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New weapons in the war on worms: Identification of putative mechanisms of immune-mediated expulsion of gastrointestinal nematodes

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Abstract

Parasitic nematode infections of humans and livestock continue to impose a significant public health and economic burden worldwide. Murine models of intestinal nematode infection have proved to be relevant and tractable systems to define the cellular and molecular basis of how the host immune system regulates resistance and susceptibility to infection. While susceptibility to chronic infection is propagated by T helper cell type 1 cytokine responses (characterised by production of IL-12, IL-18 and interferon- γ), immunity to intestinal-dwelling adult nematode worms is critically dependent on a type 2 cytokine response (controlled by CD4+T helper type 2 cells that secrete the cytokines IL-4, IL-5, IL-9 and IL-13). However, the immune effector mechanisms elicited by type 2 cytokines in the gut microenvironment that precipitate worm expulsion have remained elusive. This review focuses on new studies that implicate host intestinal epithelial cells as one of the dominant immune effector cells against this group of pathogens. Specifically, three recently identified type 2 cytokine-dependent pathways that could offer insights into the mechanisms of expulsion of parasitic nematodes will be discussed: (i) the intelectins, a new family of galactose-binding lectins implicated in innate immunity, (ii) the resistin-like molecules, a family of small cysteine-rich proteins expressed by goblet cells, and (iii) cytokine regulation of intestinal epithelial cell turnover. Identifying how the mammalian immune response fights gastrointestinal nematode infections is providing new insights into host protective immunity. Harnessing these discoveries, coupled with identifying what the targets of these responses are within parasitic nematodes, offers promise in the design of a new generation of anti-parasitic drugs and vaccines.

Keywords

Parasitic nematodes; Immune effector mechanisms; Intelectin; Resistin-like molecules; Intestinal epithelial cells

1. Introduction

Soil transmitted helminthiasis continue to be the most prevalent chronic infectious diseases of humans, with an estimated 2 billion individuals infected worldwide (Colley et al., 2001). The major public health significance and economic impact of this group of pathogens is hard to quantify, although the World Health Organisation (WHO) has estimated that more than 1000 million people world-wide are infected with one or more of the major pathogen species of humans: *Trichuris trichiura*, *Ascaris lumbricoides* and the hookworms *Necator americanus* and *Ancylostoma duodenalis* and that 39 million disability-adjusted life years (DALYs) are attributable to these four nematode species alone (Chan et al., 1994; Chan, 1997; Albonico et

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al., 1999; WHO, 2001). The most severe clinical symptoms of infection, including protein-losing enteropathy, chronic dysentery, anemia and rectal prolapse occur in the minority of heavily infected individuals (Symons, 1969; Bundy and Cooper, 1989; Grecis and Cooper, 1996; Albonico et al., 1999). However, significant detrimental clinical outcomes also occur in moderately infected individuals, including impaired nutritional status, growth retardation and lower educational achievement (Callender et al., 1992; Nokes et al., 1992; Nokes and Bundy, 1994). Beyond the direct consequences of infection, there is growing evidence from infected humans and murine model systems that chronic helminth infection can have a detrimental effect on the ability of individuals to respond to vaccination and can influence responses to other infections including malaria (Cooper et al., 2001; Chenine et al., 2005; Graham et al., 2005).

