LTα-deficient or -sufficient mice and mixed with BM cells from RORγt-deficient mice into lethally irradiated recipients. F-ECs and *Fut2* expression were diminished in recipient mice reconstituted with BM cells containing LTα-deficient RORγt$^+$ ILC3, whereas substantial numbers of F-ECs, and *Fut2* expression, were induced in recipient mice reconstituted with BM cells containing LTα-sufficient RORγt$^+$ ILC3, indicating the importance of LTα expressed by ILC3 in the induction of F-ECs (Fig. 5, F to H). When the microbiota of LTα-deficient mice or of mixed BM chimeras containing LTα-deficient ILC3 were examined, substantial numbers of SFB were observed (fig. S6, A and B). From these results, we concluded that induction and maintenance of F-ECs were also regulated by ILC3-derived LT in a commensal flora–independent manner.

Epithelial fucosylation protects against infection by *Salmonella typhimurium*

We next investigated the physiological role of epithelial fucosylation. With exception of Paneth cells, the *Fut2* expression and ileal epithelial fucosylation observed in wild-type mice were abolished in *Fut2*$^{-/-}$ mice (fig. S11, A to E). We did not detect any overt changes in mucosal leukocyte populations or in IL-22 or LT expression in ILC3 in these mice (fig. S11F and table S1). Epithelial fucosylation provides an environmental platform for colonization by *Bacteroides* species (*6*–*9*); however, it is unknown whether epithelial fucosylation affects colonization and subsequent infection by pathogenic bacteria. To assess the effects of intestinal fucosylation on pathogenic bacterial infection, we first infected GF mice with the enteropathogenic bacterium *Salmonella typhimurium*, which has the potential to attach to fucose-containing carbohydrate molecules (*42*). After infection with *S. typhimurium*, ECs from both part 1 (duodenum) and part 4 (ileum) of the mouse intestine were fucosylated, and this was correlated with Fut2 expression (Fig. 6, A and B). Previous reports have shown that expression of IL-22 in ILCs is much higher in mice infected with *S. typhimurium* (*43*, *44*). Therefore, *S. typhimurium*–induced epithelial fucosylation may be mediated by ILC3. Indeed, epithelial fucosylation was not induced in RORγt-deficient mice after *S. typhimurium* infection (Fig. 6C). To investigate whether epithelial fucosylation has a role in regulating pathogenic bacterial infection, we infected wild-type or *Fut2*$^{-/-}$ mice with *S. typhimurium* and examined disease progression. Compared with wild-type mice, *Fut2*$^{-/-}$ mice were more susceptible to *Salmonella* infection accompanied with the observation of severe inflamed cecum (Fig. 6D). Consistent with the inflammatory status of diseased mice, the numbers of infiltrating leukocytes in cecum were higher in *Fut2*$^{-/-}$ mice than in wild-type mice (Fig. 6E). Although *S. typhimurium* titers in cecal contents were comparable between wild-type and *Fut2*$^{-/-}$ mice, increased numbers of *S. typhimurium* infiltrated the cecal tissue of *Fut2*$^{-/-}$ mice (Fig. 6F). These results suggest that epithelial fucosylation is dispensable for luminal colonization by *S. typhimurium* but inhibits bacterial invasion of intestinal

