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Cutting Edge: IL-36 Receptor Promotes Resolution of Intestinal Damage

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IL-1 family members are central mediators of host defense. In this article, we show that the novel IL-1 family member IL-36γ was expressed during experimental colitis and human inflammatory bowel disease. Germ-free mice failed to induce IL-36γ in response to dextran sodium sulfate (DSS)-induced damage, suggesting that gut microbiota are involved in its induction. Surprisingly, IL-36R−deficient (Il1rl2−/−) mice exhibited defective recovery following DSS-induced damage and impaired closure of colonic mucosal biopsy wounds, which coincided with impaired neutrophil accumulation in the wound bed. Failure of Il1rl2−/− mice to recover from DSS-induced damage was associated with a profound reduction in IL-22 expression, particularly by colonic neutrophils. Defective recovery of Il1rl2−/− mice could be rescued by an aryl hydrocarbon receptor agonist, which was sufficient to restore IL-22 expression and promote full recovery from DSS-induced damage. These findings implicate the IL-36/IL-36R axis in the resolution of intestinal mucosal wounds. The Journal of Immunology, 2016, 196: 34–38.

Crohn’s disease (CD) and ulcerative colitis (UC), the two major clinical phenotypes of inflammatory bowel disease (IBD), are associated with dysregulated innate and adaptive immune responses toward gut microbiota (1). Members of the IL-1 family of cytokines are upregulated in the inflamed mucosa during experimental colitis and human IBD and contribute to intestinal inflammation (2). Interestingly, however, mice deficient in IL-1β or IL-18, or components of their processing, are more susceptible to dextran sodium sulfate (DSS)-induced colitis (3–6), and polymorphisms leading to decreased Nlrp3 expression in humans are associated with increased risk for developing CD (7). Thus, IL-1 family members may contribute to proinflammatory responses, as well as to resolution of inflammation (2, 8, 9).

Recently, information on the role of IL-36 family members, which are members of the IL-1 superfamily, has begun to emerge (10, 11). However, little data exist about the function of the IL-36/IL-36R axis in the intestine. In this article, we demonstrate that IL-36γ was induced during intestinal injury/inflammation and that IL-36R influenced neutrophil (NP) accumulation, IL-22 production, and repair of intestinal damage following injury. Treatment with an aryl hydrocarbon receptor (AhR) agonist was sufficient to induce intestinal IL-22 expression and promote recovery in Il1rl2−/− mice. Collectively, these findings support a novel contribution of the IL-36/IL-36R axis to the repair of damaged intestinal mucosa.

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Materials and Methods

Mice

Wild-type (WT) C57BL/6 and Rag1−/− mice were from The Jackson Laboratory. Ili12−/− mice were from Amgen. Germ-free (GF) mice were maintained as previously described (12). Protocols were approved by the Georgia State University and Emory University Institutional Animal Care and Use Committees.

Reagents

Abs were from eBioscience, with the exception of CD45, CD103, and CD4 (Becton Dickinson). Dead cells were identified using the Aqua Dead Cell Stain Kit (Invitrogen). Murine IL-36γ was from R&D Systems. ELISAs for IL-36γ (antibodies-online.com) and IL-22, CXCL1, and CXCL2 (eBioscience) were performed following the manufacturers’ instructions.

Isolation of colonic lamina propria cells and flow cytometry

Isolation of colonic lamina propria (cLP) cells, staining, and analyses were performed as described (13). cLP cells were defined as CD45+Ly6G−Ly6C−CD11b−F4/80−CD103− dendritic cells (DCs), Lin−CD90+ROG+NKp46+CD117−CD127− innate lymphoid cells (ILCs), and CD45+CD11b+Ly6C+Ly6G+ cells (NPs).

Microarray analysis

Microarray processing was done by the Vanderbilt Microarray Shared Resource using Murine Genome 4.0 2.0 microarray chips (Affymetrix). The Gene Expression Omnibus accession number is GSE68269 (http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?token=oligmwkanfgldc&acc=GSE68269).

Real-time PCR

RNA isolation and first-strand cDNA synthesis were performed as previously described (13). Primers were as previously described (14), with the exception of mIlf9 (F, 5′-TTGACCTTGAACCACTGGTTGG-3′; R, 5′-GGGTACCTTGCAATGGGAGTAGT-3′) and hIlf9 (F, 5′-GTCTATCGAATCTGAATTACC-3′; R, 5′-ATCTGTGCTCGTCTTTAGCTGCAAT-3′). cDNA from human IBD tissues were obtained in plate arrays (OriGene).