Intestinal nematode parasites are also a serious economic concern in the livestock industry. *Haemonchus*, *Trichostrongylus* and *Ostertagia* are the main disease-causing parasites, contributing significantly to reduced productivity and costing approximately US\$1.5 billion annually in repeated anthelmintic treatments to control infections (Newton and Munn, 1999; Newton and Meeusen, 2003). Widespread reports of anthelmintic resistance and the growing costs of developing new anthelmintic drugs (Albonico et al., 2004; Lochnit et al., 2005) require the development of more long-lived immunological intervention strategies. The development of immunologically defined laboratory models of intestinal nematode infection such as *Trichinella spiralis*, *Nippostrongylus brasiliensis*, *Heligmosomoides polygyrus* and *Trichuris muris* has facilitated new insights into the immunological basis of susceptibility and resistance to infection under controlled laboratory conditions. By employing these nematode infection models, advances have been made in understanding the cellular and molecular interactions involved in the generation and regulation of immune responses during infection. Despite unique aspects of phylogeny, biochemistry, morphology and lifecycle strategies, a consensus has emerged that immunity to intestinal-dwelling nematode worms is critically dependent on a type 2 cytokine response (controlled by CD4+T helper type 2 cells that secrete the cytokines IL-4, IL-5, IL-9 and IL-13), while susceptibility to chronic infection is propagated by type 1 cytokine responses (characterised by production of IL-12, IL-18 and interferon (IFN)- γ) [for recent reviews, see (Finkelman et al., 1997; Maizels and Yazdanbakhsh, 2003; Cliffe and Grecis, 2004; Hayes et al., 2004; Maizels et al., 2004)]. IL-4 and IL-13, acting through shared and distinct pathways that are dependent on the type 2 cytokine-associated transcription factor STAT6, appear to be the most critical cytokines for immunity; while IL-4 stimulates fluid secretion in the gut, IL-13 promotes goblet cell responses and both cytokines induce smooth muscle contraction (McKenzie et al., 1998; Urban et al., 1998, 2001; Akiho et al., 2002; Zhao et al., 2003; Finkelman et al., 2004; Madden et al., 2004). Recent studies in livestock and human populations support a role for type 2 cytokines in host resistance to infection (Jackson et al., 2004; Pernthaner et al., 2005) and provide important indications that murine hosts are appropriate systems to model immune regulation of parasitic nematode infection.

Although the requirement for type 2 cytokines in worm expulsion is well established, the immune effector cells and molecular mechanisms elicited by this type of immune response have remained elusive. In the case of *T. spiralis*, clear evidence exists that mast cells can play an important role in worm expulsion (Knight et al., 2000, 2002; Brown et al., 2003; McDermott et al., 2003). However, expulsion of a number of intestinal nematode parasites—while dependent on type 2 cytokines—can occur in the absence of classical effector mechanisms associated with type 2 responses such as B cell activation, antibody production, eosinophilia and mastocytosis (Else and Finkelman, 1998; Betts and Else, 1999; Betts et al., 2000). In recent years this has led a number of groups to adopt global gene profiling and proteomic analyses of intestinal responses associated with worm expulsion in an attempt to identify novel type 2 cytokine-dependent immune effector mechanisms involved in immunity. In our own gene profiling studies of the intestinal response following *T. muris* infection, we found 171 genes that were upregulated greater than 1.5-fold over uninfected controls. Of the 10 genes exhibiting

the most marked infection-induced upregulation, half of these were gut epithelial cell-specific genes (see Table 1). Specifically, intelectin, a family of calcium-dependent galactose-binding lectins (Komiyama et al., 1998) and calcium-activated chloride channel 3, an epithelial ion channel implicated in mucus secretion (Gruber et al., 1998; Gyomai et al., 2001; Leverkoehne and Gruber, 2002), were the two most highly upregulated genes. Pancreatic lipase-related protein 2 and pancreatic co-lipase, both members of the lipase family (Lowe, 2000) were also highly expressed. Resistin-like molecule- β , a small cysteine-rich goblet cell specific protein (Steppan et al., 2001), was in the top five epithelial-specific genes upregulated following *T. muris* infection. Interestingly, none of these dominant epithelial cell-specific genes had previously been associated with type 2 cytokine responses that are expressed around the period of worm expulsion.