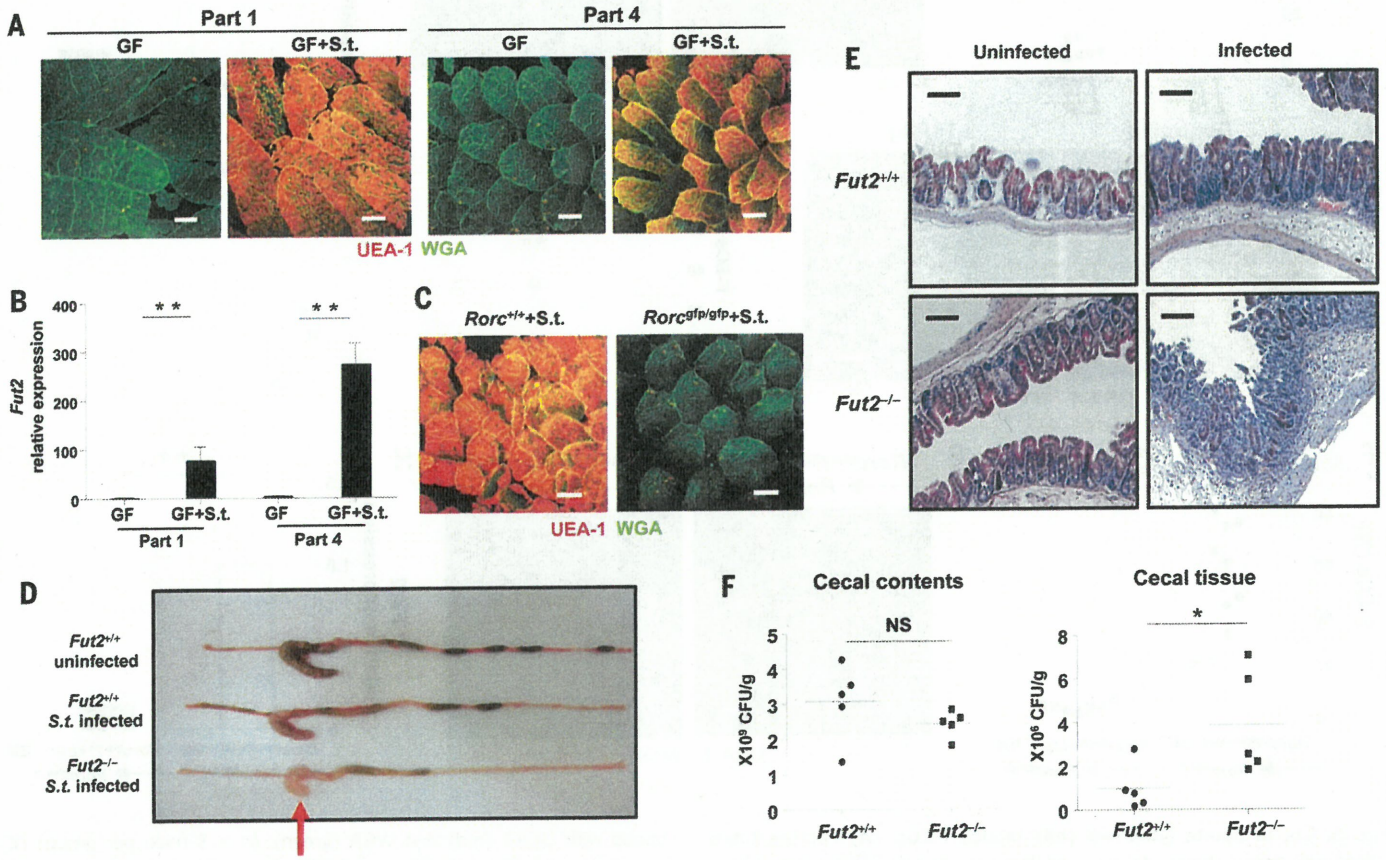

Fig. 6. Epithelial fucosylation protects against infection by *S. typhimurium*. (**A**) Whole-mount tissues from part 1 (duodenum) and part 4 (ileum) of the small intestines of germ-free (GF) or *S. typhimurium*–infected GF mice were stained with UEA-1 (red) and WGA (green) (n = 3 to 4 mice per group). Scale bars, 100 μm. (**B**) Epithelial Fut2 expression in part 1 and part 4 of the small intestines of GF and *S. typhimurium*–infected GF mice was analyzed by using quantitative PCR (n = 3 to 4 mice per group). Error bars indicate SD. **P < 0.01 by using Student's t test. (**C**) Whole-mount tissues from ileum of *S. typhimurium*–infected *Rorc*$^{+/+}$ or *Rorc*$^{gfp/gfp}$ mice were isolated and stained with UEA-1 (red) and WGA (green) (n = 3 to 4 mice per group). Scale bars, 100 μm. (**D** and **E**) *Fut2*$^{+/+}$ or *Fut2*$^{-/-}$ mice were infected with *S. typhimurium*. Red arrow shows inflammation of the cecum. Representative macroscopic images (D) and hematoxylin and eosin–stained cecal sections (E) of infected or uninfected mice (n = 5 mice per group). Scale bars, 100 μm. (**F**) Numbers of bacteria in the luminal contents, and within the tissues, of the ceca of *Fut2*$^{+/+}$ or *Fut2*$^{-/-}$ mice were counted 24 hours after infection (n = 5 mice per group). *P < 0.05 by using Student's t test. NS, not significant. Three independent experiments were performed with similar results.

