

FIGURE 1: ATP is released from necrotic and apoptotic cells as extracellular ATP (eATP). Also, adenylate kinase and synthase mediate the generation of ATP in the extracellular compartment. Extracellular purines (e.g., ATP and ADP) stimulate their receptors and modulate various biological processes. Once eATP is released, the ATP is soon hydrolyzed to AMP and adenosine by the ectonucleotidases CD39 and CD73. Adenosine binds to adenosine receptors (e.g., A_1 , A_{2A} , A_{2B} , and A_3).

responses [30]. Th2-type immune responses are also induced by dendritic cells expressing $P2X_7$. Indeed, depletion of eATP by apyrase treatment or $P2X_7$ deficiency reduces signs of inflammation in the upper respiratory tract [31]. It was recently found that the functional capacity of $P2X_7$ (i.e., its ability to promote pore formation) is associated with asthma risk or disease severity in humans [32]. Moreover, *in vivo* imaging analysis has revealed eATP release in the intestinal compartment and peritoneal cavity of mice with acute graft-versus-host disease (GVHD) [33]. Treatment with apyrase or with inhibitors of various purinergic receptors inhibits GVHD-associated intestinal inflammation. In this case, the eATP- $P2X_7$ pathway activates dendritic cells and consequently induces Th1 immune responses (e.g., $IFN\gamma$ production) and expansion of donor T cells, thus contributing to the onset of inflammation.

Several studies have revealed the pathologic roles of eATP and purinergic receptors (especially $P2X_7$) in the development of intestinal disorders, including irritable bowel syndrome (IBS) and inflammatory bowel disease (IBD) [1, 34] (Table 1). IBS is a common gastrointestinal disorder characterized by discomfort, chronic abdominal pain, and altered bowel habit. Sometimes it occurs after intestinal infection. One meta-analysis has demonstrated that the risk of IBS increases 600% after gastrointestinal infection [35]. Consistently, it has been reported that transient intestinal infection with *Trichinella spiralis* in mice causes postinflammatory visceral hypersensitivity, which is associated with $IL-1\beta$ production mediated by eATP- $P2X_7$ pathways [34] (Table 1). Because mast cells are considered to play a critical role in the development of IBS and express high levels of $P2X_7$, it is possible that the eATP- $P2X_7$ pathway in mast cells is involved in the development of IBS [36].

The eATP-purinergic receptor pathway, especially the eATP- $P2X_7$ pathway, is also involved in the development of IBD. Overexpression of $P2X_7$ receptors has been observed in the intestinal mucosa of patients with IBD—especially Crohn's disease [44]. Experimentally, $P2X_7$ -deficient mice do not develop experimental colitis, and inhibition of $P2X_7$ by A-740003, Brilliant Blue G, or KN-62 ameliorates experimental colitis by reducing the recruitment of neutrophils, T cells, and macrophages, as well as collagen deposition [44] (Table 1). The eATP- $P2X_7$ pathway is therefore now considered to be a novel therapeutic target in the treatment of IBD [43, 44] (Table 1).

Several mechanisms of eATP-mediated inflammation in the development of IBD have been proposed. First, eATP from damaged intestinal epithelial cells, which are frequently observed in IBD patients, and inflammatory cells (e.g., neutrophils and macrophages) stimulates dendritic cells to produce IL-6, IL-12, and IL-23 and $TGF\beta$, thus inducing the production of inflammatory Th1 and Th17 cells [42, 43] (Figure 2) (Table 1). Enteric neuronal cell death is frequently observed in intestinal inflammation and causes colonic motor dysfunction. The eATP- $P2X_7$ pathway is involved in enteric neuronal cell death through the pannexin-inflammasome cascade, and thus colonic motor dysfunction during colitis is prevented by targeting these pathways [41] (Table 1). We previously established mast cell-specific antibody libraries and showed that $P2X_7$ is expressed at high levels in mast cells in the colonic tissues [40]. eATP stimulates mast cells to induce the production of inflammatory chemokines (e.g., CCL2, CCL4, CCL7, CXCL1, and CXCL2), cytokines ($IL-1\beta$, IL-6, and $TNF\alpha$), and mediators (histamines and leukotriene). Thus, blockade of $P2X_7$ by a specific antibody (1F11 monoclonal antibody) inhibits mast cell activation in the colonic

TABLE 1: Recent reports indicating the critical roles of eATP in the adverse conditions of intestines (inflammatory bowel diseases and irritable bowel syndrome).