In an independent microarray study, Knight and colleagues isolated epithelial cells from the intestine of naïve and *T. spiralis*-infected mice around the period of worm expulsion and identified 216 genes that were upregulated in the epithelial cell compartment; these included goblet cell genes such as resistin-like molecule- β (RELM β) and other epithelial genes implicated in barrier function, ion exchange, tissue repair and metabolism (Knight et al., 2004). In elegant proteomic analyses of purified epithelial cells, Pemberton et al. demonstrated that the most marked change in protein expression within epithelial cells around the period of expulsion of *T. spiralis* was that of a newly described gene product, intelectin-2 (Pemberton et al., 2004b). More recently, Datta et al. performed similar analyses of epithelial gene expression around the period of expulsion of *T. muris* using a custom array containing 9000 genes. Many of the genes that were upregulated in the large intestinal epithelium were similar to those outlined in Table 1, including intelectin, calcium-activated chloride channel 3 and pancreatic lipase-related protein 2, as well as genes such as angiogenin-like protein and angiogenin-related protein (Datta et al., 2005). Therefore, in three independent studies using either *T. muris* or *T. spiralis* infection, a number of common epithelial-intrinsic genes were upregulated around the period of worm expulsion, specifically, intelectins, resistin-like molecules and machinery associated with ion exchange and barrier function.

The magnitude of the epithelial response highlighted by these microarray studies and the consistent pattern of gene expression suggest that epithelial cells themselves could be regarded as an immune effector cell against intestinal nematode parasites. Moreover, these results implicate the gene products expressed in epithelial cells in the coordinated host response to infection and potentially in contributing to worm expulsion and/or tissue repair. This review will focus on two of the most abundantly expressed and best-characterised gene products that were upregulated in the microarray results described above: (i) the intelectins, and (ii) the resistin-like molecules. In addition, a novel mechanism of worm expulsion involving immune-mediated changes in epithelial cell turnover will be discussed.

2. The intelectins

Lectins are found in mammals as either surface-bound receptors or in plasma where they exist as opsonins or agglutinins. This large family of molecules is conserved in evolution and performs a number of biological functions, including regulation of cell proliferation, recognition of tumor antigens and innate recognition of carbohydrates present in pathogen cell walls (Apostolopoulos and McKenzie, 2001; East and Isacke, 2002; Wang et al., 2004; Elola et al., 2005; Iwanaga and Lee, 2005). The mannose receptor is a well-characterised mammalian lectin that recognises mannosyl-containing residues of carbohydrates found in bacterial cell walls. Mannose receptors are found on phagocytic cells and are thought to play a critical role in innate immunity by enhancing uptake of bacteria (Ezekowitz et al., 1990; Stahl and Ezekowitz, 1998). Rather than binding mannose-rich subunits, the intelectin family is composed of calcium-dependent galactose-binding lectins. Intelectin-1 was first identified by

sequence homology to the *Xenopus* egg lectin XL35. The frog egg lectin is released upon fertilisation of the egg, whereupon it binds to galactose-containing residues in the mucin covering the egg, precipitating hardening of the egg and preventing polyspermy (Nishihara et al., 1986). Subsequently, murine intelectin-1 was found to be expressed in paneth cells in the small intestine and was hypothesised to play a role in innate defense against bacterial infections (Komiya et al., 1998). Using both reverse transcription (RT)-PCR and proteomic approaches, a novel intelectin variant was identified in mice called intelectin-2, that exhibited 91% sequence identity to intelectin-1 and was found only in the small intestine (Pemberton et al., 2004a). There are also two known intelectins in the human genome: intelectin-1 (also called lactoferrin receptor) exists as a 120 kDa disulfide-linked homotrimer expressed in the thymus, heart and intestine, while human intelectin-2 expression is restricted to the small intestine (Lee et al., 2001; Suzuki et al., 2001; Tsuji et al., 2001). Studies demonstrating that recombinant human intelectin could bind to galactofuranosyl residue-containing molecules isolated from the bacterium *Nocardia*, support a role for intelectins in innate recognition of bacteria (Tsuji et al., 2001).