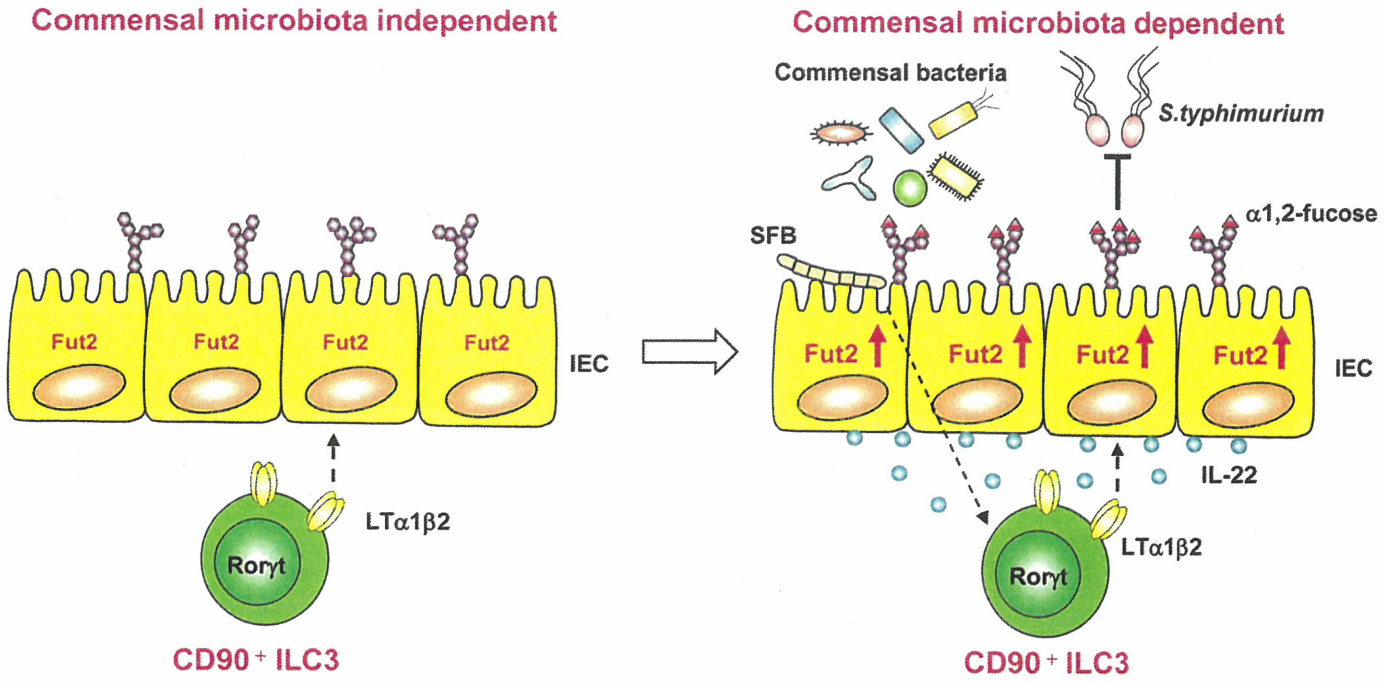

Fig. 7. Scheme for the induction and regulation of epithelial fucosylation by ILC3. IL-22– and LTα-producing ILC3 are critical cells for the induction and regulation of F-ECs. ILC3-mediated fucosylation of ECs is operated by commensal microbiota–dependent and –independent manners. Commensal bacteria, including SFB, stimulate CD90$^+$ ILC3 to produce IL-22 for the induction of Fut2 in ECs. On the other hand, LTα production by ILC3 are operated by a commensal bacteria–independent manner. ILC3-derived IL-22 and LTα induce Fut2 and subsequent epithelial fucosylation, which inhibits infection by *S. typhimurium*. IEC, intestinal epithelial cell.

tissues. Collectively, these results indicate that epithelial fucosylation, regulated by *Fut2*, has a protective role against infection by pathogenic bacteria.

Discussion

The results of recent genome-wide association studies imply that FUT2 nonsense polymorphisms affect the incidence of various metabolic and inflammatory diseases, including chronic intestinal inflammation such as Crohn's disease and infections with pathogenic microorganisms, especially Norwalk virus and rotavirus in humans (*13*–*19*). Understanding the mechanisms of regulation of Fut2 gene expression and fucosylation, one of the major glycosylation events in intestinal ECs, is therefore of great interest. Previously, it was thought that epithelial fucosylation is initiated by direct interaction between commensals and ECs (*7*). Indeed, several reports have shown that epithelial fucosylation is actively induced and used by *Bacteroides* (*8*, *9*). Here, we unexpectedly found that microbiota-epithelia cross-talk is insufficient to induce epithelial fucosylation, and rather, CD90$^+$ RORγt$^+$ ILC3 are necessary for induction of epithelial *Fut2* expression and consequent fucosylation. ILC3 located in the intestinal lamina propria express high levels of IL-22 in a commensal bacteria–dependent manner (Fig. 4I and fig. S7, A and D). This IL-22 then presumably binds to IL-22R expressed by intestinal ECs, leading