Innate PI3K p110δ Regulates Th1/Th17 Development and Microbiota-Dependent Colitis


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Innate PI3K p110δ Regulates Th1/Th17 Development and Microbiota-Dependent Colitis


The p110δ subunit of class IA PI3K modulates signaling in innate immune cells. We previously demonstrated that mice harboring a kinase-dead p110δ subunit (p110δKD) develop spontaneous colitis. Macrophages contributed to the Th1/Th17 cytokine bias in p110δKD mice through increased IL-12 and IL-23 expression. In this study, we show that the enteric microbiota is required for colitis development in germfree p110δKD mice. Colonic tissue and macrophages from p110δKD mice produce significantly less IL-10 compared with wild-type mice. p110δKD APCs cocultured with naïve CD4+ Ag-specific T cells also produce significantly less IL-10 and induce more IFN-γ- and IL-17A–producing CD4+ T cells compared with wild-type APCs. Illustrating the importance of APC–T cell interactions in colitis pathogenesis in vivo, Rag1−/−/p110δKD mice develop mild colonic inflammation and produced more colonic IL-12p40 compared with Rag1−/− mice. However, CD4+CD45RBhigh/low T cell Rag1−/−/p110δKD recipient mice develop severe colitis with increased percentages of IFN-γ- and IL-17A–producing lamina propria CD3−CD4+ T cells compared with Rag1−/− recipient mice. Intestinal tissue samples from patients with Crohn’s disease reveal significantly lower expression of PIK3CD compared with intestinal samples from non–inflammatory bowel disease control subjects (p < 0.05). PIK3CD expression inversely correlates with the ratio of IL12B:IL10 expression. In conclusion, the PI3K subunit p110δ controls homeostatic APC–T cell interactions by altering the balance between IL-10 and IL-12/23. Defects in p110δ expression and/or function may underlie the pathogenesis of human inflammatory bowel disease and lead to new therapeutic strategies. The Journal of Immunology, 2014, 192: 3958–3968.

Genetic variants that confer susceptibility to the human inflammatory bowel diseases (IBD) Crohn’s disease (CD) and ulcerative colitis highlight the importance of innate immune interactions with the enteric microbiota in both initiating and controlling inflammation (1). Commensal and pathogenic microorganisms are recognized through conserved molecular microbial patterns by pattern-recognition receptors, of which TLRs form integral components (2). Although mechanisms by which the host distinguishes commensal from pathogenic bacteria are not well defined, under normal conditions TLR signaling initiated by the enteric microbiota is protective (3). PI3Ks have emerged as important regulators of TLR signaling (4, 5). Class IA PI3Ks have five different regulatory subunits and three p110 catalytic subunits: p110α and p110β are expressed ubiquitously in tissues, whereas p110δ is enriched in leukocytes (6). Agents that activate macrophages to produce IL-12p40, the common subunit of the proximal inflammatory cytokines IL-12 and IL-23, also activate class Iα PI3K (7). Activation of PI3K in turn blocks the expression of IL-12p40 mRNA (IL12b) (7). Although inflammatory responses are essential for eradicating pathogenic microbes, excessive/prolonged activation of innate immunity is harmful to the host. PI3K-mediated negative feedback of IL-12p40 is important to prevent excessive innate immune responses.

The clearest role for PI3K in chronic inflammation is described in a mouse harboring a kinase-dead p110δ catalytic subunit of PI3K (p110δKD) (8). These mice demonstrate B and T cell defects, including defective Ag receptor signaling and impaired humoral responses. Notably, the occurrence of spontaneous colitis was demonstrated in PI3K p110δKD mice (9). Expression of IL-12p40, Th1, and Th17 cytokines was described in the intestinal and systemic immune compartments. Consistent with a homeostatic role for p110δ in the intestine, wild-type (WT) mice raised in a germfree (GF) environment markedly upregulated colonic p110δ (Pik3cd) expression when the enteric microbiota were introduced, but colitis-prone Il10−/− mice raised in the same conditions did not (9).

Given the role of the PI3K p110δ subunit in innate immune processes fundamental to the pathogenesis of IBD, host-enteric microbiota and APC–T cell interactions in p110δKD mice were further characterized. We describe a requirement for the enteric

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Abbreviations used in this article: BMDM, bone marrow–derived macrophage; CBL, cecal bacterial lysate; CD, Crohn’s disease; CNN, conventionalized; GF, germfree; GSK-3β, glycogen synthase kinase 3β; HKEC, heat-killed Escherichia coli; IBD, inflammatory bowel disease; LPMC, lamina propria mononuclear cell; MLN, mesenteric lymph node; MOI, multiplicity of infection; mTOR, mammalian target of rapamycin; TRIF, Toll–IL-1R domain–containing adaptor inducing IFN-β; WT, wild-type.