As discussed above, gene profiling analysis by a number of groups independently identified intelectin expression as a hallmark of parasitic nematode infection in the gastrointestinal (GI) tract. Subsequently, intelectin-1 expression was shown to be constitutive in the small intestine by two-dimensional gel electrophoretic studies, while upregulation of intelectin-2 was the most marked change in protein expression in the intestinal epithelium following infection with *T. spiralis* (Pemberton et al., 2004b). Critically, maximal intelectin-2 expression occurred around day 14 p.i., coincident with expression of type 2 cytokines and worm expulsion. These results were subsequently confirmed by RT-PCR and immunohistochemical staining identified paneth cells and goblet cells as the cellular source of intelectins following infection (Pemberton et al., 2004a). Gene profiling of intestinal responses following infection with *T. muris* also identified intelectin as the gene that exhibited most robust upregulation in genetically resistant mouse strains around the period of worm expulsion (see Table 1; Datta et al., 2005). We were able to confirm the microarray expression data by RT-PCR, finding that following *T. muris* infection, both intelectin-1 and intelectin-2 mRNA transcription were upregulated in the intestines of genetically resistant mice around the period of worm expulsion (Fig. 1A). In contrast, *T. muris* infection of the genetically susceptible AKR mouse strain was not associated with expression of either intelectin (unpublished observations). Immunohistochemical analysis demonstrated that there was little intelectin protein expression in the intestine of naïve mice (Fig. 1B) and identified goblet cells as the cellular source of intelectins following *T. muris* infection (Fig. 1C). Intelectins were localised to the exocrine vesicles within goblet cells (Fig. 1D), suggesting they are targeted for secretion into the intestinal lumen. The dominant expression of intelectins following *T. spiralis* and *T. muris* infections, coupled with the differential expression of intelectins in resistant and susceptible mouse strains following *T. muris* infection, implicate this family of glycoproteins in anti-nematode responses. Supporting this contention, Pemberton et al. recently found that certain inbred mouse strains naturally lack expression of the intelectin-2 gene. While most mouse strains express both intelectin-1 and intelectin-2 and rapidly expel *T. spiralis*, two strains that lack intelectin-2 (C57BL6 and C57BL10) exhibit a significant delay in worm expulsion (Pemberton et al., 2004a). While the delayed expulsion of *T. spiralis* in these mice is likely to be a multifactorial event and is unlikely to be due exclusively to the absence of intelectin-2, these results support a potential function for intelectins in contributing to rapid expulsion and host resistance to infection.

The abundant expression of intelectins in the intestinal epithelium and their localisation to secretory paneth and goblet cells in the gut suggest they are likely to be present in the intestinal lumen at high concentrations around the period of worm expulsion. Given that intelectins bind galactofuranosyl-containing residues in bacterial cell walls, intelectins may bind similar carbohydrate residues in parasitic nematodes and impair worm fitness, potentially through

influencing attachment and/or feeding behaviour or essential biological processes associated with cell proliferation and death that would render the worms more susceptible to immune-mediated expulsion. However, to date there is no evidence that intelectins directly bind to parasitic nematodes and the possibility that elevated intelectin expression following nematode infections in the GI tract may be secondary to enhanced exposure of the host to bacterial symbionts present in the gut lumen cannot be ruled out at present. Notwithstanding that, intelectins may contribute to anti-nematode responses indirectly, through binding to and altering the properties of other mucin glycoproteins that are secreted by intestinal goblet cells. Analogous to the *Xenopus* egg lectin, XL35, which binds to other glycoproteins resulting in hardening of the egg (Nishihara et al., 1986), there may be a similar cross-linking function for mammalian intelectins in the gut resulting in the formation of a 'glycoprotein cement' around the nematodes that precipitates their expulsion from the host. A recent study demonstrated that in addition to exposure to nematode parasites, intelectins are also expressed following Th2 cytokine production associated with airway inflammation (Kuperman et al., 2005). Therefore, in addition to potential direct effects on nematodes, the intelectins may also perform broader functions during type 2 inflammation including immunoregulation or tissue remodeling. Taken together, a role for the intelectins in anti-nematode responses is an attractive one that will require further investigation to define the functional contribution of this family of molecules in type 2 responses and host protective immunity.