Enteric diseases	Receptors	Functions	Reference
Inflammatory bowel disease	P2R/A2BR	Enhance co-transmigration of neutrophils and platelets across intestinal epithelial cells in IBD patients. Platelets release large amount of ATP in the lumen metabolite to adenosine via CD73 and ecto-NTPDases expressed in epithelial cells. Adenosine-A2BR pathway induces electrogenic Cl ⁻ secretion with water movement to lumen.	[37]
	P2XR	T cell receptor stimulation induces ATP synthesis and release from activated T cells through pannexin-1 hemichannels. Released ATP activates T cells and produce IL-2 and proliferation in autocrine manner. Blockage of P2X receptors (oxidative ATP) impairs the development of colitis in mice.	[38]
	P2R	ATP released from commensal bacteria acts on CD70+ CD11c+ cells reside in the intestinal lamuna propria and induces Th17 cells in mice; degradation of ATP (by apyrase treatments) ameliorates colitis in mice.	[9]
	P2Y2	Increase of P2Y2 expression in epithelial cells is observed during colitis. P2Y2 stimulation induces release of prostaglandin E2 release from the cells and promotion of intestinal microtubule stabilization and mucosal reepithelization. Those pathways take part in the wound healing during colonic inflammation. Treatment with P2Y2 agonist improves recovery from colitis in mice.	[39]
	P2X7	ATP induces activation of mast cells and enhances inflammatory responses, upregulation of P2X7 in mast cells of Crohn's disease patients, anti-P2X7 antibody treatment inhibits colitis in mice.	[40]
	P2X7	Induction of enteric neuronal cell death and alteration of intestinal motility.	[41]
	P2R	ATP induces IL-6 and CXCL1 productions from epithelial cells; ATP influences the response of epithelial cells to various TLR ligands and induces inflammatory T cells by affecting DC maturations.	[42]
	P2X7	Prophylactic systemic P2X7 blockade (A740003 and brilliant blue G) reduces inflammatory cytokines in rats.	[43]
	P2X7	Upregulation of P2X7 in epithelium, macrophage, and dendritic cells of Crohn's disease patients, P2X7-deficient mice did not develop colitis.	[44]
Irritable bowel syndrome	P2X7	Induction of IL-1 β and the development of postinflammatory visceral hypersensitivity in the <i>Trichinella spiralis</i> -infected mouse	[34]

tissues and consequently prevents the development of intestinal inflammation [40] (Table 1). In this pathway, P2X₇ expression on mast cells is important for the development of colitis, because mast cell-deficient mice reconstituted with P2X₇-deficient mast cells show amelioration of inflammatory signs. Of clinical relevance, we have found that the number of P2X₇⁺ mast cells is increased at sites of inflammation in Crohn's disease patients [40]. eATP is produced by injured epithelial cells and inflammatory cells, including neutrophils, via gap junction molecules such as connexin 43 [45]. It was reported that P2Y2 and P2X7 receptors are important for the migration of neutrophils and macrophages. In the

inflammatory condition, neutrophils transmigrated between epithelial cells to the luminal part of the intestine. In this condition, platelets translocate along with neutrophils and released eATP at the mucosal surface (Figure 2) (Table 1). Additionally, mast cells express ectoadenylate kinase and ATP synthase to mediate the extracellular conversion of ADP to ATP, which in turn promotes mast cell activation in an autocrine and paracrine manner (Figure 2). We have recently found that, in contrast to the abundance of P2X₇ expression on mast cells in the colon, there are limited levels of P2X₇ expression on skin mast cells, which is regulated by skin fibroblasts [46]. Skin fibroblasts uniquely express Cyp26b1 to

