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## Crosstalk between type 3 innate lymphoid cells and the gut microbiota in inflammatory bowel disease

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### Abstract

**Purpose of review**—Innate lymphoid cells (ILCs) are a newly-identified population of immune cells prevalent in, but not limited to, mucosal tissues that not only play a significant role in immune homeostasis and host defense, but also in disease pathogenesis. This review highlights the importance of type 3 ILCs (ILC3s) and their interactions with the intestinal microflora, both in maintaining gut health and in the development of inflammatory bowel disease (IBD).

**Recent findings**—Distinct lineages of ILCs are defined based on the presence of cell surface proteins, secretion of effector cytokines, and expression of master transcription factors that determine their differentiation and inflammatory behavior. These ILC subgroups mirror corresponding CD4<sup>+</sup> T-cell subsets, with which they share many phenotypic, morphologic, and functional attributes. ILC3s, in particular, through direct and indirect interactions with the gut microbiota, have been identified to promote protection and maintenance of epithelial integrity, but also to regulate intestinal inflammation and fibrosis, such as that observed in IBD.

**Summary**—Gut mucosal ILCs respond to environmental cues, such as diet and microflora composition, which can shape downstream immune function. As such, ILCs represent attractive targets for the development of therapeutic modalities to maintain gut health and to potentially treat IBD.

### Keywords

Innate lymphoid cells (ILCs); gut microbiota; inflammatory bowel disease (IBD); mucosal immunity

### Introduction

IBD, primarily encompassing Crohn's disease (CD) and ulcerative colitis (UC), describes a chronic and relapsing inflammatory condition of the gastrointestinal (GI) tract attributed to the combinatorial effects of immune dysregulation and environmental factors in genetically-predisposed individuals. For several years, dysregulation of the adaptive immune system,

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### Conflict of interest

None declared.

mainly of CD4<sup>+</sup> T-cells, was believed to be paramount for the development of IBD. More recently, aberrancies in gut mucosal innate immunity have been shown to play a primary, initiating role. In this context, newly-identified innate immune cells, termed ILCs, have been described that play a pivotal role in both mucosal immune homeostasis, as well as in the development of IBD. This review will discuss the involvement of intestinal ILCs, with emphasis on ILC3s, in gut health and disease, and their interactions with the microbiome during IBD.

## ILC development and lineages

As their name suggests, ILCs are of lymphoid origin, derived from the common lymphoid progenitor (CLP), and rely on interleukin (IL)-2R $\gamma$ c signaling. ILCs are distinguished by the absence of features found in other immune cells, such as the lack of recombined antigen-specific receptors typically found on B- and T-cells, and of phenotypic markers associated with monocytes, dendritic cells (DCs), granulocytes, and B- and T-cells (1). ILCs can be found throughout the anatomy of both mice and humans, but are mostly enriched in mucosal barrier surfaces of the respiratory and GI tracts, and skin (1–3). Similar to how memory T-cells, natural killer (NK)T-cells, and  $\gamma\delta$ T-cells are activated, ILCs are stimulated by stress signals, the cytokine milieu of the tissue environment, and microbes, rather than by antigens. ILCs are early effectors during an immune response and secrete cytokines classically associated with T-helper cells, and can therefore potentially mediate type 1, 2, and 3 immunity that control intracellular pathogens, helminths, and extracellular microbes, respectively.

## ILC subsets

Previously referred to by a variety of names, such as ‘natural helper cells,’ ‘nuocytes,’ and ‘innate helper cells,’ ILC nomenclature has been designed to recognize its growing diversity (4). ILCs are currently divided into subsets, based on the expression of lineage-defining transcription factors. These different subsets, their associated cytokine profiles, and the transcription factors that direct their lineages and regulate their functions are reviewed in detail elsewhere (5). ILC1s, which include NK cells, secrete interferon (IFN) $\gamma$  and tumor necrosis factor (TNF) in response to IL-12, IL-15, and IL-18, and their function is regulated by the transcription factor, T-bet (6). The second group, ILC2s, originally coined ‘nuocytes,’ is dependent on the transcription factors, GATA-3 and Bcl11b (7, 8), and produces the Th2 cytokines, IL-5 and IL-13, in response to IL-25, IL-33, and thymic stromal lymphopoietin (TSLP), as well as to helminth infection and allergic inflammation (9–12). ILC2s are also distinguished by the expression of ST2 (IL-33R), c-kit, and KLRG1. Thirdly, the ILC3 lineage is controlled by the transcription factor, ROR $\gamma$ t, and is characterized by production of IL-17 and IL-22, and the expression of c-kit and IL-23R. They can be further subdivided by expression of natural cytotoxicity receptors (NCRs), wherein NCR<sup>+</sup> ILC3s secrete IL-22 and NCR<sup>-</sup> ILC3s, which include lymphoid tissue inducer (LTi) cells, express both IL-22 and IL-17 (13).