3. Resistin-like molecules (RELMs)

Resistin (also called ADSF or found in inflammatory zone 3 (FIZZ3)) is a recently discovered 12.5 kDa adipocyte-derived hormone that plays a critical role in antagonising glucose homeostasis and insulin sensitivity (Holcomb et al., 2000; Kim et al., 2001; Steppan et al., 2001; Steppan and Lazar, 2004). Three other members of the resistin-like molecule family (RELM α (FIZZ1), RELM β (FIZZ2), and RELM γ) were subsequently identified on the basis of an unusual and conserved C-terminal cysteine-rich domain (Holcomb et al., 2000; Steppan et al., 2001; Gerstmayr et al., 2003). The resistin gene family also exhibits unusual structural features including the formation of cysteine-rich multimeric structures that are conserved in all mammalian genomes analysed so far (Patel et al., 2004). Similar to the pattern of resistin expression, RELM α is expressed abundantly in adipocytes as well as the heart and lungs of naïve mice. It is also expressed at high levels in pulmonary epithelial cells, alveolar pneumocytes and the bronchoalveolar lavage fluid in a mouse model of pulmonary inflammation (Holcomb et al., 2000). Given its widespread distribution, it is not surprising that a number of functions have been proposed for RELM α including antagonising the action of insulin, inhibition of nerve growth factor-mediated gene expression of dorsal root ganglia, inhibition of adipocyte differentiation and stimulation of myofibroblast differentiation and expression of type I collagen (Holcomb et al., 2000; Blagoev et al., 2002; Rajala et al., 2003; Liu et al., 2004a). In contrast to the relatively broad expression of RELM α , RELM β (FIZZ2) is expressed exclusively in goblet cells in the lung and GI tract (Steppan et al., 2001; Zimmermann et al., 2004) while RELM γ appears to exhibit species-specific expression patterns and can be found in nasal respiratory epithelial cells and hematopoietic cells (Gerstmayr et al., 2003; Schinke et al., 2004).

A number of research groups have identified RELMs as a dominant component of type 2 cytokine-dependent responses following nematode infection (see above). Loke et al. were the first to identify RELM α as one of the most abundantly expressed transcripts in alternatively activated macrophages that are elicited in the peritoneum following implantation of the tissue-dwelling filarial nematode, *Brugia malayi* (Loke et al., 2002). Alternatively activated macrophages express activation markers, although unlike their 'classically' activated counterparts that are promoted by proinflammatory cytokines like IFN- γ and perform microbicidal functions, alternatively activated macrophages fail to upregulate expression of

inducible nitric oxide synthase. Rather, alternatively activated macrophages express high levels of arginase and have been implicated in immune suppression, responses to tissue-dwelling helminth parasites and tissue remodeling associated with type 2 cytokine responses (Mantovani et al., 2002; Raes et al., 2002a,b; Gordon, 2003; Nair et al., 2003; Noel et al., 2004; Park-Min et al., 2005; Rauh et al., 2005). RELM α expression in macrophages was found to be dependent on IL-4 and represented 2% of total mRNA in *B. malayi*-elicited alternatively activated macrophages (Loke et al., 2002; Maizels et al., 2004; Nair et al., 2005). This level of expression was second only to YM-1, a novel protein that shares homology to mammalian chitinases and has been implicated in cell-cell interactions and immune cell chemotaxis (Jin et al., 1998; Owhashi et al., 1998, 2000; Chang et al., 2001; Sun et al., 2001). Elevated expression of RELM α was also reported in the thoracic cavity of *Litomosoides sigmodontis*-infected mice (Nair et al., 2005) and was also recently identified as a dominant response in the gut following infection with the GI nematode parasites *T. spiralis*, *N. brasiliensis* and *T. muris* (Knight et al., 2004; Nair et al., 2005; Wang et al., 2005; and see Table 1). Therefore, expression of RELM α appears to be a critical component of the programmed profile of gene expression associated with multiple nematode infections in diverse anatomical sites.

