

The expanding role of innate lymphoid cells and their T-cell counterparts in gastrointestinal cancers

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ABSTRACT

Innate lymphoid cells (ILCs) contribute to the regulation of gastrointestinal (GI) homeostasis. Over the past 15 years, there has been a large effort to dissect the mechanisms required for GI homeostasis, with a major focus on different immune cell populations and the cytokines that they produce. In contrast to T-helper (Th) cells, ILCs respond rapidly to cytokines in their microenvironment in the absence of specific antigens; however, once activated both cell populations have similar effector functions. Two effector cytokines produced by both ILC3 and Th17 cell populations, Interleukin (IL)-17 and IL-22, have taken center stage for their ability to signal directly to GI epithelial cells and promote epithelial cell survival. In this review, we outline our current understanding of ILCs in the GI tract, and focus on GI cancers associated with aberrant production of IL-17 and IL-22. We highlight evidence from both mouse and patient-based analyses and discuss how tumor cells may hijack the potential evolutionary redundancy of these two cell populations.

1. Introduction

The innate immune system is our first line of defense against pathogens. The main cellular components of the innate immune response include macrophages, monocytes, neutrophils, natural killer cells (NK) and their relatives, innate lymphoid cells (ILCs). The second arm of our defense system is governed by the adaptive immune response, which consists of B lymphocytes and T lymphocytes, including both CD4+ T-helper (Th) cells and CD8+ cytotoxic T-cells. In a number of solid tumor types, neoplastic cells can hijack the natural function of both the innate and adaptive immune system to avoid destruction and fuel their growth (Grivennikov et al., 2010; Pardoll, 2012).

At the onset of tumorigenesis, when cell intrinsic tumor suppressor mechanisms have failed, the innate immune system activates a cascade of events that are designed to eradicate neoplastic cells. In the initial response, the immune surveillance governed by sub-types of macrophages and other tissue resident immune cells results in either the direct destruction of a neoplastic cell, or the production of chemokines to attract additional innate immune cells, including NK cells that can directly lyse the tumor cells (Georgoudaki et al., 2016; Dahlberg et al., 2015). In the second phase of immune surveillance, dendritic cells (DCs) bridge the innate and adaptive immune response by collecting tumor antigens and presenting them to naïve T-cells, resulting in the

activation of cytotoxic CD8+ T-cells that complete tumor destruction (Palucka and Banchereau, 2012).

Over the past 10 years, it has become clear that tumor cells have devised mechanisms to overcome immune editing, and hijack the effector functions of both innate and adaptive immune cells. Here we will discuss recent literature for two previously under-characterized immune cell populations, ILCs and CD4+ Th17 cells, both of which are present in the tumor microenvironment. We will review our current understanding of how ILCs, in particular the ILC3 subgroup, inadvertently contribute to the initiation and progression of gastrointestinal (GI) cancers and compare this to our knowledge of the overlapping function of Th17 cells. We focus on GI cancers, as these cell types are critical in host defense to infections and the control of chronic inflammation, both of which increase the risk of colorectal cancer (CRC) development (Kim and Chang, 2014; Dejea et al., 2013).

2. Innate lymphoid cells are primarily localized to mucosal surfaces

The GI tract contains the largest concentration of immune cells in the body. Sheltered by the mucosal barrier, an immune response can be triggered by exposure to ingested antigens, chemical irritants, and dysregulation of commensal bacteria. In a thought provoking review of

Abbreviations: CRC, colorectal cancer; DSS, dextran sulfate sodium; GI, gastrointestinal; IBD, inflammatory bowel disease; ILC, innate lymphoid cell; IL, interleukin; Th, T-helper

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'The Hallmarks of Cancer', Hanahan and Weinberg discuss our emerging scientific appreciation of the extrinsic tumor-suppressive role the immune system can play, with disruption of the normal immune function capable of promoting tumor development (Hanahan and Weinberg, 2011). It is now well established that communication within the tumor microenvironment between neoplastic cells, fibroblasts, endothelial cells, and immune cells can fuel tumor progression (Klemm and Joyce, 2015). In light of this, reprogramming the tumor microenvironment, through immunotherapy, is currently a major area of research. This in principle, allows for utilization of the immune system beyond the intrinsic tumoricidal capacity of NK cells. Here we focus on the NK cell family, and more specifically the recent extension to include ILCs, with the role of this sub-family in cancer onset, progression and response to immunotherapy not clear.

ILCs develop from common lymphoid progenitors (CLP) present in the bone marrow, and require the expression of IL-2R γ c and inhibitor of DNA-binding 2 (Id2) for their maturation (Yang et al., 2011; Yokota et al., 1999; Klose et al., 2014). ILCs have a lymphoid-like morphology and are defined by the absence of surface markers for myeloid and DCs, and the lack of antigen receptors (Spits and Cupedo, 2012). While they can be detected in a number of tissues, they are relatively rare, and comprise only 0.1–13% of CD45+ leukocytes depending on the tissue examined (Kim et al., 2016). ILCs are unique in that they primarily exist as tissue resident cells at mucosal surfaces, and thus much of our basic knowledge of their function is derived from the GI tract. Here we will outline our current understanding of ILCs in IBD and GI malignancies.