In vitro stimulation

Bone marrow–derived MΦs (1 × 106 cells/ml) were stimulated with TLR agonists for 12 h.

DSS-induced colitis

Mice were provided 3% (w/v) DSS (MP Biomedicals) in the drinking water for 5 d and then switched to normal drinking water for recovery. Daily clinical assessment of DSS-treated animals was performed as described previously (13).

CD4+CD45RBhi-induced colitis

Purified WT CD4+CD45RBhi-T cells (4 × 106) were infected i.p. into Rag1−/− recipients. Colonies were harvested when clinical signs of chronic colitis were evident (4 wk).

Helicobacter hepaticus–induced colitis

H. hepaticus (1 × 109 CFU strain 51449; American Type Culture Collection) was gavaged to mice on days 0, 2, and 4. Mice also received 1 mg anti–IL-10R (Bio X Cell; 1B1.2) Ab via i.p. injection on days 0, 7, 14, and 21 after H. hepaticus infection (15).

Wound-healing assays

Mucosal wound-healing assays were performed as previously described (16).

In vivo AbR treatment

6-Formylindolindole (3, 2-h) carbazole (FICZ; Enzo Life Sciences; 1 μg/mouse) was injected i.p. on day 3 of DSS treatment for 5 d.

Histology

Colon sections were fixed in 10% formalin. Paraffin embedding, sectioning, H&E staining, and slide scanning was performed at Emory’s Winship Cancer Institute-Pathology Core.

Statistical analyses

Statistical analyses were performed using the unpaired Student t test or one-way ANOVA.

Results and Discussion

IL-36γ is expressed during experimental colitis and human IBD

Resident MΦs (Cx3cr1hiLyt6C−) are abundant in the healthy cLP, whereas a distinct subset of Cx3cr1low/intLyt6C− cells, which are predominantly inflammatory MΦs, infiltrates the colon after DSS treatment (17) (Supplemental Fig. 1A). To identify genes that are preferentially expressed by these inflammatory MΦs, we conducted microarray analysis between FACS-sorted CD45+IAb+CD11b+F4/80+ cLP MΦs isolated from healthy mice (>80% Cx3cr1hiLyt6C− “resident”) or mice treated for 5 d with DSS (>50% Cx3cr1hiLyt6C− “infiltrating”). Using hierarchical clustering, 820 genes were differentially expressed >2-fold (log2 scale) between cLP MΦs isolated from healthy control or inflamed (DSS) colon (Supplemental Fig. 1B, middle panel). Among these genes, the gene ontology processes enriched by DAVID showed “Immune Response” as the top-ranked process. Of the 62 genes in this category, the top 10 (fold change) are shown. Interestingly, the novel IL-1 family member Il1f9 (renamed IL-36γ) was the top-ranked gene that was most preferentially expressed by cLP MΦs isolated from DSS-treated mice (5.4-fold increase log2 scale), whereas other members of the IL-1 family only showed modest increases or remained unchanged (data not shown). Validation of these observations by quantitative PCR confirmed that IL-36γ mRNA, but not IL-36α or IL-36β mRNA, was highly expressed in the inflamed colon of DSS-treated mice (Fig. 1A); correspondingly, protein levels were also increased as detected by Western blot and ELISA (Fig. 1B). This increased IL-36γ expression (~5-fold) in the inflamed colon following DSS treatment was recapitulated in additional models of colitis, including the CD45RBhi transfer model (~13-fold) and the H. hepaticus model (15) (~5-fold) (Fig. 1C). Importantly, IL-36γ mRNA expression was also increased in the human colonic mucosa from individuals with IBD compared with healthy controls, and no significant differences were noted between UC and CD samples (Fig. 1D).

To investigate cellular sources of IL-36γ in the inflamed intestine, IL-36γ mRNA expression was analyzed among cLP DCs, MΦs, intestinal epithelial lymphocytes (IELs), and intestinal epithelial cells (IECs). cLP MΦs and IECs expressed ~600- and ~85-fold higher levels of IL-36γ, respectively, compared with DCs or IELs (Fig. 1E). Because DSS treatment disrupts the epithelial barrier and exposes immune cells to microbes, the role of microbiota in IL-36γ induction was explored. Conventionally housed (CVN) or GF mice were treated with DSS for 5 d, and IL-36γ mRNA expression was assessed. As shown in Fig. 1F, colonic tissue from GF mice expressed ~25-fold lower levels of IL-36γ mRNA than did CNV mice. Consistent with this observation, stimulation of bone marrow–derived MΦs with LPS or CpG significantly induced IL-36γ mRNA expression (Supplemental Fig. 1C).

