

# Induction and rescue of Nod2-dependent Th1-driven granulomatous inflammation of the ileum

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**Mutations in the NOD2 gene are strong genetic risk factors for ileal Crohn's disease. However, the mechanism by which these mutations predispose to intestinal inflammation remains a subject of controversy. We report that Nod2-deficient mice inoculated with *Helicobacter hepaticus*, an opportunistic pathogenic bacterium, developed granulomatous inflammation of the ileum, characterized by an increased expression of Th1-related genes and inflammatory cytokines. The Peyer's patches and mesenteric lymph nodes were markedly enlarged with expansion of IFN- $\gamma$ -producing CD4 and CD8 T cells. Rip2-deficient mice exhibited a similar phenotype, suggesting that Nod2 function likely depends on the Rip2 kinase in this model. Transferring wild-type bone marrow cells into irradiated Nod2-deficient mice did not rescue the phenotype. However, restoring crypt antimicrobial function of Nod2-deficient mice by transgenic expression of  $\alpha$ -defensin in Paneth cells rescued the Th1 inflammatory phenotype. Therefore, through the regulation of intestinal microbes, Nod2 function in nonhematopoietic cells of the small intestinal crypts is critical for protecting mice from a Th1-driven granulomatous inflammation in the ileum. The model may provide insight into Nod2 function relevant to inflammation of ileal Crohn's disease.**

Crohn's disease | granuloma | *Helicobacter hepaticus* | innate immunity | Paneth cells

Under physiological conditions, reciprocal interactions between the intestinal immune system and commensal microbiota elicit a basal level of immune responses that protect the mucosa from both pathogenic and nonpathogenic bacteria. Changes precipitated by either abnormal microbiota and/or dysregulation of immune responses may disrupt this homeostasis, resulting in mucosal inflammation (1–3). For example, the pathogenesis of intestinal inflammation in Crohn's disease (CD) appears to involve an inappropriate immune response against colonizing microbes (1–3). Mutations in the NOD2 gene were the first defined genetic risk factors identified for CD (4, 5). Nod2 belongs to the NLR family of cytoplasmic proteins and responds to muramyl dipeptide (MDP), a moiety of bacterial peptidoglycan, consisting of N-acetylmuramyl-L-Ala-D-Glu (6, 7). The Rip2 kinase mediates downstream signaling of Nod2, and, upon MDP stimulation, Rip2 activates NF- $\kappa$ B and MAP kinase cascades, resulting in the induction of immune response genes (8–10). Although Rip2-dependent Nod2 function(s) may be fundamentally important, CD penetrance in individuals with either NOD2 homozygous or compound heterozygous mutations is incomplete, indicating that dysregulation of Nod2 signaling alone is insufficient to induce disease (11). Moreover, Nod2-deficient mice do not develop spontaneous intestinal inflammation (10, 12). Therefore, CD pathogenesis is likely to be influenced by additional contributing factors, including the environment, altered immune regulation, and dysbiosis of colonizing microbiota (1–3, 13).

The mechanism by which NOD2 mutations contribute to CD pathogenesis remains a subject of controversy. Three models have

been proposed. The first suggests that a NOD2 “gain-of-function” mutation results in heightened sensitivity to MDP, leading to an increased inflammatory response (14). However, several studies using human patient samples have suggested that CD-associated NOD2 mutations are loss-of-function (13, 15, 16). The second model involves altered TLR2 signaling, proposing an inhibitory role of Nod2 in the TLR2-mediated Th1 responses (17). However, other groups have shown that TLR2 responses are normal in different lines of Nod2-deficient mice, and there may be a synergistic rather than a negative effect on TLR2 stimulation in human and mouse cells (10, 18–21). The third model proposes that mutations in NOD2 may result in altered mucosal host–microbe interactions (13). Nod2 is highly expressed in Paneth cells, epithelial cells of the intestinal crypts of Lieberkühn that govern innate immune responses through the secretion of antibacterial proteins and peptides such as  $\alpha$ -defensins (22–24). CD-associated NOD2 mutations primarily predispose to the development of small intestinal (ileal) lesions, corresponding to the location of Paneth cells (25). Ileal CD is characterized by a decrease of Paneth cell-produced antimicrobial  $\alpha$ -defensins, human  $\alpha$ -defensin-5 (HD5) and  $\alpha$ -defensin-6 (HD6) (26–28). Although reduced expression of  $\alpha$ -defensins was observed regardless of NOD2 genotype, individuals with the common frame-shift mutation NOD2<sup>3020insC</sup> had a more pronounced decrease compared with the other genotypes (26). This decreased expression of  $\alpha$ -defensins reported in ileal CD, whether or not there was an identified mutation in NOD2, was independent of tissue inflammation (26, 28, 29). Moreover, the levels of  $\alpha$ -defensin detected in the ileostomy fluid of CD patients are also lowest in patients with either homozygous or compound heterozygous NOD2 mutations (30). In a murine model, the expression of a subgroup of  $\alpha$ -defensins is reduced in Nod2-deficient mice (10, 31). Indeed, Nod2-deficient small intestinal crypts are unable to kill bacteria efficiently and there are increases of commensal and pathogenic bacteria in the terminal ileum of Nod2-deficient mice (32).