3. Our current understanding of the function of ILCs in the gastrointestinal mucosa

ILCs are subdivided into three groups, based on their known transcription factor and cytokine profiles (Spits et al., 2013). This subclassification parallels the descriptors for their adaptive Th-cell counterparts (Fig. 1). In contrast to Th-cells, ILCs can respond rapidly to cytokines present in the microenvironment without the need for specific antigens, providing an immediate outlet for tissue defense systems against pathogens, maintenance of epithelial homeostasis, and repair at mucosal barriers. However, once activated their effector functions

mirror that of Th-cells, a functional redundancy that tumor cells can readily hijack.

Our understanding of why ILC populations home to the GI tract is still evolving. They are thought to be present in large numbers at mucosal surfaces because their precursors express CXCR6, which is necessary for migration to the intestine, and integrin α 4 β 7, which binds to MADCAM-1, an adhesion molecule expressed within Peyer's patches (Klose et al., 2014; Satoh-Takayama et al., 2014). In adults, the lymphatic network provides a means to migrate between the mesenteric lymph node and the GI lamina propria, a mechanism by which CCR6+ ILC3s are known to assist with the removal of auto-reactive T-cells (Hepworth et al., 2015; Kim et al., 2015). However, at early stages in life, retinoic acid (RA) has been shown to induce the expression of integrin α 4 β 7 and CCR9, and reduce the expression of CCR7 on ILC1s and ILC3s resulting in their propensity to travel to the GI tract (Kim et al., 2015). In contrast, ILC2s express CCR9 facilitating direct migration to the GI tract (Kim et al., 2015). The stage of embryogenesis where the decision to migrate to the GI tract as a final destination has yet to be revealed. The proliferation of tissue-resident progenitor cells in the GI tract is able to promote self-renewal to maintain or increase ILC numbers as required (Gasteiger et al., 2015).

3.1. ILC1s are associated with inflammatory bowel disease

Group 1 ILCs are most similar to NK cells, which upon activation release perforin and granzyme molecules to directly lyse cancer cells (Vivier et al., 2008). ILC1s can be subdivided into NK cells, CD127-ILC1 cells which are functionally similar to CD4+ Th1 cells, and CD127+ ILC1 cells which have cytotoxic abilities similar to CD8+ T-cells (Klose et al., 2014; Robinette et al., 2015). ILC1s respond to IL-12, IL-15, and IL-18 within the mucosal environment (Spits et al., 2016; Klose et al., 2014; Klose et al., 2013). Additionally, it has recently been shown that ILCs are present in the small intestinal lamina propria of mice in the absence of IL-7R α , with IL-15 able to compensate for deficiency in IL-7R (Robinette et al., 2017). ILC1s require the transcription factor T-box factor (T-bet) (Klose et al., 2014), while NK cells and intraepithelial ILC1 cells also require eomesodermin (Eomes) (Spits et al., 2016). ILC1s are best defined by their production of Interferon- γ

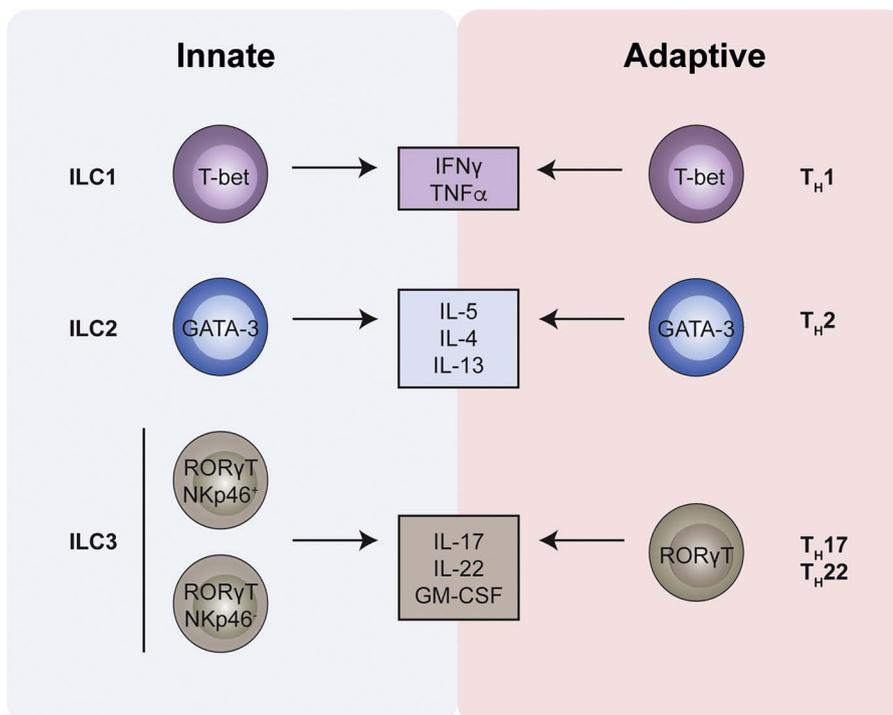


Fig. 1. Redundancy between ILC and Th populations is exemplified by cytokine signatures.

