is involved in the regulation of the stem cell compartments in other tissues, including the blood, we considered the possibility that the intestinal defects observed in the general Bmi1-deficient mice were of systemic origin (instead of tissue autonomous). To test this, we generated a Villin-Cre; Bmi1lox/lox line in which the Bmi1 gene was specifically deleted in the intestinal epithelium (although more efficiently in the duodenum than in the distal ileum and colon, data not shown). IHC analysis of 3- to 4-week-old intestinal-specific Bmi1 KO mice showed a consistent and significant
accumulation of p16INK4a-positive cells along the whole crypt-villus axis, which was associated with a reduction in the number of proliferating Ki67-positive cells when compared with that of their WT littermates (Fig. 4E). However, we did not detect a consistent reduction in the size of the tissue-specific KO intestines when compared with those found in the conventional Bmi1 null mice.

In agreement with the possibility that intestinal defects that are associated with Bmi1 deficiency originate during embryonic development, we found a massive increase in p16INK4a levels and a reduction in the number of Ki67-positive cells in the embryonic intestine at the time of villus formation (embryonic days 15 and 16) (Fig. 4E; supplementary material Fig. S3E).

The Bmi1-deficient phenotype mimics that of Notch inhibition with respect to the self-renewal and DNA repair capacity of ISCs

We performed serial culture assays of intestinal organoids (Sato et al., 2009) to further study the requirement of Bmi1 in ISC function. Intestinal organoids are derived from ISC and can be maintained indefinitely after serial passaging. We found that serially replated organoids (after passage 10) contain a high number of Bmi1-expressing cells (Fig. 5A, right panels), which was reduced following Notch inhibition by using DAPT (Fig. 5A,B). This was before the failure of organoid growth that occurred at around 3-4 days of treatment with DAPT (Fig. 5A, left panels). Interestingly, Notch inhibition in these cultures led to the transcriptional activation of p16INK4a and p19ARF (Fig. 5C) that was concomitant with a reduction in the mRNA levels of Olfm4 and Ascl2 (supplementary material Fig. S4A).

We next isolated intestinal crypt cells from Bmi1-deficient mice to measure their clonogenic capacity. Bmi1-deficient crypt cells generated organoids at a similar efficiency to their WT counterparts, but their replating capacity gradually declined from passage 5-7, and they failed to grow after passage 15-16 (Fig. 5D; supplementary material Fig. S4B). Associated with their defective long-term self-renewal, mutant organoids at passage 12-15 contained a significant
number of terminal deoxynucleotidyl transferase dUTP nick end labeling (TUNEL)-positive cells in the epithelial layer that were mostly negative for active caspase3 staining (Fig. 5E), suggesting that Bmi1 deficiency favors the accumulation of DNA breaks independently of apoptosis. To validate this finding, we determined the DNA repair capacity of Bmi1-deficient intestinal cells in response to γ-irradiation in vivo. With this aim, we irradiated Bmi1 WT or KO littermates with 12 Gy, which were then killed 2 h later and processed for IHC analysis with an antibody against γH2A.X. We found that WT intestines specifically accumulate γH2A.X staining in the villus regions, which is an indication of unrepaired DNA breaks. However, intestinal crypt cells only showed discrete γH2A.X foci as a result of efficient DNA repair, as previously published (Hua et al., 2012). By contrast, Bmi1-deficient intestines displayed an intense homogeneous γH2A.X staining pattern arising from the base of the crypts to the top of the villi (Fig. 5F), indicating that Bmi1 protein is involved in regulating DNA damage repair in the intestinal crypt cells. This is consistent with the known role of Bmi1 protein in DNA damage repair through H2A monoubiquitylation, which facilitates the recruitment of the repair machinery (Ginjala et al., 2011; Ismail et al., 2010; Pan et al., 2011).

Taken together, our results indicate that Notch signaling exerts a direct effect on the maintenance of ISCs that involves a direct cooperation with β-catenin at the chromatin level to regulate gene transcription. We identify Bmi1 as target of both Notch and β-catenin and demonstrate that intestinal Bmi1 deficiency results in reduced proliferation and limited self-renewal of the ISCs (see model in Fig. 5G).

DISCUSSION
We have identified a new mechanism for gene regulation that depends on the simultaneous activity of two crucial signaling pathways, Wnt-β-catenin and Notch, and is functional in the normal
Intestinal crypts. Importantly, we have identified Bmi1 as a target of both β-catenin and Notch, and characterized its function in ISCs. Accordingly, Bmi1 has been previously identified as a Wnt and KLF4 target in colorectal cancer cells (Yu et al., 2012). We found that Bmi1 deficiency only reproduces some of the defects that are associated with Notch inhibition, including altered proliferation and increased crypt cell differentiation into secretory cells, indicating that many other genes downstream of Notch are also required for ISC function. Moreover, Bmi1 helps to maintain the DNA integrity and self-renewal capacity of the ISC population in vitro, which should be further investigated in relation to the Notch pathway.