Although the idea that CD may result from abnormal host–microbe interactions is appealing, there is no direct experimental evidence that links loss of Nod2 function in small intestinal crypts with intestinal inflammation. Here, we show that Nod2-deficient mice inoculated with an opportunistic pathogenic bacterium, *Helicobacter hepaticus*, develop Th1-driven granulomatous inflammation of the ileum. Moreover, we find that Rip2-dependent

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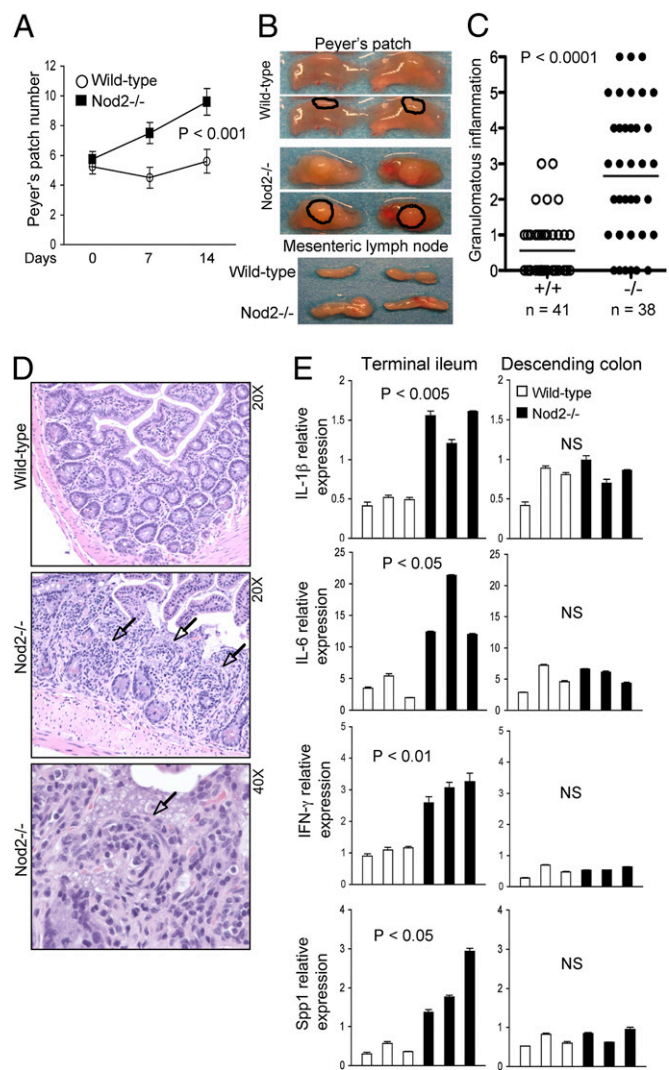
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Nod2 function in nonhematopoietic cells of the ileal crypts is required for protection from the inflammation, and we rescue the Nod2-dependent phenotype by the transgenic expression of HD5, a human Paneth cell  $\alpha$ -defensin. The data provide insight into Nod2 function in a model that may prove relevant to ileal CD.

## Results

***H. hepaticus* Induces Granulomatous Inflammation in *Nod2*-Deficient Mice.** *H. hepaticus*, a Gram-negative microaerophilic bacterium, is a common intestinal commensal bacterium in most animal facilities in the United States. Although *H. hepaticus* may induce colitis in immunodeficient mice such as common gamma-chain (IL-2R $\gamma$ )-deficient mice, it does not cause disease in most strains of wild-type mice, and thus is categorized as an opportunistic pathogen (33). We previously reported that *Nod2*-deficient mice were unable to regulate bacterial load in the ileum after de novo inoculation of *H. hepaticus* (32). This observation prompted us to characterize the mucosal response in this model. Mice were rederived and maintained under specific pathogen free, *Helicobacter*-free conditions until experimental challenge. In response to *H. hepaticus* inoculation, numbers of macroscopically visible Peyer's patches increased significantly at 14 d in *Nod2*-deficient mice in comparison with wild-type mice (Fig. 1A). In addition, the Peyer's patches and mesenteric lymph nodes were increased in size in *Nod2*-deficient mice (Fig. 1B). No gross change in the cecum or colon was observed in either strain. For histological analysis, tissue sections were scored for degree of inflammation and granuloma formation in a blind manner by one pathologist. Interestingly, *H. hepaticus*-inoculated *Nod2*-deficient mice exhibited granulomatous inflammation, which is a hallmark pathological characteristic of human CD (Fig. 1C and D and Fig. S1) (34). In the ileum, there were increased mononuclear cells in lamina propria and the appearance of epithelioid cells in the granulomatous nodules (Fig. 1D). The expression of proinflammatory cytokines IL-1 $\beta$  and IL-6, as well as the Th1 response-related genes IFN- $\gamma$  and *Spp1*, was significantly higher in the *Nod2*-deficient ileum than in that of the wild-type controls (Fig. 1E). In contrast, no differences in the expression of these genes was observed in the descending colon, highlighting a regional specificity for Nod2 function in this model (Fig. 1E). These data indicate that Nod2 is required to elicit an adequate mucosal response against *H. hepaticus* and to avert development of granulomatous inflammation.