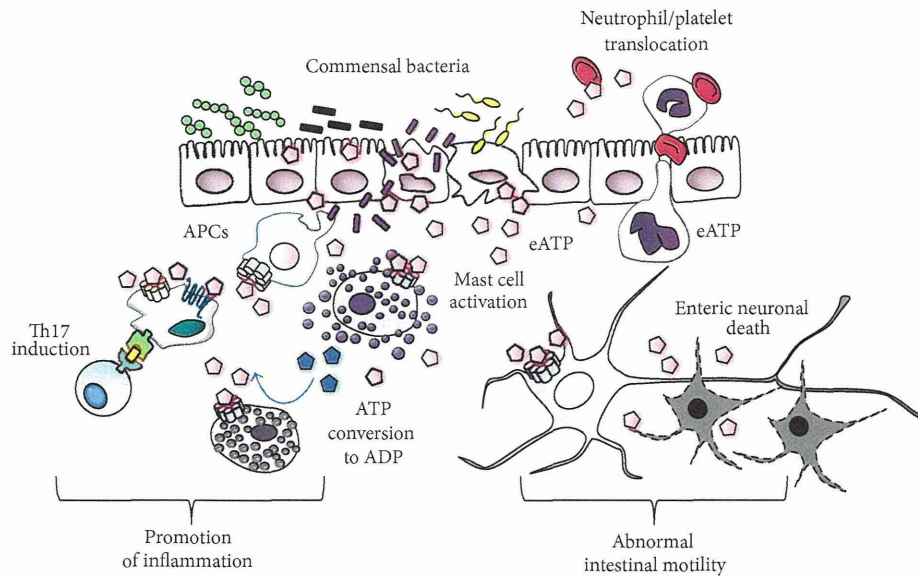


FIGURE 2: In the intestinal compartment, extracellular ATP (eATP) is released from damaged epithelial cells and commensal bacteria. Macrophages, platelets, mast cells, and neutrophils are potential source of eATP upon their activation. Neutrophils facilitate translocation of platelets across intestinal epithelium. eATP also induces Th17 cell generation, activation of mast cells, and neuronal cell death, promoting intestinal inflammation. APCs: antigen-presenting cells. eATP stimulates mast cells to induce the production of inflammatory chemokines (e.g., CCL2, CCL4, CCL7, CXCL1, and CXCL2), cytokines (IL-1 β , IL-6, and TNF α), and mediators (histamines and leukotrienes).

degrade retinoic acid within tissues or microenvironments; Cyp26b1 is responsible for inhibiting P2X₇ expression [46]. Thus, unique tissue environments determine P2X₇ expression on mast cells, which is a critical factor in the development of local inflammation.

4. Resolution of eATP-Mediated Inflammation for Maintenance of Mucosal Homeostasis

Once eATP is released, it is soon hydrolyzed to ADP, AMP, and adenosine by the ectonucleotidases CD39 and CD73; this is essential for resolving inflammatory responses (Figure 1). Indeed, CD39-deficient mice, as well as humans who have CD39 polymorphism and thus low levels of CD39 expression, have increased susceptibility to IBD [47]. Similarly, CD73 deficiency or administration of CD73 inhibitor (e.g., α , β -methylene ADP) enhances susceptibility to intestinal inflammation in mice [48–50].

Adenosine, which is derived from the dephosphorylation of eATP via CD39 and CD73 or diffuses directly from the intracellular compartment via equilibrative nucleoside transporters, binds to adenosine receptors such as A_{2A} and A₃ receptors, which are involved in both the promotion and the resolution of inflammatory responses [51–53]. A_{2A} and A₃ receptor expression on T cells and myeloid cells is a prerequisite for the inhibition of intestinal inflammation [54]. In fact, A_{2A} and A₃ adenosine receptor-selective agonists (e.g., ATP-146e and IB-MECA, resp.) ameliorate intestinal inflammation by impairing the recruitment of inflammatory cells and the production of inflammatory cytokines [55, 56].

In addition, cyclosporine, salicylates, methotrexate, and sulfasalazine, which are used to treat IBD in humans, all decrease eATP levels and increase adenosine production, partly via the stimulation of CD73-dependent adenosine production [57]. Similarly, upregulation of CD39 expression induced on dendritic cells by IL-27 hampers Th1 and Th17 cell production and consequently prevents eATP-mediated inflammation [58]. All of this evidence indicates that inhibition of eATP signaling, together with the promotion of adenosine-mediated regulatory pathways by targeting receptors or ectoenzymes, would be a beneficial strategy for the treatment of intestinal inflammation.

5. Closing Remarks

The importance of purinergic signaling was recognized almost 70 years ago. Accumulating evidence has since revealed the underlying molecular and cellular mechanisms of purinergic signal-mediated maintenance and disruption of mucosal homeostasis. Currently, the clinical relevance of some of the drugs used to treat intestinal inflammation is explained by their regulation of eATP-adenosine balance. Additionally, drugs that target purinergic receptors have now undergone clinical trials [11]. Notably, ATP-adenosine balance, as well as receptor expression levels and the cells expressing these receptors, differs among tissues and environmental conditions. Further investigations using new technologies such as *in vivo* monitoring of eATP release [59, 60] will clarify the complex mechanisms of purinergic signal-mediated immune regulation. This in turn will provide further advances in the design of drugs for preventing and

treating inflammatory diseases and maintaining immunologic health.

Conflict of Interests

The authors declare that there is no conflict of interests regarding the publication of this paper.