to the induction of Fut2 and initiation of the EC fucosylation process (Fig. 7). In contrast to the expression of IL-22, ILC3 express LT in a commensal bacteria–independent manner. Spontaneous expression of LT on ILC3 also contributes to the induction of epithelial fucosylation. To explain the mechanism underlying induction of epithelial fucosylation, we propose that epithelial fucosylation is regulated by a two-phase system orchestrated by ILC3 through the microbiota-independent production of LT and the induction of IL-22 by commensal bacteria (Fig. 7). Although other types of stimulation may also affect epithelial fucosylation, our findings reveal a critical role for ILC3.

Our results demonstrated that IL-22 produced by ILC3 is necessary and sufficient for induction of epithelial fucosylation when ILC3 are appropriately stimulated by commensal microbiota (Fig. 4, A to E). In addition to IL-22–mediated epithelial fucosylation, our results also show that the level of epithelial fucosylation is markedly reduced under LTα-deficient conditions (Fig. 5, A to C). Our findings suggest two possibilities for the IL-22/LT–mediated regulation of epithelial fucosylation. The first is that Fut2 expression and subsequent epithelial fucosylation are induced when the intensity of synergistic or additive signals from IL-22 and LT is above the threshold for activation of Fut2. For example, LT produced by ILC3 provides the baseline signal for the minimum expression of Fut2, whereas commensal-mediated IL-22 produced by ILC3 drives the maximum expression of Fut2 for the induction of epithelial fucosylation. The second possibility is that LT directly or indirectly regulates the expression of IL-22R by ECs, and vice versa, and/or the expression of IL-22. Indeed, a previous report has shown that LT produced by ILC3 regulates the expression of IL-23 by intestinal dendritic cells, as well as the subsequent production of IL-22 by ILC3 after infection with *C. rodentium* (*45*). How ILC3-derived IL-22 and LT regulate epithelial Fut2 expression remains to be further elucidated.