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microbiota to drive intestinal inflammation in p110\textsuperscript{KD} mice. Microbial-innate immune interactions, through p110\textsuperscript{a}, maintain homeostasis through regulation of both protective (IL-10) and inflammatory (IL-12p40) cytokines. Furthermore, p110\textsuperscript{a} orchestrates innate regulation of adaptive immune responses. Importantly, in human CD, decreased intestinal PI3KCD gene expression is demonstrated that inversely correlates with intestinal IL12B:IL10 ratios. Thus, p110\textsuperscript{a} appears to be a central homeostatic switch in the intestine, governing the critical balance between microbiota-induced IL-12/23 and IL-10, shaping the subsequent T cell response. Counter to prevailing paradigms in which p110\textsuperscript{a} inhibition is a strategy in inflammatory diseases (10, 11), induction of p110\textsuperscript{a} could be a potential therapeutic approach in human IBD.

Materials and Methods

Mice
All mice were maintained on a C57BL/6 background in conventional or GF housing. P89 p110\textsuperscript{a}K117D (p100\textsuperscript{a}) mice were previously obtained from R. Vihinen-Broek (Queen Mary University of London, London, U.K.). GF p100\textsuperscript{a} mice were Caesarian derived, as previously described (12), and were maintained according to standard techniques in the University of North Carolina National Gnotobiotic Resource Center. OT-II [C57BL/6-Tg(TcraTcrb)425Cbh/J] male mice were provided by T. Jing (University of North Carolina, Chapel Hill, NC). All animal experiments were in compliance with protocols approved by the International Animal Care and Use Committee of the University of North Carolina at Chapel Hill.

Reagents
LPS from Escherichia coli and Pam\textsubscript{3}CSK\textsubscript{4} were purchased from InvivoGen (San Diego, CA). Zymosan A from Saccharomyces cerevisiae was purchased from Sigma-Aldrich (St. Louis, MO). Inhibitors IC87114, rapamycin, and SB-216763 were purchased from Selleck Chemicals (Houston, TX). Cecal bacterial lysates (CBL) from C57BL/6 mice were prepared, as described previously (13). The peptide corresponding to residues 323–339 of V\textsubscript{a} was purchased from AnaSpec (Fremont, CA).

Colonie tissue explant culture
Colonie tissue explant cultures were performed, as described previously (14).

Histology
Slides were prepared for H&E staining, and a pathologist (L.B.B.) blinded to the study groups performed histological analysis using established criteria for p110\textsuperscript{a} mice (9). In T cell adoptive transfer studies, the following scoring system was used: tissue changes were categorized into inflammatory and epithelial changes and graded for severity (0 = normal, 1 = mild, 2 = moderate, 3 = marked, and 4 = severe); the sum of the two grades comprised the histopathology score. For inflammation, a score of 0 (normal) signified rare small lymphoplasmacytic aggregates confined to the lamina propria; scores of 1 (mild) and 2 (moderate) represented increasing numbers of multifocal inflammatory aggregates that were predominantly confined to the lamina propria, with occasional submucosal infiltration; a score of 3 (marked) was assigned if inflammatory infiltrates frequently extended into the submucosa and muscular layers; a score of 4 (severe) was designated if transmural inflammation was common. Epithelial changes, characterized by hypertrophy, were scored (0–4) with increasing severity and prevalence of the observed change.

Cell isolation
Bone marrow–derived macrophages (BMDMs) were cultured, as described previously (15). Splenocytes were isolated, as described (16), and further separated into CD11c\textsuperscript{+} and CD11c\textsuperscript{−}/CD11b\textsuperscript{+} cells by MACS with anti-CD11c and anti-CD11b microbeads (Miltenyi Biotec, Auburn, CA). Lamina propria mononuclear cells (LPMCs) were isolated from mouse colons, as described previously (17). LPMCs were further separated into CD11b\textsuperscript{+} and CD11b\textsuperscript{−} cells by MACS with anti-CD11b microbeads (Miltenyi Biotec).

Cell culture experiments
BMDMs or splenocytes were cultured at 1 × 10\textsuperscript{6}/ml in the presence of LPS (1 ng/ml), zymosan A (10 \mu g/ml), Pam\textsubscript{3}CSK\textsubscript{4} (5 ng/ml), or PBS, and supernatants were harvested after 4 or 24 h (BMDMs or splenocytes, respectively). Inhibitors IC87114 (0.1 or 1 \mu M), rapamycin (1 or 10 \mu M), SB-216763 (1 or 10 \mu M), or DMSO were added 1 h prior to stimulation with LPS or zymosan A. CD11b\textsuperscript{+} LPMCs were treated with IC87114 (10 \mu M) for 30 min prior to exposure to heat-killed E. coli (HKEC; multiplicity of infection [MOI] = 100) for 3 h. Total RNA was assessed for Il12b and Il10 expression by quantitative PCR.