Acknowledgments

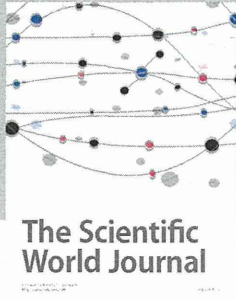
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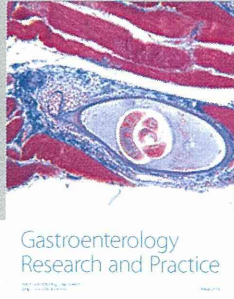
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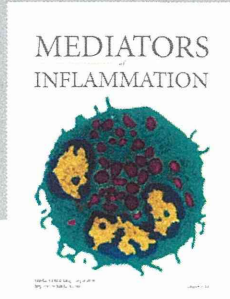
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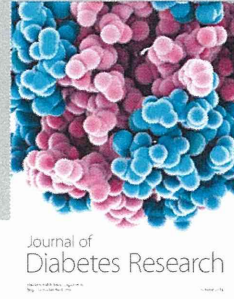
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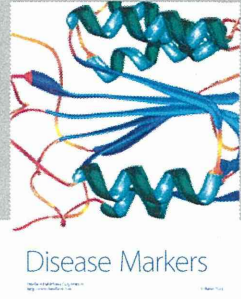
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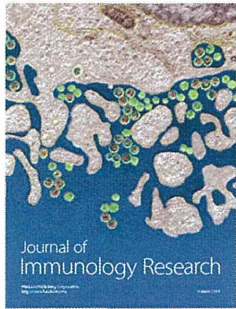
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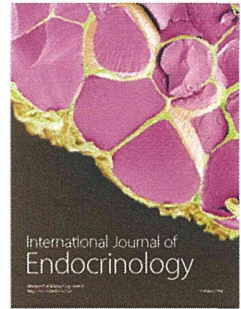
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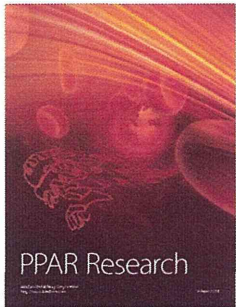
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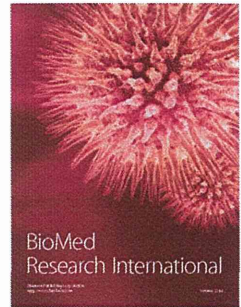
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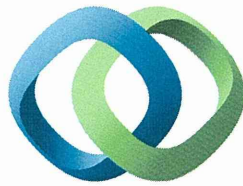
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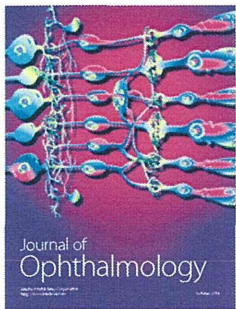


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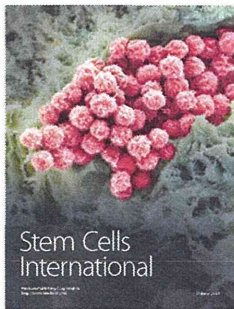


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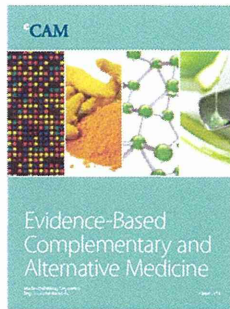
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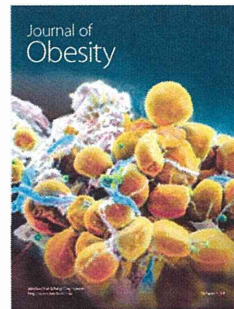
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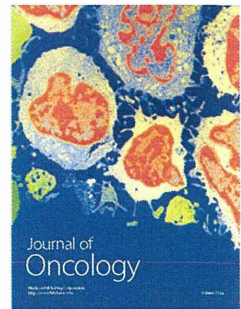
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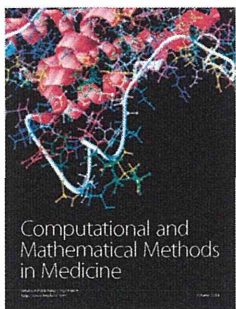
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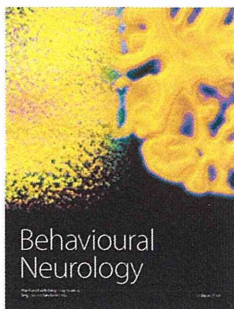
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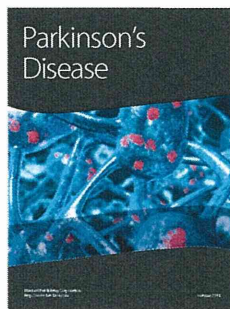
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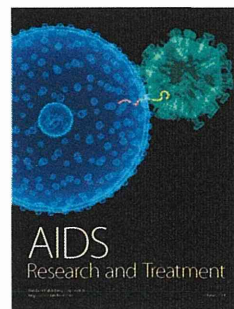
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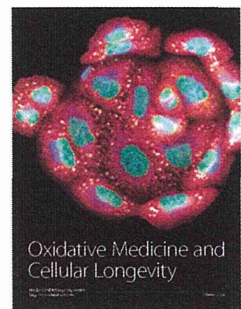
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RESEARCH ARTICLE

MUCOSAL IMMUNOLOGY

Innate lymphoid cells regulate intestinal epithelial cell glycosylation

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Fucosylation of intestinal epithelial cells, catalyzed by fucosyltransferase 2 (Fut2), is a major glycosylation mechanism of host–microbiota symbiosis. Commensal bacteria induce epithelial fucosylation, and epithelial fucose is used as a dietary carbohydrate by many of these bacteria. However, the molecular and cellular mechanisms that regulate the induction of epithelial fucosylation are unknown. Here, we show that type 3 innate lymphoid cells (ILC3) induced intestinal epithelial *Fut2* expression and fucosylation in mice. This induction required the cytokines interleukin-22 and lymphotoxin in a commensal bacteria–dependent and –independent manner, respectively. Disruption of intestinal fucosylation led to increased susceptibility to infection by *Salmonella typhimurium*. Our data reveal a role for ILC3 in shaping the gut microenvironment through the regulation of epithelial glycosylation.