## ILCs in the intestines

ILC1, ILC2, and ILC3 subsets have been characterized in the gut and gut-associated lymph nodes of both mice and humans during homeostasis, as well as during disease (14–16), and also in response to bacterial and parasitic infections (17–19). ILCs were first described in human mucosa-associated lymphoid tissues and initially defined as an NK cell subset that secretes IL-22 in response to IL-23 (20).

ILCs are rarely present in the steady state. In fact, ILCs expressing NCRs constitute only 5% of lymphocytes in human colon and small intestines (21, 22). They are even less common in naïve mice, where NCR-expressing ILCs represent only 1% of hematopoietic cells in the colon, 2% in the small intestines, and less than 1% of intraepithelial lymphocytes (23, 24).

In mice intestines, ILCs are categorized into three groups: 1) T-bet<sup>+</sup> IFN $\gamma$ -producing ILC1s, 2) ROR $\gamma$ t<sup>+</sup> IL-22-secreting ILC3s, and 3) a subset that appears to be transitional between ROR $\gamma$ t<sup>+</sup> ILC3s and T-bet<sup>+</sup> ILC1s (25). Another unique subpopulation of NCR<sup>+</sup> ILC1s is thought to inhabit the gut epithelium (26). Human intestinal ILCs resemble the subsets described in mice. These comprise Nkp44<sup>+</sup> (a human NCR) CD103<sup>+</sup> intraepithelial cells (26), Nkp44<sup>+</sup> ROR $\gamma$ t<sup>+</sup> ILC3s, Nkp44<sup>-</sup> c-kit<sup>-</sup> ILC1s, and Nkp44<sup>-</sup> c-kit<sup>+</sup> ROR $\gamma$ t<sup>+</sup> NCR<sup>-</sup> ILC3s (27).

Interestingly, plasticity between ILC subsets resembles that of CD4<sup>+</sup> T-cell lineages. NCR<sup>-</sup> ILC3s in the gut express ROR $\gamma$ t and secrete IL-17 and/or IL-22. A subset of NCR<sup>-</sup> ILC3s co-expresses T-bet, inducing secretion of IFN $\gamma$  and mirroring Th1 cells (28–30). These NCR<sup>-</sup> ILC3s are capable of producing inflammatory cytokines consistent with generating immunity against intestinal pathogens. ILC2s comprise approximately 5% of small intestinal lymphoid cells and are able to recruit and maintain eosinophils through IL-5 (31). ILC2 function in the human GI tract has not been reported, but as reported in murine studies, they may influence protection against helminth infection (32, 33).

## ILCs and IBD

Several mouse models suggest that all ILC subsets contribute to intestinal inflammation to varying degrees. One of the first studies describes that in a *Helicobacter hepaticus*-induced IBD model, an increase in colonic IL-17- and IFN $\gamma$ -producing ROR $\gamma$ t<sup>+</sup> CD127<sup>+</sup> NCR<sup>-</sup> ILC3s drives intestinal inflammation and depletion of these cells leads to abrogation of disease (30). Studies using Tbx21<sup>-/-</sup>Rag2<sup>-/-</sup> UC (TRUC) mice support these observations. TRUC mice develop microbiota-dependent colitis characteristic of UC and display an increase in colonic IL-17- and IL-22-producing NCR<sup>-</sup> ILC3s. Either depleting ILCs themselves or ablating Nod2/Ripk signaling in DCs, which activates ILCs, abrogates colitis (28, 29).