Wnt and Notch are well-known stem cell regulators in many different systems, having synergic or antagonistic effects that are context dependent. In the intestine, both pathways are required to maintain the undifferentiated compartment (Ireland et al., 2004; Korinek et al., 1998; Riccio et al., 2008; van Es et al., 2005). Nevertheless, the contribution of each signal and their orchestration is still under debate. Our results indicate that both pathways need to be simultaneously active to maintain the stem cell compartment, but suggest that this evolutionary strategy might be of general use, as indicated by the non-random distribution of TCF- and Rbpj-binding consensus sites along the entire mouse and human genomes. In this study, we provide evidence for the involvement of Bmi1 in the Wnt and Notch pathways in ISCs.
work, we focused on studying Bmi1, the expression of which depends on Notch- and β-catenin-mediated signaling, and we demonstrate that the Bmi1 promoter is directly regulated by both factors in association with the MaM coactivator. Conversely, the Notch target gene Hes1, which is also a master regulator of the absorptive and secretory lineage differentiation, represses Bmi1, suggesting that its expression is dynamically regulated in the crypt through the participation of both positive and negative signals. Notch has been previously shown to control this type of regulatory loop, also known as type I incoherent feed-forward loops (I1-IFF) in Drosophila (Guix et al., 2013; Krejci et al., 2009).

Although the original identification of Bmi1 as a target of both Notch and β-catenin was based in the use of cancer cell lines, this regulation is also found in a physiological context, such as the ISCs. Bmi1 function was known to be crucial for hematopoietic and neural stem cells, but its role in the intestine has not been defined previously. We here show that Bmi1 deletion results in reduced intestinal size, associated with increased differentiation into goblet cells and reduced proliferation of the stem cell compartment, a phenotype that partially overlaps with that produced by the absence of Notch or Rbpj signaling in the ISC compartment. Although Bmi1 null mice show a decrease in body weight, we cannot exclude that this is a secondary effect of defective intestinal function. However, several ISC markers are still detected in the intestine of Bmi1-deficient animals, and this tissue is maintained for at least 3 months (the life expectancy of these animals), which is very different from the strong intestinal phenotype that is associated with complete Notch and/or β-catenin depletion. This fact reflects the functional relevance of other Notch and β-catenin targets, such as Ephb2 or c-Myc in ISC maintenance. Of note, the severity of the Notch deletion phenotype might vary among different genetic backgrounds, as reflected by the work of Yin and colleagues (Yin et al., 2014).

By culturing normal or Bmi1-deficient ISC in Matrigel, we here demonstrate that intestinal crypt cells from Bmi1-deficient animals have incomplete self-renewal capacity associated with increased DNA damage repair, a phenotype that was confirmed in the irradiated Bmi1-deficient intestines and in agreement with the identification of the Bmi1-positive cells as a radio-resistant population with capacity to replace Lgr5-positive cells after radiation (Yan et al., 2012). Inhibition of Notch in the organoid cultures results in Bmi1 downregulation, upregulation of p16INK4a and p19ARF and a reduced number of Ki67-positive cells, before terminal organoid differentiation. These results suggest that Bmi1 contributes to proliferation and self-renewal downstream of Notch and β-catenin, probably by regulating the cell cycle through p16INK4a and p19ARF, DNA repair (Ismaiil et al., 2010), telomere length (Dimri et al., 2002; Jacobs and de Lange, 2004) and senescence (Park et al., 2004), which are known functions of Bmi1.

MATERIALS AND METHODS

Animals

All animal work was conducted according to the guidelines from Generalitat de Catalunya, and this study was approved by the committee for animal experimentation at Institut Hospital del Mar d’Investigacions Médiques (Barcelona, Spain). The mouse transgenic line Villin-CreER-T2 (in the C57BL/6 background), in which Cre recombinase expression is confined to the intestinal epithelium, was crossed with the different floxed mice to generate intestine-specific gene-targeted mice. The CreER-T2 recombinase activity was induced by injecting 2- to 3-week-old mice with tamoxifen (10 mg/kg body weight in corn oil; Sigma) intraperitoneally for three consecutive days. The general Bmi1 null mice were in an FVB/NJ background. Intestine-specific Bmi1 KO animals were obtained by crossing the previously described Bmi1lox (Arranz et al., 2012) with the Villin-Cre (from Jackson Laboratories) line (both in C57BL/6 background). In all the experiments using Bmi1-deficient mice, animals were euthanized before any obvious sign of disease was detected.