Western blot analysis
BMDMs were cultured at 1 × 10\textsuperscript{6}/ml with LPS (1 \mu g/ml), or cecal tissue from GF to conventionalized (CNV) mice was cultured. Cell or tissue lysates were collected in radioimmunoprecipitation assay buffer with protease and phosphatase inhibitors. Equal amounts of protein were loaded and run on a 10% SDS-PAGE gel. Blots were probed for phosphorylated glycogen synthase kinase-3b (GSK-3b) (Ser\textsuperscript{9}) and total GSK-3b with Abs from Cell Signaling Technology (Danvers, MA) and phosphorylated CREB (Ser\textsuperscript{133}) (EMD Millipore, Billerica, MA) and total CREB (Santa Cruz Biotechnology, Dallas, TX). Equal protein loading was confirmed by probing blots with anti-beta-actin (mAbcam 8226) from Abcam (Cambridge, MA).

Quantitative RT-PCR
Quantitative RT-PCR was performed on total RNA, as described (14). Murine primer sequences will be provided upon request. The following human primer sequences were used: PI3KCD, forward, 5′-GGCCCGG-GMGAGTAAAACTGAC-3′, and reverse, 5′-GCTGCCCCAGGGTCTACCT-ACCT-3′; IL10, forward, 5′-GGCTACTACGTCCTGAGATC-3′, and reverse, 5′-TGATGTGTGGGTCTTGGTTC-3′; IL12B, forward, 5′-GGCTC-TGCCCTGGACCTGAGGC-3′, and reverse, 5′-GGTGAATTTGATT-GGTATCCGG-3′; GAPDH, forward, 5′-GGTGAAGGTCGAGTCAAC-GGA-3′, and reverse, 5′-GAGGGATCTCGTCCTGGAGA-3′.

ELISAs
IL-12p40 and IL-10 (BD Biosciences, San Jose, CA) and IFN-\gamma concentrations (R&D Systems, Minneapolis, MN) were determined by sandwich ELISA, according to manufacturer’s instructions.

APC–CD4\textsuperscript{+} T cell coculture
Splenic APCs from WT or p110\textsuperscript{a} mice were isolated by negative selection using CD90.2 microbeads (Miltenyi Biotec). Splenic APCs were incubated overnight with CBL (50 ng/ml), and, after washing several times to remove extracellular Ag, APCs were cocultured with negatively selected CD4\textsuperscript{+} T cells (CD8\textsuperscript{a}/B220/MHC II microbeads; Miltenyi Biotec) from WT or IL10\textsuperscript{−/−} mice at a 3:2 ratio (APC:T cell) for 72 h. For Ag-specific studies, APCs were incubated overnight with LPS (10 ng/ml) and OVA peptide (323–339, 5 \mu M) (13). After washing to remove extracellular Ag, APCs were cocultured with negatively selected CD4\textsuperscript{+} T cells (CD8\textsuperscript{a}/B220/ MHC II microbeads; Miltenyi Biotec) from mice expressing a transgenic TCR that recognizes OVA epitope residues 323–339 (OT-II mice) at a 3:2 ratio (APC:T cell) for 72 h. CD4\textsuperscript{+} T cells were analyzed for intracellular cytokine expression (IFN-\gamma and IL-17A) by flow cytometry.

Flow cytometry
CD4\textsuperscript{+} T cells were stimulated for 4 h with PMA (100 ng/ml) and ionomycin (1 \mu g/ml) in the presence of GolgiStop (BD Biosciences). Cells were then washed and stained with allophycocyanin-conjugated anti-CD3 (clone 17A2; eBioscience, San Diego, CA). After fixing and permeabilizing the cells with BD Cytofix/Cytoperm (BD Biosciences), staining for intracellular PE-conjugated anti–IFN-\gamma (clone XM12; eBioscience) and FITC-conjugated anti–IL-17A (clone eBio17B7; eBioscience) was performed. Flow cytometry samples were run on a CyAn ADP Analyzer (Beckman Coulter, Brea, CA) and analyzed using Summit v4.3 (Beckman Coulter).

CD4\textsuperscript{+}CD45RB\textsuperscript{high} low T cell–adaptive transfer colitis
T cell–mediated colitis was induced in Rag1\textsuperscript{−/−} and Rag1\textsuperscript{−/−}/p110\textsuperscript{KD} (p100\textsuperscript{a}K117D) mice at 8 wk of age, as described previously (18). CD4\textsuperscript{+} T cells were isolated by negative selection (CD8\textsuperscript{a}/B220/MHC II microbeads; Miltenyi Biotec) and stained with FITC-conjugated anti-CD4 (clone GK1.5; eBioscience) and PE-conjugated anti–CD45RB (clone 16A; DB Pharmingen, San Jose, CA). CD4\textsuperscript{+} T cells were sorted into CD45RB\textsuperscript{hi} and CD45RB\textsuperscript{lo} populations using a MoFlo XDP Cell Sorter (Beckman Coulter). Mice were ip. injected with 4 × 10\textsuperscript{6} CD4\textsuperscript{+}CD45RB\textsuperscript{hi} cells, as described (18). Clinical scores were assigned, as described (19).

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Human intestinal samples

Intestinal samples were obtained from surgical resections from CD patients and subjects requiring surgical intervention for noninflammatory conditions (e.g., colon cancer). In CD patients, when available, paired inflamed and noninflamed intestinal segments, as determined by gross appearance by the processing pathologist, were obtained for analysis. The University of North Carolina Institutional Review Board approved collection of de-identified samples, and written informed consent was obtained from all patients.