***H. hepaticus* Induces Th1 Immune Responses in Peyer's Patches and Mesenteric Lymph Nodes of *Nod2*-Deficient Mice.** We found that inoculation of *H. hepaticus* significantly increased levels of CD69, an activation marker, on CD4 and CD8 T cells, and B cells in the Peyer's patches of *Nod2*-deficient mice but not of wild-type mice (Fig. S2). Because it is known that both CD and intestinal pathology caused by *H. hepaticus* are characterized by Th1 dominant chronic inflammation, we next assessed CD4 and CD8 T cells isolated from Peyer's patches and mesenteric lymph nodes for their expression of IFN- $\gamma$  and IL-4 (35, 36). *H. hepaticus* inoculation resulted in significantly increased IFN- $\gamma$  producing CD4 and CD8 T cells in both Peyer's patches and mesenteric lymph nodes in *Nod2*-deficient but not wild-type mice (Fig. 2A). Expression of Th1-related genes including IFN- $\gamma$ , T-bet (a Th1 specific transcription factor), and IL-12 $\beta$ 2 receptor was significantly higher in the Peyer's patches and mesenteric lymph nodes of *Nod2*-deficient mice (Fig. 2B). In contrast, we could not detect any changes in IL-4 or IL-17 producing CD4 T cells (Fig. 2A and Fig. S3A). Consistent with this finding, *H. hepaticus* inoculation produced no change in the expression of genes associated with other T-helper subsets, including IL-4, IL-17, Gata-3, and Foxp3 (Fig. S3B). These observations suggest that *Nod2*-deficiency renders mice susceptible to *H. hepaticus*-induced Th1 inflammatory responses in Peyer's patches and mesenteric lymph nodes in this

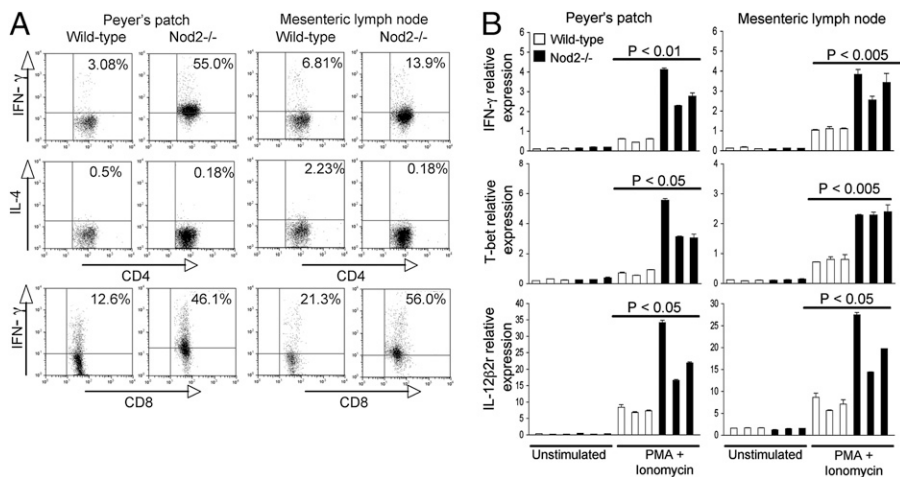


**Fig. 1.** *H. hepaticus* induces enlargement of Peyer's patches, mesenteric lymphadenopathy, and granulomatous inflammation in *Nod2*-deficient mice. (A–E) Age- and sex-matched wild-type and *Nod2*-deficient mice were inoculated with *H. hepaticus* ( $5 \times 10^8$ /mouse) via gastric gavage. (A) Intestines were removed from the mice at d 0 ( $n = 4$ ), 7 ( $n = 2$ ), or 14 ( $n = 10$  for each genotype) postinoculation and the number of macroscopically visible Peyer's patches in the small intestines was counted. The *P* values at day 14 were determined by Student *t* test. (B) Representative pictures of Peyer's patches (outlined) and mesenteric lymph nodes at day 14 postinoculation. (C) Granulomatous inflammation in the ileocecal junction of wild-type ( $n = 41$ ) and *Nod2*-deficient ( $n = 38$ ) mice at day 14 postinoculation was scored in blind manner as described in *Material and Methods*. The *P* values were determined by Student *t* test. (D) Representative pictures of H&E stained terminal ileum tissue at d 14 postinoculation. Granulomas are indicated by arrows. (E) The expression of IL-1 $\beta$ , IL-6, IFN- $\gamma$ , and *Spp1* in the terminal ileum and descending colon was examined by qRT-PCR 14 d postinoculation. Data were normalized to the expression of the  $\beta$ -actin gene. Each bar represents data from a single mouse. The *P* values were determined by Student *t* test. NS: not significant.

model, which is similar to the immune responses found in the intestines of CD patients.

**Rip2 Deficiency Mimics the *Nod2*-Dependent Phenotype.** We recently showed a deficiency in the antimicrobial capacity of ileal crypts of *Rip2*-deficient mice similar to that seen in *Nod2*-deficient mice (32). Therefore, we examined whether the *Rip2*-deficient mice also developed inflammatory responses when challenged with *H. hepaticus*.