In the gastrointestinal tract, bilateral regulation between the gut microbiota and the host creates a mutually beneficial environment. The intestinal epithelium is a physical barrier that separates the environments inside and

outside the mucosal surface. Intestinal epithelial cells (ECs) are the first line of defense against foreign antigens, including those from commensal and pathogenic bacteria. ECs play key roles in initiating and maintaining an immunologically appropriate and balanced environment in reaction to constant foreign stimulation (1). Resident commensal bacteria support the development of this functional mucosal immune system, and in turn, mucosal immune cells control the homeostasis of the gut microbiota and protect against pathogenic bacterial infection through intestinal ECs. In particular, type 3 innate lymphoid cells (ILC3) produce interleukin-22 (IL-22), which not only regulates the homeostasis of the commensal microbiota but also protects against *Citrobacter rodentium* infection, presumably by inducing EC-derived antimicrobial molecules such as RegIIIγ (2–5).

Fucosylated carbohydrate moieties expressed on intestinal ECs are involved in the creation of an environmental niche for commensal bacteria in mice and humans (6–10). Fucosylated glycans are generated by the addition of an L-fucose residue via an α1-2 linkage to the terminal β-D-galactose residues of glycan in a process catalyzed by fucosyltransferase. Two fucosyltransferases, Fut1 and Fut2, mediate intestinal epithelial fucosylation, and each enzyme acts on a distinct subset of epithelial cells. Fut1 regulates fucosylation of Peyer's patch (PP) M cells, whereas Fut2 is a key enzyme regulating intestinal columnar epithelial fucosylation and the production of secretory fucosylated ABO(H) histo-blood group antigens (11). Defective Fut2 has been shown to result in susceptibility

to *Candida albicans* infection in mice (12). In addition, inactivating polymorphisms of *FUT2* are associated with metabolic abnormalities and infectious and inflammatory diseases in humans (13–19).

The importance of epithelial fucose has been explored through studies of host–microbe interactions. Signals from commensal bacteria are required for epithelial fucosylation (6). Specific commensals, in particular *Bacteroides*, have been shown to induce epithelial fucosylation and are able to catabolize fucose for energy or incorporate it into bacterial cellular components—capsular polysaccharides—that give microbes a survival advantage in competitive environments (8, 9). Indeed, a lack of *Fut2* alters the diversity and composition of the fecal microbiota in humans and mice (20, 21). Therefore, epithelial fucose functions as a mediator between the host and commensal microbiota. Although a previous report proposed a model in which *Bacteroides*–EC interaction mediates epithelial fucosylation (7), the precise mechanisms by which *Fut2* regulates fucosylation remain largely unknown.

Microbiota induces epithelial fucosylation

Epithelial fucosylation, a major glycosylation process, occurs in the small intestine (10, 11). To assess the inductive mechanism of intestinal epithelial fucosylation, we first investigated the localization of fucosylated ECs (F-ECs) along the length of the small intestine, divided equally into four parts from the duodenum (part 1) to the terminal ileum (part 4), in naïve mice (Fig. 1A). The frequency of F-ECs, detected with the α(1,2)-fucose-recognizing lectin *Ulex europaeus* agglutinin-1 (UEA-1), was low in the duodenum and jejunum (part 1 and a portion of part 2; <15% F-ECs) and gradually increased toward the ileum (part 4; 40 to 90% F-ECs) (Fig. 1, A to C). Consistent with epithelial fucosylation, epithelial *Fut2* expression was also higher in the ileum (Fig. 1D). Because greater numbers of microorganisms are present in the distal ileum than in the duodenum (22), it may be possible that high numbers of ileal F-ECs are induced and maintained through microbial stimulation. To test this hypothesis, we examined the fucosylation status of ileal ECs (part 4) in mice treated with a mixture of antibiotics (AB), as well as in germ-free (GF) mice. The number of F-ECs was dramatically reduced in AB-treated and GF mice (Fig. 2A and fig. S1A). Furthermore, expression of epithelial *Fut2* was also reduced in AB-treated mice (Fig. 2B). Epithelial fucosylation was restored after cessation of AB treatment and in conventionalized GF mice (Fig. 2A and fig. S1A). In addition, fucosylation of goblet cells, but not Paneth cells, was lost in AB-treated and GF mice (Fig. 2C), indicating that commensal bacteria induce fucosylation of columnar epithelial cells and goblet cells, but not Paneth cells.