Cell lines and reagents

Cell lines expressing dominant-negative TCF4 (Ls174T/dnTCF4) and ICN1 (Ls174T/dntCF4/ICN1) have been previously described (Rodilla et al., 2009; van de Wetering et al., 2002) and were maintained in Dulbecco’s media with 10% fetal bovine serum (FBS). Doxycycline (Sigma) was used at 1 µg/ml. The γ-secretase inhibitor DAPT (Calbiochem) was used at 25 µM.

RT-PCR

Total RNA was extracted with the RNeasy Qiagen kit, and RT-First Strand cDNA Synthesis kit (Amersham Pharmacia Biotech) was used. The primers used for RT-PCR analyses are listed in supplementary material Table S1A. qRT-PCR was performed in a LightCycler480 system using SYBR Green I Master kit (Roche).

ChiP

Briefly, chromatin from cross-linked cells was sonicated, incubated overnight with the indicated antibodies in radioimmunoprecipitation assay (RIPA) buffer and precipitated with protein G/A-Sepharose. Cross-linkage of the co-precipitated DNA-protein complexes was reversed, and DNA was used as a template for the PCR. Antibodies against cleaved Notch1 (ab8925, Abcam) and β-catenin (BD Bioscience, catalog no. 61054) were used. For second ChiP experiments, complexes from the first ChiP were eluted through incubation in 25 µl of 10 mΜ dithiothreitol for 30 min at 37°C. After centrifugation, the supernatant was diluted with RIPA buffer and subjected to the ChiP procedure. The primers used are listed in supplementary material Table S1B.

In situ hybridization (ISH)

Intestinal samples were flushed gently with cold PBS and fixed overnight in 4% paraformaldehyde at room temperature. Samples were then dehydrated, embedded in paraffin and sectioned at 8 µm. After de-waxing and rehydration, the samples were treated twice with 2 mM HCl and proteinase K (30 µg/ml) (Biological Industries) supplemented with N2 and B27 media with 10% fetal bovine serum (FBS). Doxycycline (Sigma) was used at 1 µg/ml. The procedures for RT-PCR analyses are listed in supplementary material Table S1A. The DNA probes were obtained from complementary DNA of mouse c-Myc, Hes1, Olfm4, Ascl2 and Lgr5, and were generated through in vitro transcription with a Digoxigenin RNA Labeling Kit (Roche) according to the manufacturer’s instructions.

Intestinal crypt isolation and organoid culture in Matrigel

Mouse small intestines were collected, sliced longitudinally and thoroughly washed in cold PBS. Villi were removed by carefully scraping the surface. Remaining tissue was cut into small sections, treated twice with 2 mM EDTA for 30 min and centrifuged at 110 g to obtain the crypt-enriched fraction as previously described (Sato et al., 2009). Approximately 106 cells were seeded in 50 µl Matrigel (BD Biosciences) in 24-well plates. After polymerization, 500 µl of complete organoid medium ([DMEM/F12, Biological Industries) with penicillin (100 U/ml) and streptomycin (100 µg/ml) (Biological Industries) supplemented with N2 and B27 (Invitrogen) containing 140 mM ROCK inhibitor (Y27632, Sigma), 100 ng/ml noggin (Peprotech), 100 ng/ml R-spondin (R&D Systems), 50 ng/ml EGF (Sigma) and 20 ng/ml basic FGF (Peprotech)] was added. Medium was changed every 2 days. Incubator conditions were 37°C, 5% CO2.

Organoid immunostaining

Organoids were collected from Matrigel (BD Bioscience), placed onto a slide by using cytopsin and circled with DakoPen (Dako). Whole-mount immunostaining was performed after fixation with 4% paraformaldehyde...
and permeabilization with 0.3% Triton X-100 (Pierce). Organoids were stained with an antibody against yH2A.X (1:200; Cell Signaling, catalog no. 2577) overnight and then incubated with secondary antibody donkey-anti-rabbit Alexa Fluor 488 (Molecular Probes) for 2 h at room temperature at a 1:1000 dilution. Slides were mounted in VectaShield with DAPI (Vector). Other antibodies used were: anti-Bmi1 (1:100; Abcam, ab14389), followed by donkey anti-mouse Alexa Fluor 488, and anti-cleaved caspase3 (1:500; Cell Signaling, catalog no. 9661).

**TUNEL assay**

The TUNEL assay was performed using the DeadEnd Colorimetric Apoptosis Detection System (Promega), according to the manufacturer’s instructions.