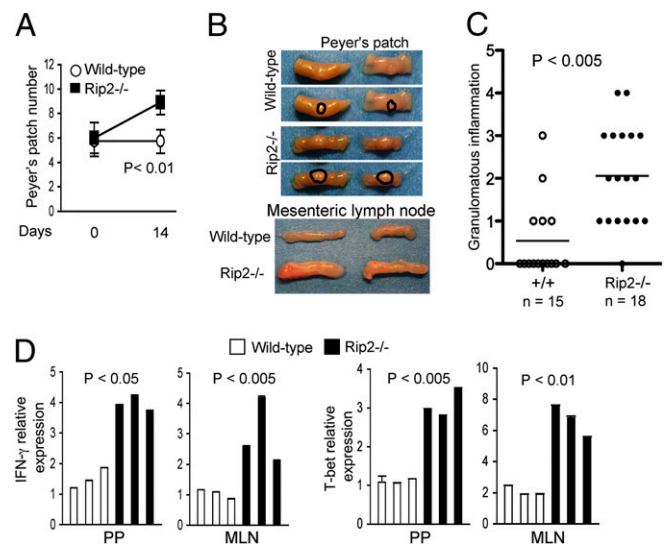
**Fig. 2.** Exaggerated Th1 immune responses in Peyer's patches and mesenteric lymph nodes in *Nod2*-deficient mice (A and B). Age- and sex-matched wild-type and *Nod2*-deficient mice were inoculated with *H. hepaticus* ( $5 \times 10^8$ /mouse) via gastric gavage. Peyer's patch and mesenteric lymph node cells were isolated at d 14 postinoculation and stimulated with PMA and ionomycin for 6 (A) or 3 (B) h. (A) The expression of IFN- $\gamma$  and IL-4 in gated CD4 or CD8 T cells was analyzed by flow cytometry. (B) The expression of IFN- $\gamma$ , T-bet, and IL-12 $\beta$ 2r was examined by qRT-PCR. Data were normalized to the expression of the  $\beta$ -actin gene. Each bar represents replicate data from a single mouse. The *P* values were determined by Student *t* test.

Similar to *Nod2*-deficient mice, *Rip2*-deficient mice inoculated with *H. hepaticus* showed (i) significant increases in the number of macroscopically visible Peyer's patches after 14 d (Fig. 3A), (ii) enlargement of the Peyer's patches and mesenteric lymph nodes (Fig. 3B), and (iii) development of granulomatous inflammation (Fig. 3C). In addition, the expression of both IFN- $\gamma$  and T-bet were also significantly higher in the Peyer's patches and mesenteric lymph nodes, consistent with a Th1 dominated immune responses (Fig. 3D). Finally, similar to *Nod2*-deficient mice, there were no significant changes in the expression of IL-4, Gata-3, IL-17A, or Foxp3 (Fig. S4). Thus, *Rip2* deficiency results in susceptibility to Th1 immune responses in the ileum following *H. hepaticus* inoculation, supporting that the protective functions of *Nod2* in this model are dependent on *Rip2* signaling.

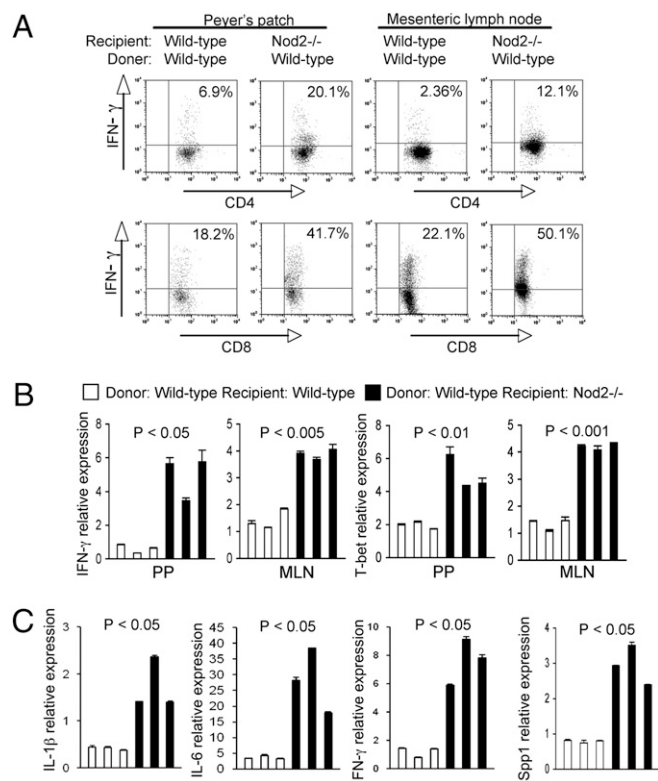
**Adoptive Transfer of Wild-Type Bone Marrow Cells Did Not Rescue the *Nod2*-Dependent Inflammatory Phenotype.** *Nod2* is expressed not only in Paneth cells but also in hematopoietic cells including monocytes, macrophages, and dendritic cells (1, 23, 37). To address whether the protective function of *Nod2* in the ileum is due to its expression in hematopoietic cells, we attempted to rescue the *Nod2*-dependent inflammatory phenotype by reconstituting *Nod2*-deficient mice using adoptive transfer of wild-type bone marrow cells from congenic CD45.1 C57BL/6 (B6.SJL-Ptprc) mice. Six weeks after the bone marrow transfer, efficiency of reconstitution was assessed by analyzing blood cells for the expression of CD45.1 (donors) vs. CD45.2 (recipients). Approximately 95% efficiency of reconstitution was evident in both strains (Fig. S5A). Compared with wild-type recipient mice, *Nod2*-deficient recipient mice again had more IFN- $\gamma$  producing CD4 and CD8 T cells (Fig. 4A), as well as higher expression of IFN- $\gamma$  and T-bet (Fig. 4B), in Peyer's patches and mesenteric lymph nodes following *H. hepaticus* inoculation. The expression of proinflammatory cytokines IL-1 $\beta$  and IL-6, as well as Th1 response-related genes IFN- $\gamma$  and *Spp1*, in the ileum was significantly higher in *Nod2*-deficient mice than in wild-type recipient controls (Fig. 4C). Similar to *Nod2*-deficient mice without bone marrow reconstitution, there were no significant changes in IL-4-producing CD4 T cells (Fig. S5B). Collectively, these results indicate that reconstitution with wild-type bone marrow cells could not rescue the *Nod2*-deficient mice from *H. hepaticus*-induced Th1 immune responses. To determine whether *Nod2*-deficient hematopoietic cells could account for the inflammation, we performed complementary bone marrow cell reconstitution experiments by adoptively transferring CD45.2+ wild-type or *Nod2*-deficient bone marrow cells into CD45.1+ wild-type mice (Fig. S6A). Wild-type recipient mice given *Nod2*<sup>-/-</sup> bone marrow cells showed no signs of inflammation. Nor was there increased expression of IFN- $\gamma$  and t-bet in Peyer's patches and mesenteric lymph node cells or increased