The innate ILC populations (left) and Th populations (right) share common transcription factors and cytokine expression profiles. The significance of these common signatures may relate to evolutionary pressure to rapidly respond to pathogens and maintain epithelial barrier function.

(IFN γ) and tumor necrosis factor- α (TNF α), similar to their Th1 counterparts (Fig. 1). ILC1s are present in both the lamina propria and intraepithelial spaces within the intestine, with elevated numbers associated with Crohn's disease, a type of IBD associated with aberrant IFN- γ expression (Fuchs et al., 2013; Bernink et al., 2013). Animal models suggest that ILC1s contribute to the pathogenesis of IBD, with depletion of ILCs and NK cells resulting in increased inflammation and epithelial damage in the intestine of *Rag1*^{-/-} mice treated with anti-CD40, a mouse model of colitis with enhanced IFN- γ production (Fuchs et al., 2013).

3.2. ILC2s contribute to the development of specialized gastrointestinal cells

ILC2s are activated in response to epithelial cell derived cytokines including IL-25, IL-33, alarmins, prostaglandin D2 (PGD2), and thymic stromal lymphopoietin (TSLP) during inflammation and infection (Kim et al., 2013; Monticelli et al., 2015). In culture, they have also been shown to expand in response to Notch ligands, which are stem cell factors secreted by stromal cells (Zhang et al., 2017). ILC2s are dependent on the transcription factors gata binding protein-3 (GATA3) and retinoic acid receptor-related orphan receptor- α (ROR α) for their maturation and development (Hoyler et al., 2012; Wong et al., 2012). Small numbers of ILC2s can be detected in the blood, with the majority localized to the mucosal surfaces of the lung, skin, and GI tract (Mjosberg et al., 2011). ILC2s are primarily known for their secretion of IL-13 and IL-15, similar to their Th2 counterparts (Fig. 1); however, they have also been shown to secrete IL-4, IL-5, IL-6, IL-8, IL-9, and GM-CSF (Walker and McKenzie, 2013). ILC2s can also secrete amphiregulin (Areg), a member of EGF family, that is linked to colon cancer (Ciardiello et al., 1991). Interestingly, it has been shown that after dextran sulfate sodium (DSS)-induced colitis, mice deficient for *Areg* were more susceptible to inflammation and epithelial damage, suggesting that ILC2s may contribute to a wound healing response (Monticelli et al., 2015). Importantly, ILC2s contribute to the development of a specialized population of epithelial cells, called tuft cells, which are a source of IL-25 that may have a fundamental role in the detection and expulsion of worms (von Moltke et al., 2016). Indeed, ILC2s are well characterized for their protective immune response against helminth parasites (Neill et al., 2010).

3.3. ILC3s are essential to management of the gastrointestinal microbiome

In humans, ILC3s are divided into two primary sub-types based on their expression of CCR6: fetal lymphoid tissue induced cells (LTi) are CCR6+, while post-natal ILC3s are CCR6- (Spits et al., 2013). The sub-classification of ILC3s is further delineated based on expression of the activating NK cell receptor (NCR) NKp44 in humans, and NKp46 in mice (Hoorweg et al., 2012). Adult ILC3s respond to IL-1 β and IL-23 (Kim et al., 2014), and similar to Th17 cells, are defined by the requirement of the transcription factor RAR-related orphan receptor gamma (Roryt) for development (Fig. 1) (Spits et al., 2013). Roryt also regulates aryl hydrocarbon receptor (AHR), a transcription factor necessary for Th17 function and the survival of ILC3s (Hughes et al., 2014; Qiu et al., 2012). The ligand for AHR is available through food by-products and the microflora, thus linking ILC3s to the microbiome (Qiu and Zhou, 2013; Zelante et al., 2013). ILC3s produce Th17-type cytokines including IL-17A, IL-17F and IL-22 either alone or in combination (Buonocore et al., 2010; Hughes et al., 2010). In some instances, ILC3s can also produce TNF α and IFN γ in addition to Th17 cytokines, consistent with the Th17/Th1 plasticity of their adaptive counterparts (Spits et al., 2013). However, the level of expression of these cytokines differs between ILC3 populations, with NCR+ ILC3 cells known to produce IL-22, but very little IL-17, while NCR- cells produce mainly IL-17 and GM-CSF (Vonarbourg et al., 2010; Glatzer et al., 2013). In some human NCR+ ILC3 cells, upon stimulation with IL-23, a potent pro-inflammatory response ensues resulting in the

release of TNF α as opposed to the release of IL-22 (Glatzer et al., 2013). Like ILC2s, NCR- ILC3s express MHCII, and can present antigen in the absence of costimulatory molecules (Hepworth et al., 2015; Hepworth et al., 2013). However, only splenic ILC3s are able to induce T-cell responses (von Burg et al., 2014). Instead, intestinal ILC3s can out-compete T-cells for IL-2, resulting in T-cell death (Hepworth et al., 2015). This provides a mechanism to limit commensal bacteria-specific CD4 T-cell responses and chronic intestinal inflammation, which together can provide a microenvironment that supports cancer development (Hepworth et al., 2015; Hepworth et al., 2013).