Statistical analysis

Statistical significance for data subsets was assessed by the two-tailed Student t test. The p values <0.05 were considered to be significant. All data are expressed as mean ± SEM.

Results

Presence of the enteric microbiota is necessary for the development of colitis in p110KD mice

To determine whether the microbiota is necessary for the development of colitis, p110KD mice were derived GF. GF p110KD mice up to 30 wk of age did not develop histological colitis (Fig. 1A, Supplemental Fig. 1A). Interestingly, GF p110KD mice produced significantly less colonic IL-10 compared with GF WT mice (Fig. 1B, left). GF p110KD and WT mice were then transitioned to CNV housing, and colonic inflammation was assessed at days 7 and 14 after transfer. Compared with GF to CNV WT mice, colons from GF to CNV p110KD mice demonstrated increased colitis scores (Fig. 1A, Supplemental Fig. 1A). However, GF to CNV p110KD mice gained weight similarly to GF to CNV WT mice (Supplemental Fig. 1B). Furthermore, colonic explants from day 7 and 14 GF to CNV p110KD mice produced significantly less IL-10 (Fig. 1B) compared with GF to CNV WT mice. At day 14, GF to CNV p110KD mice produced significantly elevated IL-12p40 (Fig. 1C) compared with WT GF to CNV mice. IL-10 is important for the maintenance of intestinal homeostasis in part through inhibition of IL-12p40 (20). The ratio of colonic IL-12p40 to IL-10 protein production therefore reflects the overall balance of intestinal pro-and anti-inflammatory cytokines. Indeed, colons from days 7 and 14 GF to CNV p110KD mice demonstrated significantly higher ratios of IL-12p40:IL-10 production (Fig. 1D) compared with GF to CNV WT mice.

Given the recent report of coregulation of IL-10 and IFN-β by p110 in dendritic cells (21), we measured IFN-β levels in colonic

![Graph A](http://www.jimmunol.org/)

**FIGURE 1.** The enteric microbiota are required for the development of colitis in p110KD mice. GF p110KD (n = 10) and age-matched WT (n = 12) mice were monitored for colitis up to 30 wk of age. Additionally, GF WT and p110KD mice were transferred to CNV housing and monitored for colitis at days 7 (n = 5 and 7, respectively) and 14 (n = 6 and 12, respectively) after transfer. (A) H&E slides of colonic tissue were scored for colitis severity using criteria described in Materials and Methods by a pathologist (L.B.B.) blinded to the experimental groups. Error bars represent mean ± SEM (**p < 0.005). (B and C) Colonic tissue explants were incubated in media for 24 h. Supernatants were collected and assayed for IL-12p40 (B) and IL-10 protein (C) production by ELISA and are expressed as the amount of cytokine (pg/ml) per 50 mg colonic tissue weight. Error bars represent mean ± SEM (**p < 0.05, *p < 0.005). (D) IL-12p40 and IL-10 protein levels from colonic tissue explant cultures in individual mice were used to determine the ratio of IL-12p40 to IL-10 production. Error bars represent mean ± SEM (**p < 0.05). (E) IFN-β protein levels from colonic tissue explant cultures were measured by ELISA and are expressed as the amount of cytokine (pg/ml) per 50 mg colonic tissue weight. Error bars represent mean ± SEM (***p < 0.005). (F) WT, p110KD, and Il10−/− BMDMs were isolated and treated with LPS (1 µg/ml), as described in Materials and Methods. Supernatants were collected and assayed for IFN-β levels by ELISA. Error bars represent mean ± SEM from two independent experiments (**p < 0.05). (G) WT and p110KD CD11b+ LPMCs were isolated, as described in Materials and Methods, and treated with HKEC (MOI = 100) for 24 h. Supernatants were collected and assayed for IFN-β levels by ELISA. Error bars represent mean ± SEM from two independent experiments (**p < 0.05).
Explant tissue cultures from GF to CNV WT and p110KD mice. Interestingly, IFN-β production was enhanced in colonic explants from day 7 GF to CNV p110KD mice compared with WT mice (Fig. 1E), in contrast to decreased levels of IL-10 production in p110KD mice. IFN-β production was increased in LPS-stimulated p110KD compared with WT BMDMs (Fig. 1F). Additionally, LPS-stimulated Il10−/−BMDMs produced more IFN-β compared with WT BMDMs (Fig. 1F), consistent with previously reported regulation of IFN-β by IL-10 (21). To assess the direct contribution of IFN-β production from colonic macrophages, CD11b+ LPMCs, comprising mostly macrophages, were isolated from p110KD mice and stimulated with HKEC. Similar to BMDMs, HKEC-stimulated p110KD CD11b+ LPMCs produced significantly more IFN-β compared with WT CD11b+ LPMCs (Fig. 1G), suggesting that p110 differently regulates IL-10 and IFN-β in macrophages.