Our findings provide further evidence of the critical roles of commensal microbiota, epithelial cells, and innate immune cells (such as ILC3) in the creation of a protective platform against infection by pathogenic bacteria (Fig. 7). Ablation of epithelial fucose allowed severe infection by the pathogenic bacteria *S. typhimurium* (Fig. 6, D to F). Although the detailed mechanisms of why *Fut2*$^{-/-}$ mice are susceptible to *Salmonella* infection remain unknown, one possibility is that fucosylated mucin produced by goblet cells blocks the attachment of *S. typhimurium* to the epithelium. Commensal microbes continuously stimulated goblet cells to release fucosylated mucin into the intestinal lumen (Fig. 2C). Indeed, in a previous in vitro study, H-type 2 antigens, which are synthesized by Fut2 in intestinal ECs, prevented the binding of *S. typhimurium* to fucosylated epithelia; this supports our present findings (*42*). Our findings suggest a protective role for ILC3-mediated mucus-associated fucosylated glycan against infection by pathogenic bacteria.

ILC3 play critical roles in regulation of immune responses during mucosal infection, especially

by producing IL-22, which promotes subsequent expression of the antimicrobial molecule RegIIIγ by ECs (*4*, *36*, *45*). In addition to this, our results describe a previously unknown biological role for ILC3 in the induction and maintenance of intestinal epithelial glycosylation, which leads to the creation of an antipathogenic bacterial platform in the intestine (Fig. 7). Furthermore, epithelial fucosylation contributes to the creation of a cohabitation niche for the establishment of normal commensal microbiota (*20*, *21*). Thus, ILC3-mediated control of epithelial-surface glycosylation might represent a general strategy for regulating the gut microenvironment. Targeted modification of these mechanisms has the potential to provide novel approaches for the control of intestinal infection and inflammation.

Materials and Methods

Mice

C57BL/6 and BALB/c mice were purchased from CLEA Japan (Tokyo, Japan). *Fut2*$^{-/-}$ and *Il22*$^{-/-}$ mice (C57BL/6 background) were generated as described previously, and *Id2*$^{-/-}$ mice were kindly provided by Y. Yokota (*33*, *46*, *47*). *Fut2*$^{-/-}$ mice were crossed onto the BALB/c background for six generations. *Rag2*$^{-/-}$ mice were kindly provided by F. Alt. *Rag1*$^{-/-}$; *Rorc*$^{gfp/gfp}$, *Il6*$^{-/-}$, *Ltα*$^{-/-}$, *Tcrβ*$^{-/-}$*δ*$^{-/-}$, and *Igh6*$^{-/-}$ mice were purchased from The Jackson Laboratory. Antibiotic-treated mice were fed a cocktail of broad-spectrum antibiotics—namely, ampicillin (1 g/L; Sigma, Bandai, Japan), vancomycin (500 mg/L; Shionogi, Osaka, Japan), neomycin (1 g/L; Sigma), and metronidazole (1 g/L; Sigma)—or were given these antibiotics in their drinking water, for 4 weeks as previously described (*48*). These mice were maintained in the experimental animal facility at the University of Tokyo. GF and SFB or *L. murinus* gnotobiotic mice (BALB/c) were maintained in the GF animal facility at the Yakult Central Institute and at the University of Tokyo. In all experiments, littermates were used at 6 to 10 weeks of age.

Isolation of bacterial DNA

The isolation protocol for bacterial DNA was adapted from a previously described method (*49*), with some modifications. Bacterial samples in the duodenum and ileum were obtained from mice aged 8 weeks. After removal of PPs and intestinal contents, the intestinal tissues were washed three times with phosphate-buffered saline (PBS) for 10 s each time so as to collect bacteria embedded within the intestinal mucus for analysis of microbial composition. These bacteria-containing solutions were centrifuged, and the pellets were suspended in 500 μL of TE buffer (10 mM Tris-HCl, 1 mM EDTA; pH 8.0). Glass beads, Tris-phenol buffer, and 10% sodium dodecyl sulfate (SDS) were added to the bacterial suspensions, and the mixtures were vortexed vigorously for 10 s by using a FastPrep FP100 A (BIO 101). After incubation at 65°C for 10 min, the solutions were vortexed and incubated again at 65°C for 10 min. Bacterial DNA was then precipitated in isopropanol, pelleted by centrifugation, washed in 70% ethanol, and resuspended in TE buffer. Extracted bacterial DNA was subjected to 16*S* rRNA gene clone library (*50*).