ILC3s are the most abundant ILC in the human intestine at steady state, and are found in cryptopatches, lymphoid follicles, and throughout the lamina propria (Bernink et al., 2013; Klose and Artis, 2016). ILC3s constitute the majority of the ILCs in the lamina propria of the ileum of mice, with corresponding characterization of the healthy human colon not yet described (Bernink et al., 2013). In Crohn's disease patients, IL-17A and IL-17F are elevated in CD3- cells, which are most likely to be ILC3s (Geremia et al., 2011). It is believed that ILCs contribute to an inflammatory feedback loop in Crohn's disease, with the loss of mucosal barrier function and exposure to microbial antigens resulting in a chronic state of inflammation. This would prolong the activation of ILC3s, resulting in an increase in IL-17 that could repair the epithelial barrier (Geremia et al., 2011), although, the persistent increase in IFN γ secreting ILC1s are known to enhance the inflammatory response that contributes to the disease (Bernink et al., 2013). A current thought is that a switch between IFN γ to IL-22 producing ILCs could have therapeutic utility in Crohn's disease (Bernink et al., 2015).

ILC3s are best characterized for their roles in anti-bacterial immunity, tissue homeostasis, and repair following chronic inflammation (Buonocore et al., 2010; Mortha et al., 2014). However, different ILC3 subsets appear to have different functions within this context. NCR+ IL-22-producing ILC3 cells prevent colonization by pathogenic bacteria, and can signal directly the colonic stem cell compartments to maintain epithelial integrity (Sato-Takayama et al., 2008; Sanos et al., 2009). This is achieved in part through IL-22 mediated induction of the expression of the antimicrobial peptide RegIII γ and α (1,2)-fucosylation of intestinal epithelial cells, which maintain homeostatic interactions with the microbiota (Pham et al., 2014). On the other hand, NCR- IL17-producing ILC3s have a pathogenic role in colitis, facilitated by their expression of GM-CSF in response to IL-1 β secretion by macrophages and DC derived IL-23 (Mortha et al., 2014; Pearson et al., 2016). Moreover, blockade of IL-17 and IFN γ using neutralizing antibodies in *Rag*^{-/-} mice infected with *H. hepaticus* resulted in reduced colitis pathology (Buonocore et al., 2010). Understanding the balance between these two populations will be essential to understanding the maintenance of the epithelial barrier. A simple explanation may stem from the tissue localization of ILC3s, with NCR-ILC3s located below crypts in cryptopatches and thus may be involved directly in epithelial maintenance, while NCR+ ILC3s are found throughout the lamina propria and thus are able to respond rapidly to pathogen infection (Eberl et al., 2004).

3.4. Cross talk between ILCs and the relationship to epithelial cells

There is increasing evidence that there is cross-regulation between ILC subsets. In the steady state GI tract, the microbiota can induce the differentiation of Th17 cells (Ivanov et al., 2008), and alter the number of IL-22 producing ILC3 cells, with the number of IL-22-producing ILC3s lower in germ free mice after weaning (Sawa et al., 2011). The repression of ILC3s is believed to be mediated by the epithelial cell derived IL-25 (also termed, IL-17E), which acts on IL-17BR + ILC2 or CD11c + DCs (Sawa et al., 2011). Consistently, IL-25 expression is reduced and IL-22 producing ILC3s are expanded following epithelial damage by DSS-induced colitis (Sawa et al., 2011). Moreover, mice with epithelial-deletion of IKK α (a noncanonical NF κ B-dependent gene)