PI3K p110 regulates macrophage production of IL-10 in response to pathogen-associated molecular patterns

WT and p110KD BMDMs were exposed to TLR agonists (LPS [TLR4], 5 ng/ml; Pam3CSK4 [TLR2/1], 5 ng/ml; zymosan A [TLR2/6], 5 μg/ml), and cytokine production was measured. BMDMs from p110KD mice produced less IL-10 in response to all TLR agonists tested compared with WT BMDMs (Fig. 2A).

**FIGURE 2.** Defective p110 activity alters macrophage production of IL-10 and IL-12p40 in response to bacterial products. BMDMs were stimulated with LPS (5 ng/ml), Pam3CSK4 (5 ng/ml), or zymosan A (5 μg/ml) for 8 h. Supernatants were collected and assayed for IL-10 (A) and IL-12p40 (B) production by ELISA. Error bars represent mean ± SEM from three independent experiments (p < 0.05). (C) The ratio of IL-12p40 to IL-10 from individual experiments was calculated. Error bars represent mean ± SEM from three independent experiments (p < 0.05, **p < 0.005).

**FIGURE 3.** A p110-specific inhibitor decreases IL-10 and augments IL-12p40 production in WT macrophages stimulated with bacterial products. WT, p110KD, and Il10−/−BMDMs were cultured with a p110-specific inhibitor (IC87114, 0.1, 1, or 10 μM) for 1 h prior to stimulation with LPS (1 ng/ml, BMDMs). Supernatants from WT and p110KD BMDMs were collected after 8 h of culture and assayed for IL-10 (A) and IL-12p40 (B) production by ELISA. Error bars represent mean ± SEM from three independent experiments (p < 0.05, **p < 0.005, ***p < 0.0005). (C) Supernatants from WT and Il10−/−BMDMs were collected after 8 h of culture and assayed for IL-12p40. Error bars represent mean ± SEM from three independent experiments (p < 0.05, **p < 0.005, ***p < 0.0005). (D and E) WT and p110KD CD11b+ LPMCs were incubated with a p110-specific inhibitor (IC87114, 10 μM) 1 h prior to stimulation with HKEC (MOI = 100) for 3 h. Quantitative RT-PCR was performed in duplicate for Il10 (D) and Il12b (E), expression levels normalized to β-actin expression and calculated as fold induction over unstimulated cells. Error bars represent mean ± SEM for three independent experiments (p < 0.05).
Additionally, p110\textsuperscript{KD} BMDMs exposed to TLR agonists produced significantly more IL-12p40 compared with WT BMDMs (Fig. 2B), in agreement with our previously published data (9). Consequently, the ratio of IL-12p40:IL-10 production in TLR ligand–treated p110\textsuperscript{KD} BMDMs was consistently increased compared with WT BMDMs (Fig. 2C). LPS- or zymosan A–stimulated CD11b\textsuperscript{+} and CD11c\textsuperscript{+} splenocytes from p110\textsuperscript{KD} mice also produced less IL-10 and more IL-12p40 than WT splenic cells (Supplemental Fig. 2A–D).

To further validate these findings, LPS-stimulated WT BMDMs were treated with p110 isoform–specific chemical inhibitors. LPS-activated WT BMDMs demonstrated a dose-dependent decrease in IL-10 production (Fig. 3A) and increase in IL-12p40 (Fig. 3B, left) with specific chemical inhibition of p110 (IC87114). Interestingly, p110 inhibition in WT BMDMs markedly enhanced IL-12p40 production above levels produced by p110\textsuperscript{KD} BMDMs. It is possible that there is compensation by other PI3K isoforms in p110\textsuperscript{KD} BMDMs but not in chemically inhibited WT BMDMs. Indeed, we have previously shown that phosphorylation of Akt in LPS-stimulated p110\textsuperscript{KD} BMDMs is not completely abrogated (9). PI3K p110\textsuperscript{a} and p110\textsuperscript{b} inhibition (PIK-90 and TGX-221, respectively) did not alter LPS-stimulated IL-10 production (Supplemental Fig. 2E, 2F) or IL-12p40 (Supplemental Fig. 2G, 2H) in WT BMDMs, in agreement with reported results in dendritic cells (21). As a control, p110\textsuperscript{b}-specific inhibition of LPS-activated p110\textsuperscript{KD} BMDMs did not alter IL-10 or IL-12p40 expression (Fig. 3A, 3B). However, in p110\textsuperscript{b} BMDMs, p110\textsuperscript{b} inhibition decreased IL-10 (Supplemental Fig. 2F) production, and p110\textsuperscript{a}- or p110\textsuperscript{b}-specific inhibition modestly enhanced LPS-induced IL-12p40 expression (Supplemental Fig. 2G, 2H), suggesting that, in the absence of p110 function, other isoforms may have modest effects on IL-10/IL-12p40 regulation.