expression of IL-1 $\beta$ , IL-6, IFN- $\gamma$ , and *Spp1* in the ileum (Fig. S6B and C). Taken together, these data suggest that *Nod2* expression in nonhematopoietic cells protects *H. hepaticus*-challenged mice from small intestinal inflammation.

**Restoration of Paneth Cell Antimicrobial Function of *Nod2*-Deficient Mice Rescued the Ileum from Th1 Inflammatory Responses.** Because *Nod2*-deficient mice have impaired clearance of *H. hepaticus* from the ileum (32), defective antimicrobial function of the crypts may underlie the susceptibility of *Nod2*-deficient mice to inflammation in this model. We thus examined whether transgenic expression of



**Fig. 3.** *Rip2*-dependence of Th1 inflammatory responses in *H. hepaticus* challenged mice. (A–C) Age- and sex-matched wild-type and *Rip2*-deficient mice were inoculated with *H. hepaticus* ( $5 \times 10^8$ /mouse) via gastric gavage. (A) Intestines were removed from the mice at days 0 (wild-type,  $n = 4$ ; *Rip2*<sup>-/-</sup>,  $n = 4$ ) or 14 (wild-type,  $n = 8$ ; *Rip2*<sup>-/-</sup>,  $n = 10$ ) postinoculation and number of macroscopically visible Peyer's patches in the small intestine was counted. The *P* value was determined by Student *t* test. (B) Enlarged Peyer's patches (outlined) and mesenteric lymphadenopathy in *Rip2*-deficient mice. Representative pictures at day 14 postinoculation are shown. (C) Granulomatous inflammation in the ileocecal junction of wild-type ( $n = 15$ ) and *Rip2*-deficient ( $n = 18$ ) mice at day 14 postinoculation was scored in a blind manner as described in *Material and Methods*. The *P* values were determined by Student *t* test. (D) Peyer's patch and mesenteric lymph node cells at day 14 were stimulated with PMA and ionomycin for 3 h. The expression of IFN- $\gamma$  and T-bet was examined by qRT-PCR. Each bar represents replicate data from a single mouse. The *P* values were determined by Student *t* test.



**Fig. 4.** Reconstitution of wild-type hematopoietic cells into *Nod2*-deficient mice did not rescue Th1 inflammatory phenotype. (A–C) *H. hepaticus* ( $5 \times 10^8$ /mouse) was inoculated into wild-type and *Nod2*-deficient mice 6 wk after reconstitution with CD45.1 C57BL/6 bone marrow cells. (A and B) Peyer's patch and mesenteric lymph node cells were isolated at day 14 and stimulated with PMA and ionomycin for 6 (A) or 3 (B) h. (A) The expression of IFN- $\gamma$  and IL-4 in gated CD4 or CD8 T cells was analyzed by flow cytometry. (B) The expression of IFN- $\gamma$ , and T-bet examined by qRT-PCR. (C) The expression of IL-1 $\beta$ , IL-6, IFN- $\gamma$ , and Spp1 in the terminal ileal tissue was examined by qRT-PCR. (B and C) Data were normalized by the expression of the  $\beta$ -actin gene. Each bar represents replicate data from a single mouse. The *P* values were determined by Student *t* test.

human Paneth cell  $\alpha$ -defensin 5 (HD5 or DEFA5) in *Nod2*-deficient mice could rescue crypt function and avert development of Th1-driven inflammation in the ileum. Prior studies have demonstrated that HD5-transgenic mice express physiologically relevant levels of HD5 in a Paneth cell-specific manner and can regulate both pathogenic and commensal bacteria in the small intestine (38, 39). HD5-transgenic mice were intercrossed with *Nod2*-deficient mice and the expression of *Nod2* and HD5 in the ileum of littermates with three genotypes *Nod2*<sup>+/-</sup>, *Nod2*<sup>-/-</sup>, and *Nod2*<sup>-/-</sup>/HD5<sup>+</sup> was confirmed by RT-PCR (Fig. 5A). Crypts were isolated from the ileum of littermates with the three genotypes and stimulated with carbamylcholine (CCH) to induce secretion of antimicrobial compounds from Paneth cells. Consistent with our previous data (32), *Nod2*<sup>-/-</sup> crypts failed to induce efficient bacterial killing (Fig. 5B). However, crypts from *Nod2*<sup>-/-</sup>/HD5 transgenic mice showed efficient bacterial killing, which was comparable to wild-type crypts, indicating that transgenic expression of HD5 can successfully restore bacterial killing activity of the ileal crypts from *Nod2*-deficient mice (Fig. 5B). Moreover, the HD5 transgene successfully regulated *H. hepaticus* in vivo because the increased loads of *H. hepaticus* in feces and the terminal ileum of *Nod2*<sup>-/-</sup> mice were reduced in *Nod2*<sup>-/-</sup>/HD5 mice to levels similar to *Nod2*<sup>+/-</sup> control mice (Fig. S7A and B). We then examined the outcome of restored crypt function on *H. hepaticus*-induced Th1-driven inflammation. Consistent with