IL-36R contributes to colonic wound healing

To evaluate the biological functions of IL-36γ in vivo, Ili12−/− mice were treated with DSS for 5 d, and the se-
verity of colonic inflammation was assessed. Consistent with a proinflammatory role for the IL-36 pathway (10), we observed modestly decreased disease activity index (DAI) in Il1rl2<sup>−/−</sup> mice compared with WT (Il1rl2<sup>+/+</sup>) mice as early as day 1 of DSS treatment, which persisted until day 5 (Fig. 2A). To evaluate recovery and repair from acute mucosal injury, DSS was replaced with normal water at day 5, and a progressive increase in the DAI for Il1rl2<sup>−/−</sup> mice was observed, which eventually matched that of Il1rl2<sup>+/+</sup> mice on day 7 (Fig. 2A). Although Il1rl2<sup>−/−</sup> mice eventually recovered from colitis, the DAI of Il1rl2<sup>−/−</sup> mice continued to increase until they had to be euthanized because they were moribund and met humane endpoint criteria. Examination of Il1rl2<sup>−/−</sup> colons at sacrifice revealed significant shortening compared with Il1rl2<sup>+/+</sup> colons (Fig. 2B). Additionally, histological analyses of Il1rl2<sup>−/−</sup> colons showed significantly enhanced mucosal damage/inflammation compared with Il1rl2<sup>+/+</sup> colons (Fig. 2C, 2D). Because Il1rl2<sup>−/−</sup> mice failed to recover from DSS-induced colitis, the role of IL-36R in colonic wound recovery was further examined by mechanically generating mucosal wounds using an endoscope equipped with biopsy forceps. Images captured from the wound sites were used to quantify colonic mucosal wound healing at 2 and 4 d postinjury (Fig. 2E). Analogous to the defective repair observed with acute DSS treatment, Il1rl2<sup>−/−</sup> mice showed a significant delay in wound healing (35.1% wound closure compared with 51.7% in Il1rl2<sup>+/+</sup> mice, Fig. 2F). Interestingly, impaired wound healing in Il1rl2<sup>−/−</sup> mice correlated with a significant reduction in NΦ accumulation in the wound bed (Supplemental Fig. 2A, 2B). Because NΦs can aid in wound repair (18), these cells were examined in the wound beds of Il1rl2<sup>+/+</sup> and Il1rl2<sup>−/−</sup> mice following mucosal biopsy. As shown in Supplemental Fig. 2A and Supplemental Fig. 2B, wound beds in Il1rl2<sup>−/−</sup> mice exhibited a significant reduction in NΦ accumulation compared with Il1rl2<sup>+/+</sup> mice. Consistent with these observations, treatment of colonic explants or IEC cultures with IL-36<sup>G</sup> significantly induced expression of the NΦ chemokines CXCL1 and CXCL2 (Supplemental Fig. 2C, 2D). These data were also supported by evidence showing that IECs constitutively expressed Il1rl2 mRNA during the steady-state and following treatment of mice with DSS (data not shown). Collectively, these results suggest an important role for IL-36G in promoting wound healing of damaged intestinal mucosa.

**IL-36R contributes to DSS-induced IL-22 production**

IL-22 is a barrier-protective cytokine that stimulates epithelial proliferation and restitution, the secretion of antimicrobial peptides, and protection from intestinal inflammation (19). Because Il1rl2<sup>−/−</sup> mice displayed impaired recovery from DSS-induced damage, the role of IL-36R in IL-22–mediated intestinal barrier protection was investigated. Interestingly, upon DSS treatment, IL-36γ expression preceded that of IL-22, with IL-36γ peaking on day 3, followed by IL-22 beginning on day 4 and peaking on day 5 (Fig. 3A). These data suggested that IL-36γ may regulate IL-22 production following DSS-

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**FIGURE 1. IL-36γ is expressed during experimental colitis and human IBD.** (A) IL-36α, IL-36β, and IL-36γ mRNA expression in colons of WT mice treated with DSS for 5 d. (B) ELISA and Western blot analyses of IL-36γ in colons of WT mice treated as in (A). (C) IL-36γ mRNA expression in colonic tissue from healthy controls, DSS (5 d), CD45RB<sup>hi</sup>, and H. hepaticus models of colitis. (D) IL-36γ mRNA expression in healthy controls, IBD, UC, or CD human mucosa samples. (E) IL-36γ mRNA expression from cLP DCs, MΦs, IELs, and IECs from WT mice treated as in (A). (F) IL-36γ mRNA expression in colons of WT mice housed under CNV or GF conditions and treated as in (A). Data are representative of two or three independent experiments with four or five mice/group. *p < 0.05.