Interestingly, ILC3s have also been detected in CD and UC patients, with isolated colonic ILCs expressing increased *IL-17*, *IL-22*, *RORC*, aryl hydrocarbon receptor (*AHR*), and *IL-23R* (34). Overall, current studies suggest that NCR<sup>-</sup> ILC3s are pathogenic in the context of IBD. However, the same is not true for ILC3s that express NCR. In fact, studies show that IBD patients have decreased IL-22-secreting NCR<sup>+</sup> ILC3s that is associated with CD (22,

27). NCR<sup>+</sup> ILC3s are key producers of IL-22, which is critical in maintaining intestinal epithelial barrier integrity, and a reduced number of these cells may predispose these individuals to dampened gut mucosal protection. Similarly, during acute *Citrobacter rodentium* infection, blocking IL-22 or depleting IL-22<sup>+</sup> ILCs aggravates disease outcome (35, 36). As such, the possibility exists that during chronic intestinal inflammation, a decrease in IL-22<sup>+</sup> ILC3s is unfavorable for IBD patients due to the lack of appropriate epithelial barrier function.

Increased intestinal ILC1s, both in the epithelial and lamina propria (LP) compartments, have also been reported in experimental IBD models (25, 26). These ILC1s express Nkp46 and a similar Nkp44<sup>+</sup> ILC1 counterpart is also increased in CD patients (26, 27), suggesting that ILC1s may have a pathogenic role in CD. Interestingly, a role for ILC2s during IBD has not yet been defined. A study, however, investigating collagen deposition in human intestinal tissues showed an increase in infiltrating IL-13-expressing killer cell immunoglobulin-like receptor (KIR)<sup>+</sup> cells in the muscularis of fibrotic CD patients compared to controls. These IL-13R<sup>+</sup> KIR<sup>+</sup> ILCs are reported to promote fibrosis via IL-13, preventing matrix protein degradation in myofibroblasts and inducing disproportionate collagen deposition (37), suggesting the potential role of ILC2s in inducing inflammation-associated fibrosis in CD.

## ILC interactions with the commensal flora

In contrast to intestinal DCs and macrophages, direct interaction between ILCs and commensal microbes has not yet been proven, and at present, expression of toll-like receptors (TLRs) on ILCs has not been reported. Evidence exists, however, that ILCs are able to act in response to microbiota through communication with both epithelial cells and intestinal mononuclear phagocytes via cytokines/cytokine signaling.

## Regulation of ILC function by the microbiome

Studies show that human ROR $\gamma$ <sup>+</sup> ILCs can indirectly respond to TLR2 agonists by secreting IL-2, which in turn induces IL-22 (38). Similarly, flagellin activation of TLR5 in LP mononuclear phagocytes leads to IL-23 production and augments IL-22 by ROR $\gamma$ <sup>+</sup> ILCs. Increased IL-22 can lead to subsequent expression of antimicrobial peptides, such as Reg3g, by intestinal epithelial cells (IECs) (39–41), thus promoting gut mucosal protection.

IL-1 $\beta$  expression by intestinal macrophages in response to the gut microflora also induces IL-22 from ROR $\gamma$ <sup>+</sup> ILCs (42, 43). IL-1 $\beta$  can stimulate granulocyte macrophage colony stimulating factor (GM-CSF) from ILC3s, and IL-10 and retinoic acid from resident DCs and macrophages, which support the proliferation of intestinal T-regulatory cells (Tregs). Blocking GM-CSF by ILC3s abolishes tolerance to food antigen; however, it is unknown whether Treg-associated tolerance towards the microbiome is affected. Therefore, homeostasis can also be regulated by interactions between ILCs and intestinal mononuclear phagocytes (44). In fact, CX3CR1<sup>+</sup> mononuclear phagocytes develop in the intestine after commensal colonization and are critical for IL-22 production by ROR $\gamma$ <sup>+</sup> ILCs (45, 46). In contrast, microbiota-stimulated IL-25 from IECs can decrease constitutive IL-22 production by ROR $\gamma$ <sup>+</sup> ILCs (47). In the absence of symbiotic microbiota, epithelial-derived IL-25 is

decreased. Besides TLRs, NK cells and NCR<sup>+</sup> ROR $\gamma$ t<sup>+</sup> ILCs may directly sense commensal flora through NCRs, such as Nkp44 and Nkp46, which can be stimulated by elements derived from commensal bacteria (48, 49).