Chemical inhibition of p110 in Il10\textsuperscript{-/-} BMDMs led to a dose-dependent increase in IL-12p40 production (Fig. 3C), suggesting that p110-mediated decreases in IL-12p40 are in part independent of the inhibitory actions of IL-10. Relevant to mucosal innate inflammatory responses, WT CD11b\textsuperscript{+} colonic LPMC treated with HKEC demonstrated diminished Il10 (Fig. 3D) and enhanced Il12b (Fig. 3E) expression in the presence of the p110-specific inhibitor. As a control, expression of neither cytokine was altered in CD11b\textsuperscript{+} colonic LPMC from p110\textsuperscript{KD} mice treated with the p110-specific inhibitor.

**FIGURE 4.** Phosphorylation of p110 targets is altered in macrophages and colons from p110\textsuperscript{KD} mice. (A and B) BMDMs from WT and p110\textsuperscript{KD} mice were treated with LPS (1 \(\mu\)g/ml), and cell lysates were collected for Western blot analysis after the indicated times. (A) Blots were probed for phosphorylated GSK-3\textsuperscript{b} (Ser\textsuperscript{9}) and total GSK-3\textsuperscript{b}. Figure shows representative results from three independent experiments. Quantitative analysis of p-GSK-3\textsuperscript{b} relative light units (RLU) is normalized to total GSK-3\textsuperscript{b} and actin. Error bars represent mean ± SEM (*p, 0.05 compared with WT). (B) Blots were probed for phosphorylated CREB (Ser\textsuperscript{133}) and total CREB. Representative results from two independent experiments are displayed. Quantitative analysis of p-CREB RLU is normalized to total CREB. Error bars represent mean ± SEM from three independent experiments (*p, 0.05 compared with WT). (C) GF WT and p110\textsuperscript{KD} mice were transferred to CNV housing and colonized with a commensal enteric microbiota (GF:WT, \(n\) = 2; p110\textsuperscript{KD}, \(n\) = 2; GF to CNV:7-d WT, \(n\) = 1; 7-d p110\textsuperscript{KD}, \(n\) = 1; 14-d WT, \(n\) = 2; 14-d p110\textsuperscript{KD}, \(n\) = 1; 7-d WT, \(n\) = 1; 7-d p110\textsuperscript{KD}, \(n\) = 1; 14-d WT, \(n\) = 2; 14-d p110\textsuperscript{KD}, \(n\) = 1). Mice were sacrificed at the indicated times after colonization, and cecal tissue was collected and protein extracted. Blots were probed for the indicated proteins/phosphoproteins. Quantitative analysis of p-GSK-3\textsuperscript{b} RLU is normalized to total GSK-3\textsuperscript{b} and actin. Error bars represent mean ± SEM (*p, 0.05, **p, 0.005 compared with WT).
Mammalian target of rapamycin and GSK-3β act downstream of p110δ in macrophages to regulate cytokine production

PI3Ks modulate multiple downstream signaling pathways, of which mammalian target of rapamycin (mTOR) and GSK-3β have been previously shown to regulate cytokine secretion in macrophages (22). PI3K p110δ KD BMDMs treated with LPS demonstrated impaired phosphorylation of GSK-3β and CREB (Fig. 4A, 4B, respectively), but not p70 S6 kinase (downstream of mTOR; data not shown). Furthermore, colonic expression of p-GSK-3β was attenuated in GF to CNV p110δ KD mice compared with GF to CNV WT mice (Fig. 4C). BMDMs from WT and p110δ KD mice were exposed to mTOR or GSK-3β inhibitors (rapamycin or SB-216763, respectively) prior to LPS stimulation. Rapamycin decreased IL-10 (Fig. 5A, 5C) and increased IL-12p40 (Fig. 5B, 5D) protein and mRNA expression in WT and p110δ KD TLR-stimulated BMDMs. These same trends were observed in WT and p110δ KD CD11b+ and CD11c+ splenocytes (Supplemental Fig. 3A–D). Inhibition of GSK-3β in p110δ KD BMDMs and splenocytes increased IL-10 protein (Fig. 5E, Supplemental Fig. 3E, 3F) and mRNA expression (Fig. 5G), whereas p110δ KD BMDMs and splenocytes decreased IL-12p40 protein (Fig. 5F, Supplemental Fig. 3G, 3H) and mRNA (Fig. 5H) expression. Hence, mTOR and GSK-3β are downstream of p110δ and are relevant for regulation of IL-10 and IL-12p40.

**APC p110δ regulates T cell cytokine production**

To begin to determine whether resident APCs regulate intestinal T cell phenotype and function, T cell cytokines and lineage markers were measured in p110δ KD colons. Colonic Tbx21 and Rorc transcripts (Fig. 6A, 6B), the hallmark transcription factors of Th1 (23) and Th17 cells (24), respectively, were increased in GF to CNV p110δ KD mice at days 7 and 14 posttransition compared with matched GF to CNV WT mice. Likewise, increased Ifng and Il17a transcripts (Fig. 6C, 6D) were detected in cecal tissue from days 7 and 14 GF to CNV p110δ KD compared with matched GF to CNV WT mice.