It has been shown that epithelial fucosylation can be induced by the mouse and human commensal *Bacteroides thetaotaomicron* (6). However, on the basis of bacterial 16S ribosomal RNA (rRNA) gene clone library data obtained from

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isolated ileal mucus samples from naive mice (Fig. 2D), we did not detect *B. thetaiotaomicon* in our colony, suggesting that other commensals can induce epithelial fucosylation. To identify which indigenous bacteria are responsible for the induction of F-ECs, we analyzed mucus-associated bacterial populations residing in the mouse duodenum (part 1) and ileum (part 4). In contrast to the predominance of *Lactobacillus* in the duodenum, segmented filamentous bacteria (SFB) predominated in the ileum (Fig. 2D); this is consistent with previous studies (23, 24). SFB are Gram-positive bacteria that preferentially colonize the epithelial surface of the terminal ileum, where they induce T helper 17 (T_H17) cells (25, 26). Similar to their effect on T_H17 cell-inducing microbiota (27), vancomycin, ampicillin, and to some extent metronidazole—but not neomycin—extinguished epithelial fucosylation (fig. S1, B and C). Furthermore, consistent with the emergence of SFB, epithelial fucosylation is initiated after weaning (6, 28). To investigate whether SFB have the potential to induce F-ECs, we examined mono-associated gnotobiotic mice and found that F-ECs were induced in SFB but not in *Lacto-*

bacillus murinus mono-associated mice (Fig. 2E). Together, these results suggest that epithelial fucosylation in the terminal ileum is induced by commensal bacteria, including SFB, under physiological conditions.

ILC3 are required for epithelial fucosylation

We next investigated the cellular and molecular mechanisms of F-EC induction. Commensal bacteria, including SFB, induce the proliferation of intraepithelial lymphocytes and immunoglobulin A (IgA)-producing cells and the development of T_H17 cells; they also modulate the function of ILCs (3, 4, 25–27, 29). To assess whether epithelial fucosylation is induced directly by commensal bacteria or is mediated by mucosal immune cells, we first analyzed the epithelial fucose status of T cell-, B cell-, and Rag-deficient mice. The number of F-ECs was not decreased in T cell- or B cell-deficient mice (fig. S2), indicating that T cells and B cells are dispensable for the induction of epithelial fucosylation. Although SFB induce T_H17 cells (25, 26), T_H17 cells are not required for epithelial fucosyl-

ation because IL-6, a critical cytokine for T_H17 cell differentiation in the intestine (30), was also not necessary for the induction of F-ECs (fig. S3, A to C). We next analyzed RAR-related orphan receptor- γ t (ROR γ t)-deficient mice, which lack the ILC3 subset, in addition to T_H17 cells (30, 31). ROR γ t-deficient mice exhibited a marked decrease in the number of F-ECs, accompanied by a decrease in *Fut2* expression in ileal ECs (Fig. 3, A to D). These findings suggest that ILC3 are critical inducers of F-ECs. This was further supported by our observation of few F-ECs in the ileum of Id2-deficient mice, which do not develop any of the ILC subsets (Fig. 3, E to G) (31, 32). Although both ROR γ t- and Id2-deficient mice lack PPs (33, 34), PPs are not necessary for epithelial fucosylation because PP-null mice, generated by treatment with monoclonal antibody (mAb) to IL-7R during fetal growth, had normal levels of F-ECs (fig. S4). ILC3 in the small intestine are aberrantly expanded in Rag-deficient mice (35), and elevated numbers of F-ECs were observed in these mice (Fig. 3, H and I), supporting the notion that F-ECs are induced by ILC3. Because ILC3 express higher levels of CD90, they