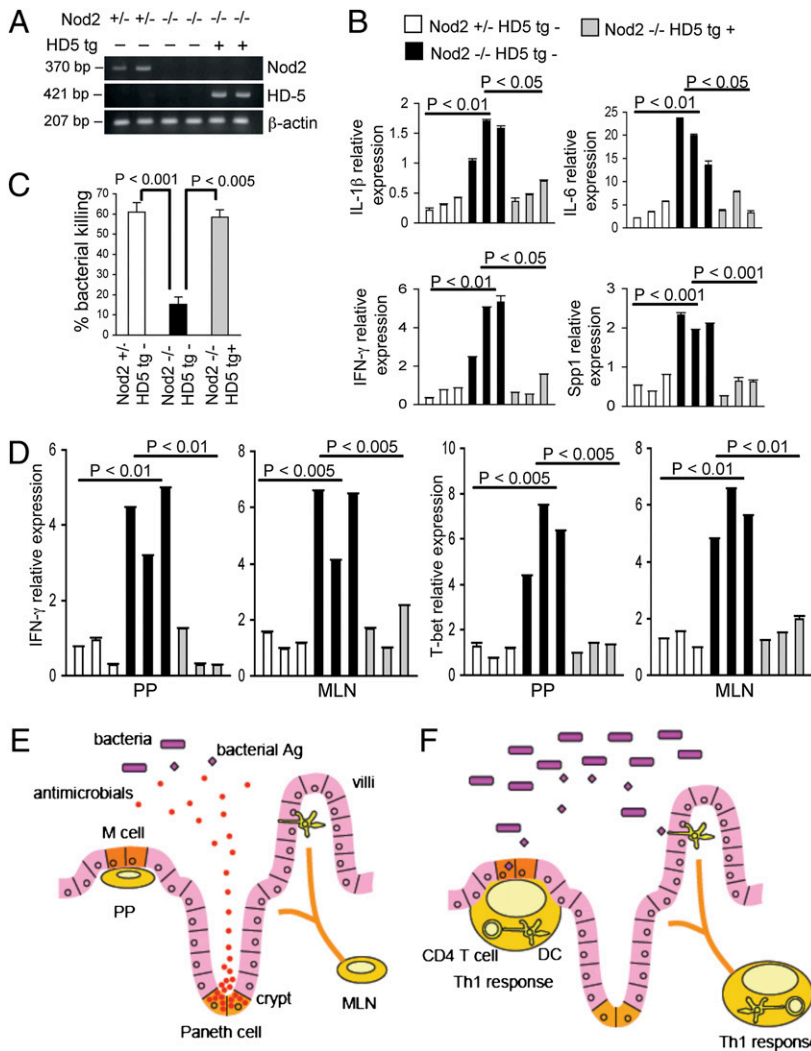
earlier findings (Fig. 1E), the expression of IL-1 $\beta$ , IL-6, IFN- $\gamma$ , and Spp1 in the ileum, and of IFN- $\gamma$  and T-bet in the Peyer's patches and mesenteric lymph nodes, was significantly higher in *Nod2*-deficient (*Nod2*<sup>-/-</sup>) mice than in heterozygous (*Nod2*<sup>+/-</sup>) littermate controls after 14 d (Fig. 5C and D). In contrast, the expression of those genes in crypt-rescued *Nod2*<sup>-/-</sup>/HD5 mice were comparable to both heterozygous (*Nod2*<sup>+/-</sup>) littermate controls (Fig. 5C and D) and wild-type mice (Figs. 1E and 2B). Moreover, blind scoring for granulomatous inflammation of the ileal mucosa showed that *Nod2*<sup>-/-</sup> mice, but not *Nod2*<sup>-/-</sup>/HD5 transgenic mice, had significantly increased inflammation compared with *Nod2*<sup>+/-</sup> controls (Fig. S7C). Together, these data indicate that *H. hepaticus*-induced Th1 inflammatory responses in the ileum are dependent on crypt antimicrobial function and that restoration of the bactericidal activity of small intestinal crypts is sufficient to rescue the phenotype of *Nod2*-deficient mice and to protect them from inflammatory responses in the ileum.