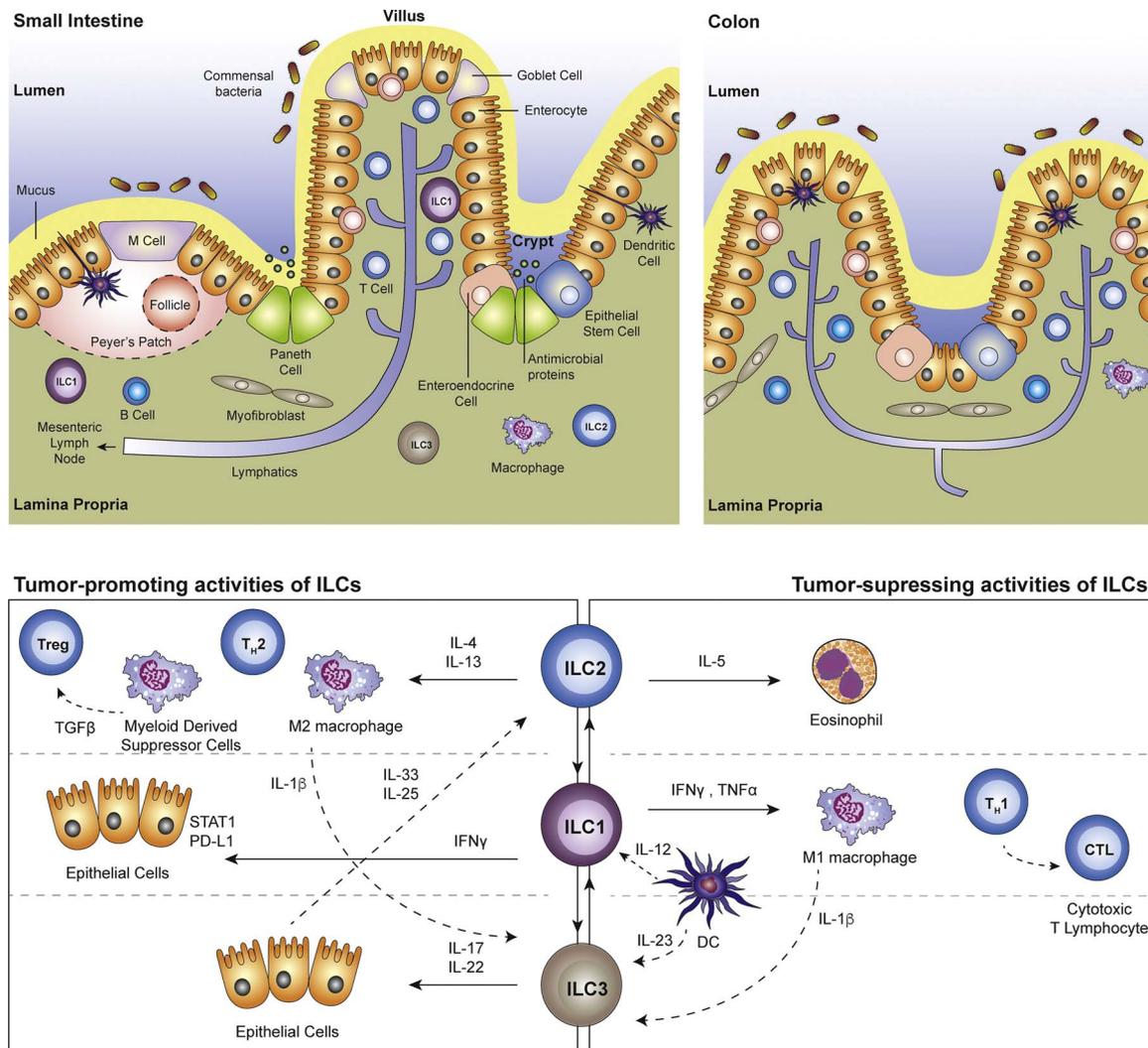


Fig. 2. ILCs are located throughout the gastrointestinal mucosa. In the adult mouse, ILC1s, ILC2 s, and ILC3 s are present throughout the intestine (top panel, left), and are less well characterised in the colon (top panel, right). They traffic to the intestinal tract through the mesenteric lymph node, where they take up residence within the lamina propria. In gastrointestinal cancers, which arise within the colon, ILCs may have both pro- and anti-tumorigenic roles (bottom panel), which primarily stems from their known cytokine expression profiles. How this relates to their Th-counterparts has yet to be clearly defined.

are highly susceptible to *C.rodentium* infection and DSS-induced colitis, which was associated with less IL-22-producing ILC3 infiltration and the subsequent reduction of antimicrobial peptide expression (Giacomin et al., 2015). Mechanistically, deficiency of IKK α leads to elevated TSLP which can promote the function of ILC2. These results further highlight the relationship between ILC subsets and epithelial cells. However, the interaction whether direct or indirect between ILC2 and ILC3 remains to be elucidated. Since both ILC2 and ILC3 have been shown to be anti- and pro-tumorigenic, it will become increasingly important to further delineate their role in CRC (Fig. 2).

4. Link between innate lymphoid cells and the progression of gastrointestinal cancers

It is now well appreciated that the growth and progression of cancers of the GI tract can be fueled by cytokines produced within the tumor microenvironment. It is clear from the overlap in localization, transcriptional activity, cytokine profiles and effector functions that ILCs strongly resemble different Th-cell subsets. Here we will summarize our understanding of the role of ILCs in GI cancers, and how they, together with their Th counterparts, may inadvertently aid tumor growth.