**FIGURE 2. IL-36R contributes to colonic wound healing.** (A) DAI of Il1rl2<sup>+/+</sup> and Il1rl2<sup>−/−</sup> mice treated for 5 d with DSS, followed by normal water for 8 d. (B) Image and length of Il1rl2<sup>+/+</sup> and Il1rl2<sup>−/−</sup> colons from mice, treated as in (A), at 13 d. H&E staining (C) and histology scoring (D) of colon sections from Il1rl2<sup>+/+</sup> and Il1rl2<sup>−/−</sup> mice, treated as in (A), at 13 d. Endoscopic images at 2 and 4 d (E) and quantification at 4 d of wound repair (F) in Il1rl2<sup>+/+</sup> and Il1rl2<sup>−/−</sup> mice after biopsy-induced injury. Arrows indicate the wound bed. Data are representative of three independent experiments with five mice/group. *p < 0.05.
induced damage. Therefore, IL-22 expression in the colon of Il1r2+/+ and Il1r2−/− mice following DSS treatment was quantitated. After 5 d of DSS treatment, Il1r2−/− mice had significantly reduced IL-22 protein expression compared with Il1r2+/+ mice (Fig. 3B). IL-22 protein expression in Il1r2−/− colons returned to baseline by day 8, because these mice repaired intestinal damage, whereas Il1r2−/− mice failed to induce IL-22 at day 8, because intestinal damage progressed. Interestingly, robust IL-22 expression in Il1r2−/− colons following DSS was abolished in GF mice, similar to IL-36γ expression (data not shown). These data demonstrate that the IL-36 pathway is involved in DSS-induced IL-22 expression.

In the DSS model, IL-22–producing NΦs provide a major contribution to the resolution of colonic injury (14). Thus, we explored whether there are defects in IL-22–producing NΦs following DSS treatment in the absence of IL-36R. Indeed, a significant decrease in IL-22 production by NΦs from Il1r2−/− mice was observed compared with Il1r2+/+ mice with regard to frequency (Fig. 3C) and absolute cell number (Fig. 3D), whereas T cells and ILCs did not exhibit significant differences. These data are consistent with the observations of Zindl et al. (14), showing that IL-22–producing NΦs are important contributors to the resolution of DSS-induced colonic damage and suggest that IL-36R is involved in the differentiation of this important cell type. Of note, very low levels of IL-22 were detected in Il1r2−/− and Il1r2−/− wound beds following mucosal biopsy (data not shown), suggesting that the extent and type of injury dictate whether the IL-36 pathway may predominantly control NΦ recruitment and/or differentiation into IL-22 producers.

**FICZ induces IL-22 and resolution of colonic damage in Il1r2−/− mice**

Because IL-22–producing NΦs were significantly reduced in colons of DSS-treated Il1r2−/− mice (Fig. 3C, 3D), we next investigated whether boosting IL-22 production from other cellular sources in vivo could complement this defect. The AhR pathway was shown to induce IL-22 production from CD4+ T cells and ILC3s in the intestine (20, 21); therefore, we treated Il1r2−/− mice with the AhR agonist FICZ during the course of DSS treatment beginning at day 3. Although Il1r2−/− mice failed to recover from DSS-induced intestinal mucosal damage and had to be euthanized, consistent with Fig. 2A and 2B, FICZ-treated Il1r2−/− mice showed a significant reduction in DAI (Fig. 4A) and histological damage (Fig. 4B, 4C) and were able to fully recover from intestinal damage, similar to Il1r2+/+ mice or Il1r2−/+ mice treated with FICZ. Importantly, FICZ treatment enhanced IL-22 mRNA expression in Il1r2−/− mice during DSS-induced damage (Fig. 4D); however, we do not exclude the possibility that FICZ mediated protective effects independent of IL-22 induction.

Collectively, these data implicate the IL-36/IL-36R axis in the repair of intestinal mucosal wounds. Although the IL-36 pathway plays a pathogenic role in chronic psoriatic disorders (10), it is beneficial during acute intestinal damage. NΦs may play a central role in IL-36–mediated resolution of intestinal damage by phagocytosing and killing bacteria and/or producing IL-22 and other proresolving factors (22) that contribute to epithelial barrier repair and control of inflammation. Future insight into the functions of the IL-36 pathway during acute and chronic mucosal inflammation may contribute to the development of novel therapeutic strategies aimed at manipulating this cytokine axis.

**Disclosures**

J.E.T. was an employee at Amgen during the time of the studies and owns Amgen stock. The other authors have no financial conflicts of interest.

**References**