## Discussion

Since the discovery of a genetic association between *NOD2* mutations and CD in 2001 (4, 5), there has been much debate over how *NOD2* mutations lead to disease pathogenesis. Unlike apparent gain-of-function *NOD2* mutations associated with Blau syndrome or early onset sarcoidosis, CD-associated mutations in the *NOD2* gene seem to be loss-of-function, which may likely alter host-microbe interactions through various mechanisms (13). Several studies have attempted to recapitulate CD-like intestinal inflammation using chemical inducers (such as DSS or TNBS) or adoptive transfer of hematopoietic cells in mice with *Nod2* null or frame-shift mutations (14, 40–43). Despite many interesting observations, these mouse models were limited due to the fact that inflammation was induced mainly in the colon, whereas in CD, *NOD2* mutations are mostly associated with ileal inflammation (25). Unlike these previous studies, our current model shares multiple features with *NOD2* mutation-associated CD. First, the inflammation in this model is localized to the ileum. The expression of proinflammatory cytokine genes was increased in the ileum but not in the descending colon in *H. hepaticus* inoculated *Nod2*-deficient mice (Fig. 1E). Second, like CD, our model shows a profound Th1-mediated inflammation with elevated expression of Th1 related genes in the ileal mucosa and increased IFN- $\gamma$  producing CD4 and CD8 T cells in Peyer's patches and mesenteric lymph nodes (Figs. 1E and 2A and B). Third, the inflammation in our model is accompanied with granuloma formation, which is one of pathological hallmarks of human CD (Fig. 1C and D). Fourth, an interplay of intestinal microbiota and genetic susceptibility is important in both human CD and this model (2) because *H. hepaticus* inoculation was required to induce inflammatory responses in *Nod2*-deficient mice. Lastly, both human CD and our model involve Peyer's patches (Fig. 1A and B). Clinical observations suggest that Peyer's patches and M cells are the initial sites of inflammation in ileal CD (44), and significant inflammation of Peyer's patches was evident in this mouse model. Taken together, these observations indicate that our model shares many salient features with ileal CD. Therefore, although *Nod2* is pleiotropic in both expression and function, our model may help discern the physiological function of *Nod2* most relevant to ileal CD.

*Nod2* is expressed in hematopoietic cells including monocytes, macrophages, and dendritic cells (1, 23, 37) as well as in the small intestinal epithelium, with high levels in Paneth cells and lower expression in other epithelial cells (1, 22, 23, 45). In *NOD2*-associated CD pathogenesis, a major debate exists over whether expression in hematopoietic cells or intestinal epithelial cells is most vitally linked to pathology. Our data indicate that Th1 inflammatory responses in *H. hepaticus*-inoculated *Nod2*-deficient mice are associated with the function of *Nod2* in small intestinal crypts rather than in bone marrow-derived cells. Specifically, we





**Fig. 5.** Restoration of ileal crypt function by defensin transgene rescued Th1 inflammatory phenotype in *Nod2*-deficient mice. (A) Generation of *Nod2*<sup>-/-</sup>/HD5 transgenic mice. The expression of *Nod2* and HD5 in the terminal ileum of *Nod2*<sup>+/-</sup>, *Nod2*<sup>-/-</sup>, and *Nod2*<sup>-/-</sup>/HD5 transgenic (HD5 tg) mice was determined by RT-PCR analysis using primers specific for *Nod2* and HD5. Primers for β-actins were used as an internal control. (B) Successful restoration of crypt function in bacterial killing activity by introducing defensin transgene into *Nod2*-deficient mice. Crypts isolated from the terminal ileum of *Nod2*<sup>+/-</sup>, *Nod2*<sup>-/-</sup>, and *Nod2*<sup>-/-</sup>/HD5 tg littermates were stimulated with CCH for 30 min. Secretions were mixed with *E. coli* ( $1 \times 10^3$  cells) and bacterial killing was measured by counting colonies of serial dilutions. (C and D) *Nod2*<sup>+/-</sup>, *Nod2*<sup>-/-</sup>, and *Nod2*<sup>-/-</sup>/HD5 tg littermates were inoculated with *H. hepaticus* ( $5 \times 10^9$ /mouse) via gastric gavage. (C) The expression of IL-1β, IL-6, IFN-γ, and Spp1 in the terminal ilea was examined 14 d postinoculation by qRT-PCR. (D) Peyer's patch and mesenteric lymph node cells at day 14 were stimulated with PMA and ionomycin for 3 h. The expression of IFN-γ and T-bet was examined by qRT-PCR. (C and D) Data were normalized by the expression of the β-actin gene. Each bar represents replicate data from a single mouse. The *P* values were determined by Student *t* test. (E and F) Model of ileal CD. Please see Discussion for details. (E) Normal terminal ileum without *NOD2* mutations. (F) Terminal of ileum with loss-of-function *NOD2* mutations or null mutations, the host-microbiota balance in the ileum shifts, in part due to impaired antimicrobial functions of Paneth cells (Fig. 5F). The resulting changes in composition, surface-association or concentration of bacteria, or bacterial antigens, can overstimulate the mucosal immune system, particularly if the surface epithelium is compromised. This scenario may invoke a tendency for lymphocytes in Peyer's patches and mesenteric lymph nodes to initiate a Th1 immune response, which initially may be insufficient to cause overt mucosal inflammation in most cases and remains subclinical. However, if additional risk factors exist, be they genetic, environmental, dietary, or microbiological, the Th1 immune responses may escalate and the ileum may develop chronic pathological inflammation. Although our animal experimental data supports this disease model, future studies in human CD disease are required to further test the validity of this proposed mechanism.