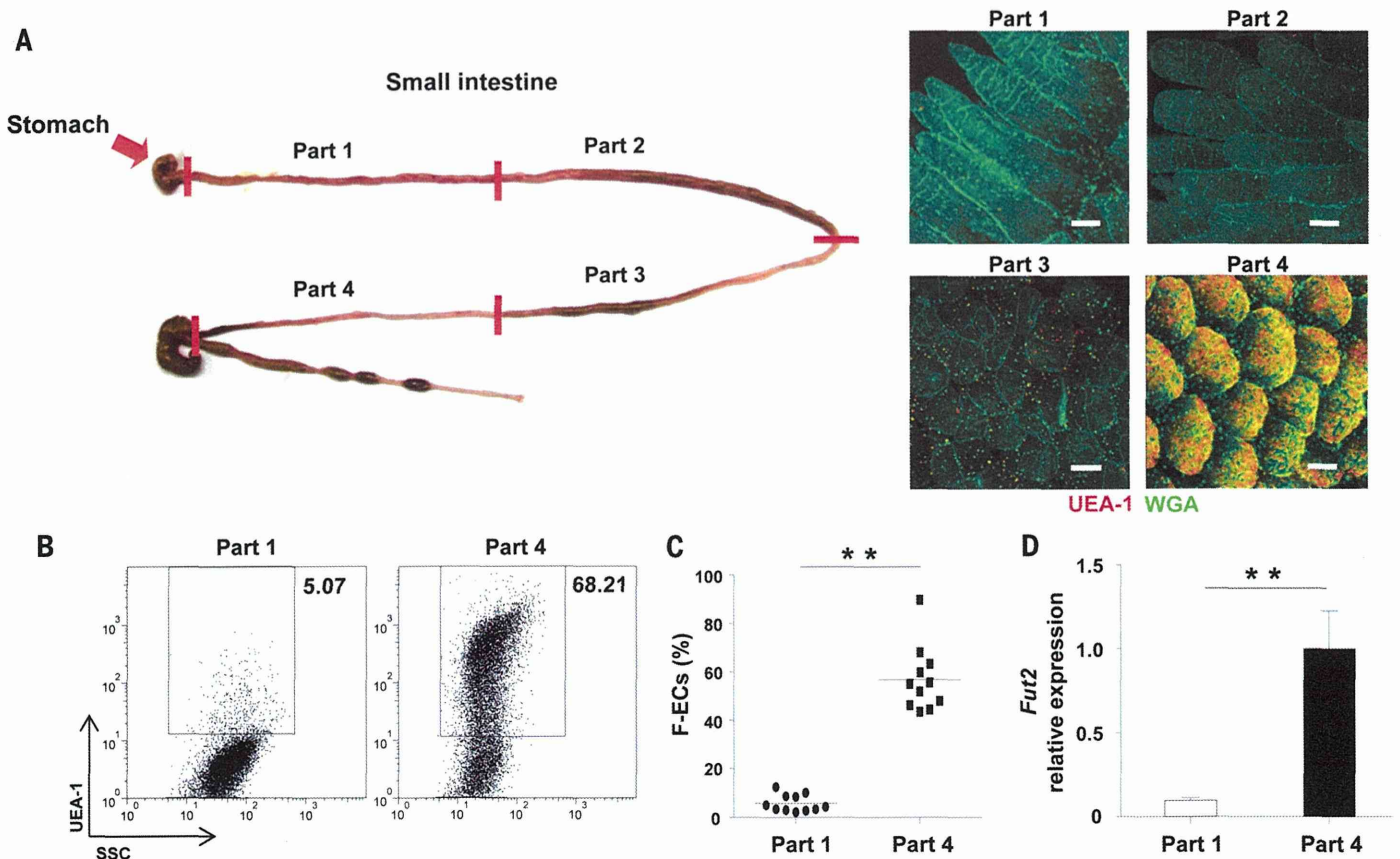


Fig. 1. F-ECs are dominant in the ileum. (A) Mouse small intestines were divided equally into 4 parts (parts 1, 2, 3, and 4), from the proximal (duodenum) to the distal (ileum) ends (left), and whole-mount tissues were stained with UEA-1 (red) and WGA (green) to detect F-ECs (UEA-1⁺ WGA⁺ cells) (right). Scale bars, 100 μ m. Data are representative of three independent experiments. (B and C) Flow cytometric analysis of intestinal ECs isolated from part 1 and part 4 of the small intestines of C57BL/6 (B6) mice. Representative

dot-plots are shown in (B). Percentages and mean numbers (horizontal bars) of fucosylated epithelial cells ($n = 11$ mice per group) are shown (C). SSC, side scatter. Data of two independent experiments are combined. (D) Expression of *Fut2* in ECs isolated from part 1 and part 4 of the small intestine isolated from five to six mice per group. Error bars indicate SD. ** $P < 0.01$ by using Student's *t* test. Data are representative of two independent experiments.

can be depleted with a mAb to CD90 (36, 37). To identify whether ILC3 induce F-ECs, we treated wild-type and Rag-deficient mice with a mAb to CD90. *Fut2* expression and the number of F-ECs were markedly decreased after depletion of

ILCs in both wild-type and Rag-deficient mice (Fig. 3, J to M, and fig. S5, A and B). Substantial numbers of SFB were still observed in ROR γ t⁻, Id2⁻, and CD90⁺ ILC-depleted mice (fig. S6, A and B). Therefore, the defective epi-

thelial fucosylation in these models was not attributable to the absence of F-EC-inducing commensals. Collectively, these results indicate that CD90⁺ ILC3 are required for the induction and maintenance of F-ECs.