4.1. ILC1s may be associated with colitis-associated cancer

A direct role for ILC1s in CRC has not been explored. Given the link between IBD, which has a dominant ILC1 signature (Bernink et al., 2013), and increased risk of CRC (Karvellas et al., 2007) it is likely that ILC1s may contribute to the early onset and growth of GI tumors. It could be argued that this may be associated with IFN γ , the dominant cytokine produced by ILC1s, which has known functions in CRC progression. However, a contribution of IFN γ to tumorigenesis is not likely to be black and white. *In vitro* IFN γ has been shown to promote apoptosis (O'Connell et al., 2000), inhibit angiogenesis (Beatty and Paterson, 2001), and inhibit proliferation (Wang et al., 2015) of CRC cells. *In vivo*, IFN γ has also been shown to promote colon epithelial apoptosis and inhibit proliferation, which was linked to attenuated chronic inflammation (Schmitt et al., 2012). Similarly, using the *Apc*^{Min} mouse model of familial adenomatous polyposis, the genetic deletion of a single *Ifn* γ allele was attributed to augmented CRC progression (Wang et al., 2015). Since IFN γ is required for the Th1 response, which is known to enhance the activity of cytotoxic effector cells, including CD8⁺ T-cells, NK cells, and macrophages (Whitmire et al., 2005; Reiter, 1993; Haabeth et al., 2011; Hoepner et al., 2013), it is possible that lack of an immune mediated lyses of tumor cells attributed to this

observation. Indeed, IFN γ is able to upregulate MHC class I expression on tumor cells which in turn promotes a CD8 T-cell mediated cytotoxic response (Martini et al., 2010). IFN γ is also a potent mediator of signal transducer and activator of transcription-1 (STAT1) activation, which is linked to the upregulation of PD-L1 expression on tumor cells, and their ability to evade cytotoxic T-cells (Garcia-Diaz et al., 2017). Indeed, ILC1s have been shown to play a role in immune surveillance in other cancers, including non-small-cell lung cancer (Djenidi et al., 2015). How ILC1 derived IFN γ may contribute to the success or failure of current cancer immunotherapy approaches will be an interesting area of research.

Along a similar line of thought, TNF α is associated with the pathogenesis of IBD, with biological inhibitors of this cytokine a major pharmaceutical success story (Levin et al., 2016). Like IFN γ , TNF α also has a role in anti-tumor immunity, through the recruitment of macrophages and DCs (Villeneuve et al., 2005). However, like IFN γ , this is not a simple correlation as dysregulated TNF α can also promote tumor formation and growth in CRC models, where therapeutic blockade of TNF α has been shown to prevent tumor formation (Popivanova et al., 2008). The disparity in our understanding of the role of each of these cytokines in CRC may stem from our understanding of the dominant source, and location, of the cells actively secreting and responding to them. Clarification of the presence and function of ILC1s in this context may assist with delineating the pro and anti-tumorigenic properties of IFN γ and TNF α .

4.2. ILC2s may support pro-tumorigenic immune cells in gastrointestinal cancers

While direct investigations into the role of ILC2s in CRC have yet to be performed, the frequency of ILC2s in peripheral blood mononuclear cells is increased in gastric cancer patients compared to healthy controls (Bie et al., 2014). There is emerging evidence that prototypical ILC2-type cytokines may play a significant role in CRC, since IL-4, IL-15 and IL-33 have been detected in CRC cells (Di Stefano et al., 2010; Kuniyasu et al., 2001; Zhou et al., 2013), and can promote the secretion of IL-13, which has been suggested to trigger tumor promoting myeloid derived suppressor cells to secrete TGF β or polarize macrophages towards their pro-tumorigenic M2 phenotype (Dhakal et al., 2014; Gabrilovich and Nagaraj, 2009). However, *Il13*^{-/-} mice have comparable colonic tumor formation to wild-type mice, suggesting that IL-13 secretion does not contribute directly to CRC (Ingram et al., 2013). IL-15 has been shown to suppress colitis-associated cancer (CAC) by promoting anti-tumor immunity (Bahri et al., 2015). In contrast, IL-4 deficient mice developed fewer CRC tumors compared to wild-type mice (Osawa et al., 2006). IL-33-induced ILC2s have been shown to protect against acute colitis, which was associated with Areg, since *Areg*^{KO} mice had increased disease (Monticelli et al., 2015). Depletion of Areg in *Apc*^{Min} mice can also lead to reduced tumor burden compared to wild-type mice, implicating Areg in intestinal tumorigenesis (Guzman et al., 2013). TSLP has also been linked to CRC (Yue et al., 2016). Among the other cytokines secreted by ILC2s, clear roles for IL-6 and GM-CSF in CRC have been elucidated (Grivennikov et al., 2009; Wang et al., 2014a). However, the dominant cellular source of these cytokines driving tumor progression has yet to be determined. It is likely, that tumor cells have taken advantage of growth factors secreted by numerous cell types to ensure a growth advantage.