Consequently, we next investigated whether T cell–dependent IL-12p40 and IL-10 expression was altered in p110δ KD APCs. Splenic CD4+ T cells from WT mice were cultured with either WT or p110δ KD splenic APCs pulsed with CBL. CBL-pulsed p110δ KD APCs cultured with naive WT CD4+ T cells produced decreased levels of IL-10 (Fig. 6E) and increased levels of IL-12p40 (Fig. 6F).
compared with WT APCs. WT and p110\(^{KD}\) APCs cultured with
IL10\(^{−/−}\) CD4\(^{+}\) T cells demonstrate that IL-10 expression is largely
derived from APCs (Fig. 6E). As expected, CBL-pulsed p110\(^{KD}\) APCs also produced significantly less IL-10 (Fig. 6E) and more IL-
12p40 (Fig. 6F) compared with WT APCs in the absence of CD4+
T cells.

Next, to study Ag-specific APC–T cell interactions, splenic
CD4\(^{+}\) T cells from OVA-specific transgenic TCR mice (OT-II
mice) were cocultured with OVA-pulsed and LPS-activated WT
and p110\(^{KD}\) APCs. OVA-loaded p110\(^{KD}\) APCs induced signifi-
cantly more IFN-γ-producing (Fig. 6H, 6I) and IL-17A–producing
(Fig. 6H, 6J) CD4\(^{+}\) T cells compared with OVA-loaded WT
APCs (Fig. 6G, 6I, 6J). However, T cell proliferation was in-
duced to a similar extent by both WT and p110\(^{KD}\) APCs
(Supplemental Fig. 4A–C). These data suggest that cytokine
production by p110\(^{KD}\) APCs directs differentiation of Ag-specific
Th1 and Th17 CD4\(^{+}\) T cells.

These results suggest a model in which defective p1106,
through regulation of IL-10 and IL-12p40, leads to inflammatory effector
T cell development. To test this model in vivo, we generated

FIGURE 6. APC p110\(^{d}\) regulates T cell differentiation.
(A–D) GF WT and p110\(^{KD}\) mice were transferred to
CNV housing. Colonic tissue was collected from WT and
p110\(^{KD}\) mice sacrificed at days 0 (n = 12 and 10, re-
spectively), 7 (n = 5 and 7, respectively), and 14 (n = 6 and
12, respectively) after transfer. Quantitative RT-PCR
was performed in duplicate for Tbx21 (A), Rorc (B), Ifng
(C), and Il17a (D) expression normalized to β-actin
expression. Error bars represent mean ± SEM (*p < 0.05).
(E and F) WT and p110\(^{KD}\) APCs were cultured overnight
with CBL (50 µg/ml) and then cocultured with WT or
IL10\(^{−/−}\) CD4\(^{+}\) T cells at a ratio of 3:2 for 72 h. Supernatants
were collected and assayed for IL-10 (E) and IL-
12p40 (F) production by ELISA. Error bars represent mean ± SEM for three independent experiments (*p < 0.05).
(G–J) WT and p110\(^{KD}\) APCs were stimulated with LPS (10 ng/ml) and OVA peptide (5 mM) overnight
and then cocultured with WT CD4\(^{+}\)CD62L\(^{-}\) OT-II T cells
at a ratio of 3:2 for 72 h. T cells were assayed for IL-17A
and IFN-γ production by flow cytometry. CD4\(^{+}\) lymphocytes were gated using forward and side scatter.
Representative flow cytometry plots show IFN-γ- and IL-
17A–producing WT CD4\(^{+}\) OT-II T cells cocultured with
LPS- and OVA-stimulated WT (G) and p110\(^{KD}\) (H)
APCs. Plots are representative of results from three in-
dependent experiments with similar results. Quantifica-
tion of the percentage of total CD4\(^{+}\) T cells producing
IFN-γ (I) and IL-17A (J) was determined from the flow
cytometry analysis. Error bars represent mean ± SEM
from three independent experiments (*p < 0.05).
**Discussion**

We previously described the development of spontaneously occurring Th1- and Th17-mediated colitis in p110\(\text{KD}\) (9). In the present series of experiments, we further elucidate intestinal host-microbial and APC–T cell interactions mediated by p110. Colitis in p110\(\text{KD}\) mice is dependent on host responses to the enteric microbiota, as has been described in other murine colitis models (26). In the absence of the enteric microbiota, p110\(\text{KD}\) mice did not develop intestinal inflammation, whereas, after reconstitution with commensal enteric microbiota, colons from p110\(\text{KD}\) mice demonstrated histological inflammation, impaired IL-10, and increased IL-12p40 production (Fig. 1). Consequently, altered IL-10 and IL-12p40 production by p110\(\text{KD}\) APCs in response to microbial products and cognate interactions with T cells orchestrates pathogenic adaptive immune responses contributing to intestinal inflammation.