16S rRNA gene clone library analyses

For 16*S* rRNA gene clone library analyses, bacterial 16*S* rRNA gene sequences were amplified by means of polymerase chain reaction (PCR) with the 27F (5′-AGAGTTTGATCCTGGCTCAG-3′) and 1492R (5′-GGTTACCTTGTTACGACTT-3′) primers. Amplified 16*S* rDNA was ligated into the pCR4.0 TOPO vector (Invitrogen, Carlsbad, CA), and the products of these ligation reactions were then transformed into DH-5α–competent cells (TOYOBO, Osaka, Japan). Inserts were amplified and sequenced on an ABI PRISM 3100 Genetic Analyzer (Applied Biosystems, Foster City, CA). The 27F and 520R (5′-ACCGCGGCTGCTGGC-3′) primers and a BigDye Terminator cycle sequencing kit (Applied Biosystems) were used for sequencing. Bacterial sequences were identified by means of Basic Local Alignment Search Tool (BLAST) and Ribosomal Database Project searches (*50*).

Immunohistochemistry

Immunohistochemical analyses were performed as previously described, with some modifications (*51*). For whole-mount immunofluorescence staining, the mucus layer was removed by flushing the small intestine with PBS; then, the appropriate parts of the small intestine were fixed with 4% paraformaldehyde for 3 hours. After being washing with PBS, whole-mount tissues were stained for at least 3 hours at 4°C with 20 μg/mL UEA-1 conjugated to tetramethylrhodamine B isothiocyanate (UEA-1-TRITC; Vector Laboratories, Burlingame, CA) and 10 μg/mL wheat germ agglutinin (WGA) conjugated to Alexa Fluor 633 (Invitrogen). For whole-mount fluorescence in situ hybridization analysis, we modified the protocol previously described (*52*). After fixation with 4% paraformaldehyde, intestinal tissues were washed with 1 mL PBS and 100 μL hybridization buffer (0.9 M NaCl, 20 mM Tris-HCl, 0.1% SDS) containing 2 μg EUB338 probe (5′-GCTGCCTCCCGTAGGAGT-3′) conjugated to Alexa Fluor 488 (Invitrogen). After overnight incubation at 42°C, the tissues were washed with 1 mL PBS and stained for 3 hours with 10 μg/mL WGA conjugated to Alexa Fluor 633 in PBS. After being washed with PBS, all tissues were analyzed under a confocal laser-scanning microscope (TCS SP2; Leica Microsystems, Wetzlar, Germany).

Cell preparations

A standard protocol was used to prepare intestinal ECs (*53*). Tissues of the small intestine were extensively rinsed with PBS after removal of PPs. After the intestinal contents had been removed, the samples were opened longitudinally and cut into 1-cm pieces. These tissue pieces were mildly shaken in 1 mM EDTA/PBS for 10 min at 37°C. After passage through a 40-μm mesh filter, intestinal ECs were resuspended in minimum essential medium containing 20% fetal calf serum (FCS). Lamina propria (LP) cells were collected as previously described (*54*), with some modifications. Briefly, isolated small intestine was shaken for 40 min at 37°C in RPMI 1640 containing 10% FCS and 1 mM EDTA. Cell suspensions, including intestinal ECs and intraepithelial lymphocytes, were discarded, and the remaining tissues were further digested with continuous stirring for 60 min at 37°C with 2 mg/mL collagenase (Wako) in RPMI 1640 containing 10% FCS. After passage through a 190-μm mesh, the cell suspensions were subjected to Percoll (GE Healthcare) density gradients of 40 and 75%, and the interface between the layers was collected to retrieve LP cells. Stromal cells were identified as CD45$^-$ Viaprobe$^-$ cells. For fluorescence-activated cell-sorting (FACS) analysis of ILCs, isolated LP cells were further purified by magnetic-activated cell sorting so as to eliminate CD11b$^+$, CD11c$^+$, and CD19$^+$ cells. CD11b$^-$ CD11c$^-$ CD19$^-$ Viaprobe$^-$ CD45$^+$ LP cells were used to detect ILCs.