4.3. ILC3s stimulate the growth and expansion of neoplastic gastrointestinal cells

Among the three subsets of ILCs, the role of ILC3 is gaining increased research interest for its potential tumor promoting activities. The function of the NCR+ IL-22-producing ILC3 subset in preventing aberrant microbial colonization in the intestine is an evolutionary adaptation that may inadvertently promotes the growth of mutant

epithelial cells that express the receptors needed for IL-17 and IL-22 mediated pro-tumorigenic STAT3 activation (Kirchberger et al., 2013). This line of thought has been further fueled by a recent observation, whereby tumor development was decreased in *Rag*^{-/-}; *Il17*^{-/-} mice, while both *Rag*^{-/-} and wild-type mice developed large tumors following IL-23 transgene injection (Chan et al., 2014). This observation suggests that IL-23 activates an innate source of IL-17, independent to T cells, that contributes to intestinal tumorigenesis. IL-22 producing ILCs have also been shown to promote tumor growth in a bacterial model of CRC, with depletion of IL-17+ and IL-22+ ILCs preventing tumor formation (Kirchberger et al., 2013). In this model; however, IL-17 played only a minor role in tumor growth, with inhibition of IL-17 resulting in reduced inflammation, while inhibition of IL-22 significantly reduced tumor burden. The discrepancies between the role of ILC derived IL-17 and IL-22 could potentially be explained by the differences in localization and function of the NCR+ and NCR- ILC3 subsets.

5. Is the evolutionary redundancy of ILC3s and Th17 cells hijacked by tumor cells?

The similarities between ILCs and their Th-cell counterparts leaves one to question when they arose during evolution, if they co-evolved to ensure robust immunity, or if selective pressure led to shared cytokine expression signatures that tumors use to their advantage. The substantial heterogeneity of both the ILC3 and Th17 lineages suggests that they may still be evolving under pressure from a changing microbial environment.

5.1. IL-17 produced by Th17 cells is associated with gastrointestinal cancer progression

Although both ILC3 and Th17 cells produce IL-17A, with the majority of the literature to date on IL-17A in CRC attributed to Th17 cells. Human tumor-infiltrating Th17 cells have been extensively documented in patients with CRC, and their polarization was found to be mediated by tumor-associated macrophages (Kryczek et al., 2009). An increase in Th17 cells has been linked to poor prognosis in CRC patients (Tosolini et al., 2011) and IL-17A can promote CAC, with *Il17*^{-/-} mice having reduced tumor burden (Hyun et al., 2012). IL-17A deficiency has also been shown to alleviate CRC in *Apc*^{Min} mice (Chae et al., 2010).

Once IL-17A is secreted, it binds to IL-17 receptors A (IL-17RA) and C, with IL-17RA expressed on both hematopoietic cells and non-hematopoietic cells including colonic epithelial cells and cancer-associated fibroblasts (Wang et al., 2014b). Engagement of the receptor complex leads to activation of mitogen activated protein kinases (MAPK), NF κ B and C/EBP signaling. This results in the production of chemokines that recruit neutrophils, T-cells, and myeloid cells (Lan et al., 1999). Additionally, IL-17A can induce the production of a range of anti-microbial proteins including β -defensin, S100A7, S100A8, S1200A9 and lipocalin-2 (Kao et al., 2004; Liang et al., 2006). These observations suggest that IL-17 has a major role in inflammation and protection against infection. Indeed, *il17a*^{-/-} mice are susceptible to *C. rodentium* infection, where the major source of IL-17A is T cells (Ishigame et al., 2009).

Both IL-17 producing CD3- and CD3+ cells are present in the intestine of IBD patients (Geremia et al., 2011), and the expression of IL-23 is known to be elevated in CRC patient tumors (Grivennikov et al., 2012; Langowski et al., 2006). IL-23 and IL-1 β are essential to the development of both human ILC3s and Th17 cells, with both IL-23 and IL-1 β derived from CX3CR1+ mononuclear phagocytes (MNP) or CD14-dendritic cells in the human intestine (Bernink et al., 2015; Longman et al., 2014). Tumor infiltrating neutrophils and DCs have also been shown to secrete IL-23 in the GI tract (Kvedaraitė et al., 2016). Following the observation that *Apc*^{Min}; *Il23p19*^{-/-} mice have a reduced tumor burden, which correlated with reduced IL-17 expression in the

distal colon (Grivennikov et al., 2012), the pathogenesis of IL-23 was primarily linked to Th17 cells. This was further supported when *IL23p19*^{-/-} mice were shown to be resistant to CAC, antibody-mediated inhibition of IL-23 reduced CAC burden, and syngeneic tumor transplants into mice deficient for IL-23R did not grow (Langowski et al., 2006; Wu et al., 2009). However, we now appreciate that IL-23 creates an environment that can readily prime ILC3 cells, and following antigen presentation fuel Th17 cells, suggesting that much of the IL-17 literature in GI cancers may need to be revisited.