observed that reconstitution of *Nod2*-deficient mice with wild-type bone marrow cells did not reverse the *H. hepaticus*-induced Th1-driven inflammation (Fig. 4). Conversely, wild-type mice reconstituted with *Nod2*-deficient bone marrows cells were not susceptible to *H. hepaticus*-induced Th1 inflammation (Fig. S6). These observations point to the role of *Nod2* in nonhematopoietic cells as most relevant to the observed phenotype of our model. Impaired antimicrobial function of Paneth cells in *Nod2*-deficient mice was previously reported (10, 31, 32), and here we show restoration of Paneth cell antimicrobial function by transgenic expression of α-defensin HD5 (Fig. 5A and B). Remarkably, restoration of crypt function reversed the Th1 granulomatous inflammation in the ileum (Fig. 5C and D). This rescue by transgenic expression of HD5 further supports the hypothesis that *H. hepaticus*-induced Th1-driven granulomatous inflammation of the ileum depends on *Nod2* function in the small intestinal crypts, most probably in Paneth cells. Moreover, the *Nod2*-mediated preservation of intestinal homeostasis likely involves Rip2 kinase, as *Rip2*-deficient mice exhibited very similar inflammatory responses in this model (Fig. 3). Therefore, the *Nod2*-Rip2 signaling pathway in non-hematopoietic cells appears central to mediating host-microbial interactions in the small intestine through the regulation of ileal crypt function. In humans, although studies indicate that the *NOD2*<sup>3020insC</sup> mutation is linked to reduced α-defensin (26), further studies are needed to establish which cell types—hematopoietic or nonhematopoietic—play the predominant role in *NOD2*-associated inflammatory disease.

We propose the following model of *Nod2* function in the small intestinal mucosa. In mice with functional *Nod2*, Paneth cells in the crypts secrete antimicrobial proteins that regulate mucosa-associated and luminal microbiota (Fig. 5E). Under physiological conditions, only limited immune activation occurs through responses to nonpathogenic bacteria and associated antigens, as detected by epithelial cell receptors, uptake by M cells and/or sampling by transepithelial dendrites of dendritic cells. These responses are host-beneficial and the steady-state level of activation, referred to as “physiological inflammation,” bolsters mucosal protection. In contrast, with *Nod2* loss-of-function or null mutations, the host-microbiota balance in the ileum shifts, in part due to impaired antimicrobial functions of Paneth cells (Fig. 5F). The resulting changes in composition, surface-association or concentration of bacteria, or bacterial antigens, can overstimulate the mucosal immune system, particularly if the surface epithelium is compromised. This scenario may invoke a tendency for lymphocytes in Peyer's patches and mesenteric lymph nodes to initiate a Th1 immune response, which initially may be insufficient to cause overt mucosal inflammation in most cases and remains subclinical. However, if additional risk factors exist, be they genetic, environmental, dietary, or microbiological, the Th1 immune responses may escalate and the ileum may develop chronic pathological inflammation. Although our animal experimental data supports this disease model, future studies in human CD disease are required to further test the validity of this proposed mechanism.

## Materials and Methods

**Mouse Strains and *H. hepaticus* Infection.** C57BL/6 mice were purchased from Taconic Farms. CD45.1 C57BL/6 (B6.SJL-Ptprc) mice were kindly provided by Dr. Shannon Turley (DFCI, Boston, MA). *Nod2*- and *Rip2*-deficient mice (kindly provided by Dr. Richard Flavell, Yale University, New Haven, CT) were backcrossed to C57BL/6 for 12 generations and rederived into specific pathogens-free, *Helicobacter*-free conditions and maintained in isolated barrier units thereafter at Taconic Farms (8, 10). HD5 transgenic mice were established as described (38) and backcrossed to C57BL/6 mice for seven generations. HD5 transgenic mice were rederived into specific-pathogen free, *Helicobacter*-free conditions and intercrossed with *Nod2*-deficient mice to generate *Nod2*<sup>-/-</sup>/HD5 transgenic mice. Culture and inoculation of *H. hepaticus* was performed as described previously (32) and is detailed in *SI Materials and Methods*.

**Histological Scoring of Granulomatous Inflammation.** H&E-stained paraffin sections of intestinal tissue were randomly coded and scored for degrees of granulomatous inflammation in a blind manner by a pathologist (A.M.) as previously described and detailed in *SI Materials and Methods* (46).

**Isolation and Activation of Cells from Peyer's Patch and Mesenteric Lymph Node.** Cells from Peyer's patches and mesenteric lymph nodes were isolated by crushing them between the rough surface of glass slides and passing them through a 40- $\mu$ m cell strainer. The cells were cultured in RPMI-1640 containing 10% FBS, 100 U/mL penicillin, and 00 U/mL streptomycin and activated in the presence of PMA (20 ng/mL) and ionomycin (1  $\mu$ M) or

left untreated for 3 h before isolation of RNA from the cells. For the detection of intracellular cytokines, the cells were stimulated in the presence of 2  $\mu$ M monensin (eBioscience) for 6 h.

**Flow Cytometry.** Antibodies and detailed methods are described in *SI Materials and Methods*. Cells were analyzed by FACSCalibur (Becton Dickinson) followed by analysis using FlowJo software.

**Crypt Isolation and Bacterial Killing Assays.** Crypt assays were performed as described (32) and is detailed in *SI Materials and Methods*.

**Quantitative Real-Time PCR Analysis.** Quantitative real-time PCR (qRT-PCR) analysis was performed as described and is detailed in *SI Materials and Methods* (10).

**Statistical Analysis.** Data were subjected to Student *t* test for analysis of statistical significance, and *P* < 0.05 was considered to be significant.

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