Antibodies and flow cytometry

For flow cytometric analysis, isolated intestinal ECs were stained with UEA-1-TRITC, anti-CD45–Pacific blue (PB; Biolegend, San Diego, CA), and Viaprobe (BD Biosciences, East Rutherford, NJ). Viaprobe$^-$ CD45$^-$ UEA-1$^+$ cells were identified as F-ECs. After blocking with anti-CD16/32 (FcγRII/III) (BD Biosciences), the following antibodies were used to stain spleen and LP cells: anti-CD45–PB (Biolegend), anti-CD11b–phycoerythrin (PE), anti-Foxp3-fluorescein isothiocyanate (FITC) (eBioscience, San Diego, CA), anti-CD11c–allophycocyanin (APC), anti-CD11b–FITC, anti-Gr-1-Alexa647, anti-CD3-APC, anti-B220-PE, anti-B220-APC, anti-IgA-FITC, anti-CD4-eFluor450, anti-CD90.2–FITC, anti-IL-17-PE, and anti-IFNγ-FITC (all from BD Biosciences), and Viaprobe. CD11b$^-$ CD11c$^-$ CD19$^-$ LP cells were purified by using anti-CD11b, anti-CD11c, and anti-CD19 MicroBeads (Miltenyi Biotec, Bergisch Gladbach, Germany). The results were obtained by using a FACSAria cell sorter (BD Biosciences) with FlowJo software (TreeStar, Ashland, Oregon).

Intracellular staining of Foxp3 and cytokines

Isolated LP cells were incubated for 4 hours at 37°C with 50 ng/mL phorbol myristate acetate (Sigma), 500 ng/mL ionomycin (Sigma), and GolgiPlug (BD Bioscience) in RPMI 1640 containing 10% FCS and penicillin and streptomycin. After incubation, cells were stained with antibodies against surface antigens for 30 min at 4°C. The cells were fixed and permeabilized with Cytofix/Cytoperm solution (BD Bioscience), and cytokines were stained with the fluorescence-conjugated cytokine antibodies. A Foxp3 staining buffer set (eBioscience) was used for intracellular staining of Foxp3.

Depletion of CD90$^+$ ILCs

Depletion of CD90$^+$ ILCs was performed as previously described, with some modifications (*36*). Two hundred and fifty micrograms of a mAb to CD90.2 or an isotype control rat IgG2b (BioXCell, West Lebanon, NH) was given by means of intraperitoneal injection a total of three times at

3-day intervals. Intestinal ECs and LP cells were collected 2 days after the final injection.

Hydrodynamic IL-22 gene delivery system

pLIVE control plasmid (Takara Bio, Shiga, Japan) or IL-22–expressing pLIVE vector (pLIVE-*mIl22*) was introduced into 8-week-old antibiotic-treated C57BL/6 or *Rorc*$^{gfp/gfp}$ mice. Ten micrograms per mouse of plasmid diluted in ~1.5 mL TransIT-EE Hydrodynamic Delivery Solution (Mirus Bio, Madison, WI) was injected via the tail vein within 7 to 10 s. To assess IL-22 expression, serum IL-22 was quantified by means of an enzyme-linked immunosorbent assay (R&D Systems, Minneapolis, MN).

Generation of PP-null mice

mAb to IL-7R (A7R34) was kindly provided by S. Nishikawa. PP-null mice were generated by injecting 600 μg of mAb to IL-7R into pregnant mice on embryonic day 14 (*55*).