Recent studies have shown that certain phytochemicals derived from vegetables can influence ILC survival and cytokine secretion through expression of AHR (50–52). Indirectly, the microbiota can modulate generation of the tryptophan-derived AHR ligand, indole-3-aldehyde, which can promote ILC3 function. *Lactobacillus* spp. utilize tryptophan and control the availability of its byproduct that augments IL-22 production by ILC3s (53). It is well documented that AHR promotes Th17 differentiation, as well as the maintenance and function of ILC3s (54). However, recent investigation of AHR-deficient mice show that these mice actually possess increased numbers of intestinal Th17 cells, as well as decreased IL-22 from ILC3s, that is permissive for outgrowth of Th17-skewing segmented filamentous bacteria (SFB) (55). Taken together, these data suggest that commensal bacteria and their metabolic products have the ability to regulate ROR $\gamma$ t<sup>+</sup> ILCs.

Commensal bacteria can colonize barrier surfaces and directly interact with IECs. Germ-free or antibiotic-treated mice show decreased IEC-derived IL-7 (25, 56), a key cytokine in the homeostasis and function of ILC2s and ILC3s. In fact, microbiota-dependent IL-7 production from IECs is necessary for ILC3 ROR $\gamma$ t expression (25), whereas lack of IFN $\gamma$  signaling in IECs dampens IL-7 (56); thus, implicating commensal bacteria in regulating both IFN $\gamma$ -producing NK cells and IL-7-dependent ILCs. The expression of IL-1 family members, such as IL-18, IL-33, and IL-1 $\beta$  can also stimulate responses from ILC1s, ILC2s, and ILC3s, respectively (43, 57, 58); however, a direct influence by commensal bacteria has not been well-characterized.

Given the proximity of commensal bacteria, IECs, and ILCs, it is logical to assume that the gut microbiota may affect ILC development. However, current studies show that the microbiota is not required for development of most ILC subsets, such as NK cells and GATA3<sup>+</sup> ILC2s (12, 59, 60). Nonetheless, the numbers of NCR<sup>+</sup> ROR $\gamma$ t<sup>+</sup> ILC3s are decreased, and a lack of IL-22 and *Rorc* expression is observed in the small intestinal LP of germ-free and antibiotic-treated mice (23, 25, 35). In contrast, and under these same conditions, normal development proceeds in all ROR $\gamma$ t<sup>+</sup> ILC3s (47, 61–63). In fact, LTi cells and secondary lymphoid structures are still generated in the fetus before birth (64). After birth however, the formation of lymphoid follicles is impaired in germ-free mice, suggesting a compromise in function of LTi-like ROR $\gamma$ t<sup>+</sup> ILC subsets (65, 66). As such, the effect of the microbiome on ILC development is still controversial and further investigation is warranted.

Even in the absence of microbial colonization, around the third trimester of gestation in mice, ILC3s are present in the fetal gut. Compared to ILCs in the adult gut, these cells produce less IL-22, indicating that IL-22 production depends on the presence of the microbiome (67). Upon binding to the IL-22R expressed on IECs, IL-22 activates STAT3 and induces antimicrobial peptides, such as Ref3g and Reg3b, in a *Citrobacter rodentium* infection model (36, 68, 69). In IBD patients, ILC3s in contact with the intestinal microbiota in the afferent limb of the gut express more cytokines than those not interacting with the

microbiome, in the efferent limb of the gut. It appears that this functional difference is dependent on stimulation of ILC3s by CX3CR1<sup>high</sup> CD14<sup>high</sup> mononuclear phagocytes that have been activated by microbes (70).

Together, these studies suggest that the gut microbiota can shape the development and function of ILCs, primarily through indirect interactions with myeloid and epithelial cell populations, and describe a well-developed network among ILCs, IECs, and the gut microbiota.

### Regulation of the microbiota by ILCs

ILCs can also reciprocally regulate the commensal flora through various mechanisms. For example, cytokines derived from ILCs can influence the composition and compartmentalization of the intestinal microbiota. T-bet deficient ILC1s are impaired in producing IFN $\gamma$ , and mice lacking T-bet develop colitis dependent on IL-17-expressing ROR $\gamma$ <sup>+</sup> ILCs and dysbiosis of *Helicobacter typhlonius* (28). Moreover, ILC2s may represent key players in controlling the anatomical restraint of commensal microbiota when the epithelial barrier is compromised. While not yet proven within the GI tract, ILC2s within the respiratory tract produce amphiregulin, which maintains epithelial barrier function and restores lung epithelium in the event of airway damage due to infection (12). Additional studies are required to demonstrate that ILC1s and ILC2s can directly regulate the commensal microbiota.