Class I\(_{\text{b}}\) P13Ks regulate macrophage and dendritic cell responses to bacteria (5). Taken together, our results and those of others (21) elucidate a model in which p110 is an intracellular integrator of environmental signals that is involved in the restoration of inflammatory responses to homeostasis, mediated in part by IL-10. Regulation of IL-10 expression involves both PI3K-dependent and inflammatory responses to homeostasis, mediated in part by IL-10.
FIGURE 8. Adoptive transfer of CD4+CD45RB\(^{hi}\) T cells into Rag\(^{1-}\) /p110\(^{KD}\) recipient mice leads to severe colitis. Eight-wk-old Rag\(^{1-}\) \((n = 13)\) and RKO/p110\(^{KD}\) \((n = 14)\) recipient mice were given 4 x 10\(^5\) CD4+CD45RB\(^{hi}\) T cells admixed with 2 x 10\(^{6}\) CD4+CD45RB\(^{low}\) T cells by i.p. injection to induce colitis, as described in Materials and Methods. Mice were assessed for colitis severity at 24 d after adoptive transfer. (A) Clinical disease activity scores were determined, as described in Materials and Methods. Error bars represent mean ± SEM \((\ast p < 0.05)\). (B) (original magnification ×20, H&E) Colon sections from Rag\(^{1-}\) /p110\(^{KD}\) recipients were harvested and taken for histological evaluation. Representative sections are shown. (C) H&E slides of colonic tissue were scored for colitis severity by a pathologist (L.B.B.) blinded to the experimental groups, as described in Materials and Methods. Error bars represent mean ± SEM \((**p < 0.005)\). (D–F) Supernatants from 24-h colonic tissue explants were collected and assayed for IL-10 (D) and IL-12p40 (E) production by ELISA and are expressed as the amount of cytokine (pg/ml) per 50 mg colonic tissue weight. Error bars represent mean ± SEM \((p < 0.05)\). (F) IL-12p40 and IL-10 protein levels from colonic tissue explant culture in individual mice were used to determine the ratio of IL-12p40 to IL-10. Error bars represent mean ± SEM \((**p < 0.005)\). (G and H) MLNs from Rag\(^{1-}\) /p110\(^{KD}\) recipients were analyzed by flow cytometry for intracellular IFN-\(\gamma\) (G) and IL-17A (H) expression in CD3+CD4+ T cells. Each point on the graphs represents MLN cells from one mouse. Error bars represent mean ± SEM \((p < 0.05)\). (I and J) LPMCs were analyzed by flow cytometry for IFN-\(\gamma\) (I) and IL-17A (J) expression in CD3+CD4+ T cells. Each point on the graphs represents pooled LPMCs from three mice. Error bars represent mean ± SEM \((p < 0.05)\). Most colony-stimulating factor-independent LPMCs from Rag\(^{1-}\) /p110\(^{KD}\) recipients were analyzed by flow cytometry to evaluate the ratio of IL-12p40 to IL-10. Error bars represent mean ± SEM \((p < 0.05)\). (K) Rag\(^{1-}\) /p110\(^{KD}\) recipients were analyzed by flow cytometry to evaluate the ratio of IL-12p40 to IL-10. Error bars represent mean ± SEM \((p < 0.05)\). (L) Rag\(^{1-}\) /p110\(^{KD}\) recipients were analyzed by flow cytometry to evaluate the ratio of IL-12p40 to IL-10. Error bars represent mean ± SEM \((p < 0.05)\). (M) Rag\(^{1-}\) /p110\(^{KD}\) recipients were analyzed by flow cytometry to evaluate the ratio of IL-12p40 to IL-10. Error bars represent mean ± SEM \((p < 0.05)\). (N) Rag\(^{1-}\) /p110\(^{KD}\) recipients were analyzed by flow cytometry to evaluate the ratio of IL-12p40 to IL-10. Error bars represent mean ± SEM \((p < 0.05)\).
Thus, p110\(\delta\) is a therapeutic target in IBDs to induce IL-10 production. Indeed, paired connect samples from individual patients. Data were analyzed using a paired \(t\) test (**\(p<0.05\)). Intestinal PIK3CD expression normalized to GAPDH expression from patients with CD was assessed at inflamed sites (\(n=14\)) and compared with noninflamed sites (\(n=14\)) from the same patient. Lines connect samples from individual patients. Data were analyzed using a paired \(t\) test (\(*\ *p<0.05\)).

Interestingly, in the absence of T cells, RKO/\(\delta\) KD mice developed mild histopathologic colonic inflammation. The development of mild colonic inflammation in RKO/\(\delta\) KD mice could be explained by the presence of non–\(\text{hepaticus}\) Helicobacter species in our mouse colony (data not shown). The ability of \(H.\ \text{hepaticus}\) to induce innate immune-driven colonic inflammation in the absence of adaptive immune cells has been well described (42, 43).

Recently, p110\(\delta\) inhibition has been targeted for the treatment of chronic rejection of tissue transplants, systemic lupus erythematosus, and certain lymphoid cell malignancies (10, 11, 44). Although preliminary clinical results are promising, this study highlights a potentially untoward consequence of p110\(\delta\) inhibition—enhanced intestinal and innate inflammatory processes initiated by APCs.

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**Disclosures**

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**References**