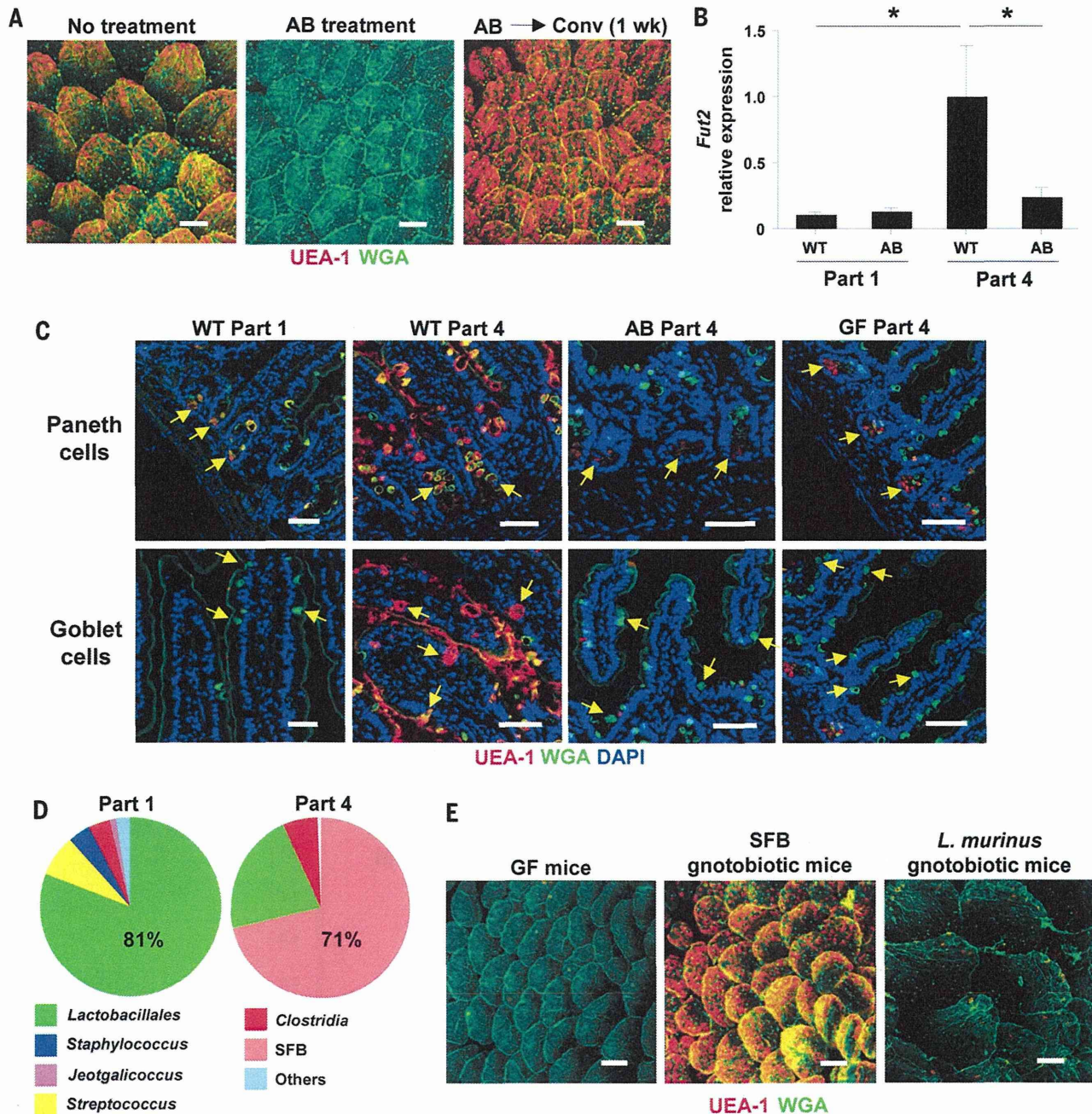


Fig. 2. Commensal bacteria induce epithelial fucosylation under homeostatic conditions. (A) Whole-mount ileal tissues of AB-treated mice and conventionalized AB-treated mice were stained with UEA-1 (red) and WGA (green) ($n = 3$ mice per group). Scale bars, 100 μ m. Data are representative of two independent experiments. (B) *Fut2* expression in ECs isolated from part 1 (duodenum) and part 4 (ileum) of the small intestines of wild-type (WT) and AB-treated mice ($n = 3$ mice per group). Error bars indicate SD. $*P < 0.05$ by using Student's *t* test. Data are representative of two independent experiments. (C) Tissues from part 1 and part 4 of the small intestines of WT, AB-treated, and GF mice were stained with UEA-1 (red), WGA (green),

and 4',6-diamidino-2-phenylindole (DAPI) (blue). Arrows show Paneth cells (top) and goblet cells (bottom). Scale bars, 50 μ m. Data are representative of two independent experiments. (D) Bacterial populations isolated from the mucus fraction of part 1 and part 4 of mouse small intestine were analyzed by means of 16S rRNA gene clone library. Representative graphs were constructed from samples (part 1, $n = 480$ clones; Part 4, $n = 477$ clones) isolated from five different mice (95 or 96 samples were obtained from each mouse). (E) Ileal tissues of GF, SFB, or *L. murinus* mono-associated mice ($n = 3$ mice per group) were stained with UEA-1 (red) and WGA (green). Scale bars, 100 μ m. Data are representative of two independent experiments.