Emerging evidence, however, suggests that ROR $\gamma$ <sup>+</sup> ILC3s have the ability to regulate bacterial populations in the intestine. In the healthy intestine, ROR $\gamma$ <sup>+</sup> ILC3s are major producers of IL-22 (36, 47, 63). In the absence of ROR $\gamma$ <sup>+</sup> ILC3s, an increase in serum IgG titers specific for intestinal commensals occurs (71), indicating potential disruption in epithelial barrier integrity and spread of commensal bacteria to peripheral tissues. Following dextran sodium sulfate (DSS) administration to ROR $\gamma$ <sup>+</sup>-deficient mice that induces intestinal epithelial damage, generation of hyperactive B-cells results, promoting colitis (71). As such, ROR $\gamma$ <sup>+</sup> ILC3s may be necessary to inhibit intestinal damage induced by pathogenic B-cells.

CX3CR1<sup>+</sup> phagocytes are also important for IL-22 production by ROR $\gamma$ <sup>+</sup> ILC3 cells. Studies on mice lacking CX3CR1<sup>+</sup> phagocytes show an increased presence of commensal bacteria in mesenteric lymph nodes (MLNs) and greater susceptibility to DSS-induced colitis (45, 72). Blocking IL-22 or depleting ILCs results in outgrowth of *Alcaligenes* (normally found in Peyer's patches and MLNs) into the liver and spleen, and induces systemic inflammation (63), suggesting that ILCs indeed play a role in anatomical containment of commensal bacteria. ILC3-derived IL-22 can also act on the intestinal epithelium to induce expression of tissue protective mucins and antimicrobial peptides, such as RegIII $\beta$ , RegIII $\gamma$ , S100A8 and S100A9 (73). Systemic inflammation is ameliorated after introduction of IL-22 and mice lacking Muc2 or RegIII $\gamma$  show a lack of spatial segregation of commensal bacteria, suggesting an important, albeit indirect, role for ILCs in limiting bacterial outgrowth and inflammation (74, 75). Similarly, S100A8 and S100A9 bind to calprotectin to inhibit proliferation of commensal bacteria and support containment of these bacteria (63). Finally, consistent with the results in mice, *Alcaligenes*-specific responses are detected in CD patients (63).

## Conclusion

ILC3s are a subset of ILCs that are enriched in the mucosa of experimental models of IBD as well as in inflammatory lesions of IBD patients. Because of their prime location, ILC3s are optimally positioned to instantaneously react to both environmental and inflammatory signals received from the gut microbiota, IECs, and other immune cells within the GI tract. Their role in IBD appears to be complex, and not yet fully elucidated, but is greatly influenced by the intestinal cytokine milieu, as well as interactions with the commensal flora and with both hematopoietic and non-hematopoietic mucosal cells. Although several studies cited within this review were performed prior to the identification of ILCs (indeed, early papers referred to ILCs as a subset of NK cells), they support a clear role, particularly for ILC3s, during homeostatic and disease states that is influenced by interactions with the intestinal microbiota (summarized in Figure 1). Nonetheless, future studies are imperative to further define lineage development of gut ILC subsets, to determine the role of other ILC subsets in IBD, and to better describe the reciprocal relationship between mucosal ILCs and the gut microenvironment, and the implications of these interactions during gut health and disease.