**Immunohistochemistry**

Intestinal samples were embedded in paraffin and sectioned at 4 µm. After de-waxing and rehydration, endogenous peroxidase activity was quenched (20 min, 1.5% H2O2) and antigen retrieval was performed depending on the antibody. Paneth cells were stained with a rabbit antibody against lysozyme (1:5000; Dako, A0099). Goblet cells were stained with Alcian Blue (pH 2.5; Sigma) and counterstained with Nuclear Fast Red (Sigma). Other primary antibodies were against: green fluorescent protein (1:200; Takara, 632460); β-catenin (1:2000; Sigma, C2206); Bmi1 (1:200; Abcam, ab14389); EphB2 (1:500; R&D Systems); Myc (1:100; Santa Cruz, sc-764); Ki67 (1:500; Novocastra, M1); p16INK4a (1:50; Santa Cruz, sc-1207; or 1:150; Santa Cruz, sc-1661). All primary antibodies were diluted in PBS containing 0.05% BSA and incubated overnight at 4°C, unless indicated otherwise. Sections were then incubated with specific horseradish peroxidase (HRP)-labeled secondary antibody, and staining was developed using diaminobenzidine peroxidase substrate kit (Dako Cytomation). BrdU (1:250; Abcam, ab6326) was incubated for 2 h at room temperature, and the secondary antibody system used was a biotinylated anti-rat antibody (Dako, E0468) incubated for 1 h at room temperature, followed by the Vectastain ABC kit (Vector, PK6100). Staining was developed as described above. For staining with antibodies against cleaved Notch1 (1:200; Cell Signaling, no. 4147) and Bmi1 (Cell Signaling, no. 6964), incubations were performed in histoblock solution (PBS 3% BSA, 20 mM MgCl2, 0.3% Tween 20, 5% FBS), and for staining of yH2A.X (1:200; Cell Signaling, no. 2577), incubations were performed in PBS 1% normal goat serum (Dako), 0.1% surfactant-AMPS (Thermo Scientific) and 0.05% BSA. Incubations were performed overnight at 4°C, samples were then incubated with HRP-labeled anti-rabbit polymer (Dako Envision) and developed using FITC-coupled Tyramide Signal Amplification System (PerkinElmer).

**References**


**Immunoprecipitation assays**

Purified intestinal murine crypt cells were lysed for 30 min at 4°C in 300 µl PBS plus 0.5% Triton X-100, 1 mM EDTA, 100 mM sodium orthovanadate, 0.25 mM PMSF and complete protease inhibitor cocktail (Roche). Supernatants were pre-cleared for 2 h with 1% bovine serum albumin (BSA), 1 µg IgGs and 50 µl sepharose Protein A (SPA) beads and incubated overnight with 3 µg of specific anti-β-catenin antibody. Antibody-protein complexes were then captured with 30 µl SPA beads for 2 h, extensively washed in lysis buffer, and the precipitates were analyzed by western blotting.

**Bioinformatics analysis**

The human genome was scanned for the detection of Rbpj-[CG][CT]-GTGGGAA[AC] and TCF4- [GT][TA][TA][CA][TA][GG] binding sites in both forward or reverse strands using a modified version of a previously described program (Romano et al., 2008) that identifies local genomic regions with colocalization of several binding sites. P values were obtained by the Z-scores derived from observed and permuted distributions of the binding sites. Graphs and statistics were built with R Statistical package.

**Promoter analysis and luciferase assays**

The Bmi1-luc reporter was generated by cloning the region from −2009 to +484 of the human Bmi1 gene into the pGL2 basic vector (Promega), which was then verified by sequencing. The primers used were GLprimer1 and GLprimer2 from the human promoter. Luciferase reporter assays were performed in HEK-293T cells. Cells were seeded in 12-well plates at a density of 5×10⁴ cells/well. In the different experiments, 250 ng or the indicated amounts of ICN1, Mastermind, dominant-negative Rbpj, dominant-negative TCF4, small hairpin RNA against Hes1 (shHes1; MISSION, TRCN0000018989) or irrelevant DNA, plus 150 ng RSV-β-galactosidase and Bmi1 promoter-luciferase (Bmi1prom-luc) plasmids were transfected into triplicate wells using polyethylenimine (PEI) (Polysciences). Immunofluorescence images of intestinal sections and organoids were taken by using confocal microscopy with a Leica SP5 TCS upright microscope and the Leica Application Suite Advanced Fluorescence software.

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**Competing interests**

The authors declare no competing financial interests.

**Author contributions**

E.L.-A., V.R., L.P., J.G., M.I. and A.C.R. designed and supervised the experimental work. A.B. and S. Gutarra helped with the animal experiments. S. Gutarra and S. Gonzalez helped with the animal work. P.M.-C., P.F.-S., F.R., A.B. and L.L.E. designed and supervised the experimental work. A.B. and L.L.E. conceived the study, analyzed the data and wrote the manuscript.

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