In vivo treatment with LTβR-Ig and antibody to IL-22

Neutralization antibody to IL-22 was purchased from eBioscience. Eight-week-old Rag-deficient mice were injected intraperitoneally with antibody to IL-22 a total of five times at 3-day intervals (on days 0, 3, 6, 9, and 12). Plasmid pMKIT-expressing LTβR-Ig and LTβR-Ig treatment was performed as described previously (*56*). Four-week-old C57BL/6 mice were injected intraperitoneally once a week for 3 weeks (on days 0, 7, 14, and 21) with LTβR-Ig fusion protein or control human IgG1 at a dose of 50 μg per mouse. Intestinal ECs were analyzed 3 days after the indicated injection time points.

Adoptive transfer of mixed BM

For mixed BM transfer experiments, *Rorc*$^{gfp/gfp}$ mice were irradiated with two doses of 550 rad each, 3 hours apart. BM cells (1×10^7) from *Rorc*$^{gfp/gfp}$ mice was mixed with BM cells (1×10^7) from C57BL/6 or *Ltα*$^{-/-}$ mice and intravenously injected into irradiated recipient mice. BM chimeric mice were used for experiments 8 weeks after the BM transfer.

Isolation of RNA and real-time reverse transcriptase PCR analysis

Intestinal ECs and subsets of LP cells were sorted with a FACSAria cell sorter (BD Biosciences). The sorted cells were lysed in TRIzol reagent (Invitrogen), and total RNA was extracted in accordance with the manufacturer's instructions. RNA was reverse-transcribed by using a SuperScript VILO cDNA Synthesis Kit (Invitrogen). The cDNA was subjected to real-time reverse transcriptase–PCR (rRT-PCR) by using Roche (Basel, Switzerland) universal probe/primer sets specific for *Ltα* (primer F: 5′-tcctcagaagcacttgacc-3′, R: 5′-gagttctgcttgctggggta-3′, probe No. 62), *Ltβ* (primer F: 5′-cctggtgacctgttgttg-3′, R: 5′-tgctcctgagccaatgatct-3′, probe No. 76), *Il22* (primer F: 5′-tttcctgaccaaactcagca-3′, R: 5′-tctggatgttctggtcgtca-3′, probe No. 17), *Il22r1* (primer F: 5′;-tgctctgttatctgggctacaa-3′, R: 5′-tcaggacacgttggacgtt-3′, probe No. 9), *Il10rβ* (primer F: 5′-attcggagtgggtcaatgtc-3′, R: 5′-gcatctcaggaggtccaatg-3′, probe No. 29), *Fut2* (primer F: 5′-tgtgacttccaccatcatcc-3′, R: 5′-tctgacagggtttggagctt-3′, probe No. 67), and *Gapdh* (primer F: 5′-tgtccgtcgtggatctgac-3′, R: 5′-cctgcttcaccaccttcttg-3′, probe No. 80). RT-PCR analysis was performed with a Lightcycler II instrument (Roche Diagnostics) to measure the expression levels of specific genes.

Infection with S. typhimurium

Streptomycin-resistant wild-type *S. typhimurium* was isolated from *S. typhimurium* strain ATCC 14028. *Fut2*$^{-/-}$ (BALB/c background) and control littermate mice pretreated with 20 mg of streptomycin 24 hours before infection were given 1×10^8 colony-forming units of the isolated *S. typhimurium* via oral gavage. After 24 hours, the mice were dissected, and the cecal contents were collected. Isolated cecum was treated with PBS containing 0.1 mg mL^{-1} gentamicin at 4°C for 30 min so as to kill bacteria on the tissue surface. The cecum was then homogenized and serial dilutions plated in order to determine the number of *S. typhimurium*. Sections of proximal colon were prepared 48 hours after infection. Infiltration of inflammatory cells was confirmed with hematoxylin and eosin staining.

Statistical analysis

Statistical analysis was performed with an unpaired, two-tailed Student's *t*-test. *P* values <0.05 were considered statistically significant.

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SUPPLEMENTARY MATERIALS

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Figs. S1 to S11
Table S1

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