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\*of special interest

\*\*of outstanding interest

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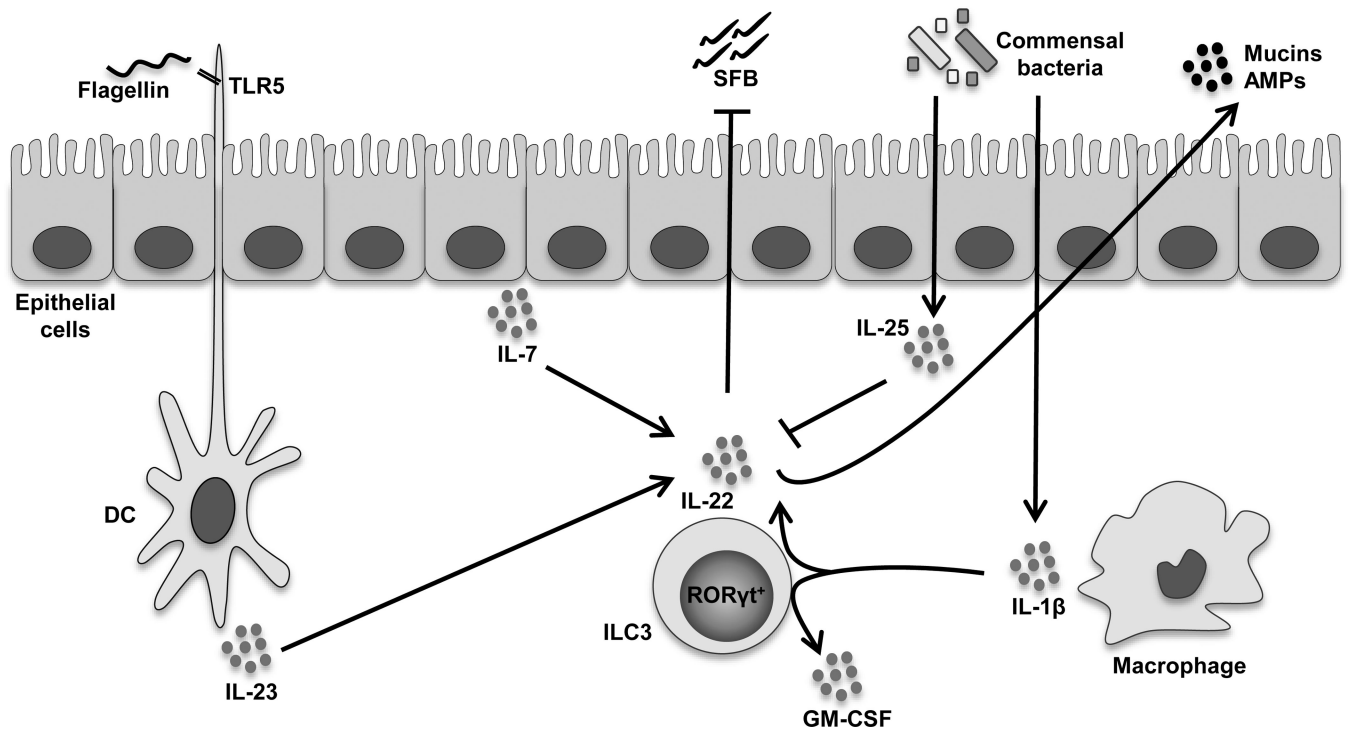
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### Key points

- ILCs are a novel population of innate lymphocytes that are selectively enriched at mucosal sites, comprise subpopulations that are distinct phenotypically and functionally, and are involved in both the maintenance and loss of homeostasis at mucosal surfaces, such as in the GI tract.
- Type 3 ILCs (ILC3s) are major producers of IL-22 in response to microbial products, mucosal antigen presenting cells, as well as the local cytokine milieu, and appear to possess effector function in mouse models of IBD.
- Gut-derived ILC3s expressing natural cytotoxicity receptors (NCRs) may be protective by promoting epithelial integrity and barrier function, while NCR-ILC3s may be pathogenic by inducing intestinal inflammation.
- Dysregulation in the quantity and composition of ILC subsets is observed in IBD patients compared to controls.
- Interactions between ILC3s and the gut microbiota reciprocally regulate each other's functions and greatly influence the role each play during intestinal health and disease.



**Fig. 1. Interactions between type 3 innate lymphoid cells (ILC3s) and the gut microbiota**  
Emerging evidence suggests that crosstalk between ILC3s and components of the intestinal microflora has the ability to support both maintenance of gut homeostasis, as well as induce chronic intestinal inflammation. Central to this process is IL-22, which promotes gut health by inducing the production of epithelial-derived antimicrobial peptides (AMPs) and mucins. ROR $\gamma$ t<sup>+</sup> ILC3s are major producers of IL-22 in response to microbial products, mucosal antigen presenting cells, as well as the local cytokine milieu. Flagellin, the principal component of bacterial flagella, induces TLR5 in dendritic cells (DCs) and promotes IL-23 secretion, which enhances IL-22 from ILC3s. IECs produce IL-7 in response to elements of the gut microbiota, which also stimulates IL-22 from ILC3s. Intestinal macrophage-derived IL-1 $\beta$  has the ability to induce both IL-22 and GM-CSF from ILC3s to support dietary antigenic tolerance. However, commensal bacteria may also induce IECs to produce IL-25, decreasing IL-22 production. In the absence of ILC3-derived IL-22, segmented filamentous bacteria (SFB) demonstrate unrestricted growth, which encourages pathogenic Th17 immune responses that can promote colitis in mice.