5.2. IL-22 produced by ILCs is associated with gastrointestinal cancer progression

In naïve mice, ILC3s are the main source of IL-22, a cytokine that is known to stimulate the proliferation and survival of colonic epithelial cells (Kirchberger et al., 2013). Polymorphisms in *IL22* are associated with an increased risk of CRC (Thompson et al., 2010), although how these polymorphisms impact on protein expression levels and function is not clear. The level of IL-22 expressed in human colon tumors has been linked to tumor growth and metastasis, which is thought to be mediated by STAT3 activation and upregulation of associated anti-apoptotic and pro-proliferation genes (Jiang et al., 2013). In contrast to IL-17A producing Th17 cells, IL-22 producing Th17 cells have been less well documented in CRC.

Once IL-22 is secreted, it interacts with a heterodimeric receptor complex, consisting of IL-22R1 and IL-10R2, with IL-22R1 expressed exclusively by non-hematopoietic cells (Tachiiri et al., 2003). Engagement of the receptor complex results in the phosphorylation and activation of STAT3, which regulates the production of anti-microbial peptides such as RegIII β , RegIII γ , S100A8, S100A9 and β -defensin in order to limit pathogen survival (Pickert et al., 2009; Zheng et al., 2008). This has been best demonstrated in the *C. rodentium* infection model, in which Ror γ t ILC3 deficient mice rapidly succumb to infection, attributed to attenuated IL-22 signaling (Tumanov et al., 2011; Guo et al., 2014). Under homeostatic conditions, IL-22 signaling is inhibited by IL-22 binding protein (IL-22BP), a soluble receptor secreted by immature DCs (Martin et al., 2014). When tissue damage occurs, expression of IL-22BP is downregulated, allowing IL-22 exert its tissue repair functions (Martin et al., 2014). In a CAC model, IL-22BP deficient mice have accelerated tumor development (Huber et al., 2012). Most importantly, IL-22-driven STAT3 activation has been implicated in several mouse models of CRC including a bacterial-induced CRC mouse model, where depletion of ILC3 blocked the development of invasive CRC and neutralization of IL-22, to a greater extent than IL-17, resulted in less intestinal inflammation and reduced tumor burden (Kirchberger et al., 2013). However, the study did not address which sub-lineage of ILC3s were responsible for the tumor development. Other studies suggest that in the early stages of inflammation-associated CRC, IL-22 may protect against tumor development, while at later stages IL-22 evokes a pro-tumorigenic function (Huber et al., 2012). Our understanding of the source and function of IL-22 in CRC is really only just beginning to become clear.

6. Implications for the success and failures of cancer therapeutics

Pending the stage of CRC at the time of diagnosis, patients will undergo standard-of-care chemotherapeutic treatments. It is now appreciated that chemotherapy drastically alters the microbial environment (Roy and Trinchieri, 2017), which would indirectly alter the ILC and Th17 profiles of a patient. As a result of their location, ILCs would be the first population of cells to respond to chemotherapy induced changes to a microbial environment, in particular ILC3s, which would result in an increase in the presence of IL-17A and IL-22. NCR+ IL-22 producing ILC3 cells are essential to the proliferation of intestinal stem cells that express IL-22R (Lindemans et al., 2015), facilitating tissue repair and cancer growth, which one could predict would negate the

intended function of a chemotherapeutic. Indeed, serum IL-22 levels correlate with chemoresistance in CRC patients, which was attributed to the induction of the IL-22 induced pro-survival activities of STAT3 (Wu et al., 2013; Wu et al., 2014). A similar scenario is emerging for IL-17, with expression levels shown to increase following Fluorouracil (5 FU) treatment, a standard of care chemotherapeutic in CRC, resulting in the activation of IL-17 mediated pro-survival pathways in colonic epithelial cells (Wang et al., 2014b). IL-17 also been shown to mediate resistance to anti-angiogenic therapies (Chung et al., 2013). Whether these observations relate solely to the innate response, or linger as a result of the adaptive response remain to be revealed. However, these observations warrant a better understanding of the innate and adaptive source of IL-17 and IL-22 following chemotherapeutic treatments. It is likely that their role in preventing bacterial infections, chronic inflammation and mediating repair of normal tissues following multiple rounds of chemotherapy will need to be weighed against their likelihood of promoting extrinsic resistance as reagents targeting these cytokines, and their associated transcription factors, are developed for clinical use.

7. Concluding remarks

Our understanding of the role of ILCs in the tumor microenvironment is only just beginning, with the relative contribution of ILC3s and Th17 cells to tumor progression not clear. ILCs are unique in that they do not need antigen sensing for their activation, and thus respond to environmental triggers more rapidly than T-cells. This distinctive feature also suggests that they may be the first to trigger the growth and progression of a tumor, which may be sustained by their adaptive T-cell counterparts. The tumor promoting functions shared by these cell populations are most likely related to cytokine secretion, which are amenable therapeutic targets. Thus, the success of anti-cytokine therapies alone or in combination with other treatment options will depend on our understanding of the timing of cytokine expression during tumor onset, progression, and standard-of-care therapeutic treatments.

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