Similarly, expression of RELM β was found to be a common response in the GI tract following infection with *T. spiralis*, *N. brasiliensis* and *T. muris* (Artis et al., 2004b). Critically, maximal expression of RELM β was associated with expression of type 2 cytokines and worm expulsion following all three infections despite differences in lifecycle strategies and biological niches favoured by these different species (Artis et al., 2004b). In the case of *T. muris* infection, RELM β expression was only observed following infection of resistant mouse strains that develop type 2 cytokine responses but not in animals susceptible to chronic infections (Artis et al., 2004a,b; Wang et al., 2005), demonstrating that RELM β expression is not a generic response to nematode infection; rather, its expression is restricted to environments in which protective type 2 responses dominate. Consistent with a restricted expression profile, there was no demonstrable upregulation of RELM β mRNA or protein following protozoan infection in the GI tract (Artis et al., 2004b). Unlike RELM α that appears to be expressed in macrophages or epithelial cells in the GI tract, RELM β expression appears to be restricted to goblet cells (Artis et al., 2004b) (see Fig. 2).

In vitro studies demonstrated that IL-4 and IL-13 could directly induce expression of RELM β mRNA in a goblet cell-like intestinal epithelial cell line (He et al., 2003; Artis et al., 2004b). Further, administration of rIL-13 to normally susceptible AKR mice following infection with *T. muris* resulted in enhanced RELM β expression and worm expulsion while blockade of IL-4 receptor signalling in normally resistant strains inhibited RELM β responses (Artis et al., 2004b). Consistent with a role for type 2 cytokines in regulating expression, the RELM β promoter contains numerous binding sites for the type 2 cytokine-associated transcription factor STAT6. Early reports suggested RELM β expression was restricted to the GI tract, however it is now clear that cells in the lung express this family member, either following infection with *N. brasiliensis* or the induction of type 2 cytokine-dependent airway inflammation (Zimmermann et al., 2004; Nair et al., 2005). There is limited analysis of RELM γ expression, although nematode infection-induced upregulation of RELM γ has been reported in the GI tract following *T. muris* infection (Wang et al., 2005).

The picture that emerges is one in which expression of RELMs occurs in multiple tissues following exposure to diverse nematode parasites. So what might be the functions of this family of molecules? There are a number of possibilities, including direct anti-parasitic effects, tissue repair and immune regulation. Evidence for a possible role for RELM β as an effector molecule that directly targets nematode parasites comes from studies with *T. muris* and *Strongyloides stercoralis*. RELM β binds specifically to structures associated with the lateral alae in both parasites. In the case of *T. muris*, the lateral alae are modified into a structure called the bacillary

band (Fig. 3A and B). This band is composed of numerous epidermal glandular and non-glandular cells, some of which contain dendritic processes that run between pore cells and adjacent nerve cells and are implicated in neuro- and/or chemo-sensory functions (Gibbons, 2002; see Fig. 3C). In *S. stercoralis*, RELM β binds to the lateral alae that overlie nerve-rich lateral cords and in vitro assays showed that RELM β could inhibit nematode chemotaxis towards host tissue extract (Artis et al., 2004b). Therefore, coupled with other effector mechanisms, a possible function for RELM β may be to disorient nematode parasites in their GI niche and contribute to their expulsion. A disorientation function for RELMs that might contribute to worm expulsion is supported by the demonstration that RELM family members can bind to neurons and influence their function in vertebrates (Holcomb et al., 2000). Further, it is noteworthy that many current anti-nematode drugs target worm neuro- and chemo-sensory functions, perhaps via a common pathway targeted by host-derived RELMs.

No receptors for any of the RELMs have been identified in mammalian genomes to date. However, it is possible that in addition to an anti-parasitic function, RELMs may also perform an autocrine or paracrine function on other mammalian cells. For instance, local expression of RELM β in the lung and GI tract may influence cells of the innate and adaptive immune system to augment type 2 cytokine responses or sensitise the tissue to these cytokines and so promote host protective immunity. In addition, the putative role for RELM α in deposition of alpha smooth muscle actin and collagen in a lung model of fibrosis (Liu et al., 2004a), suggest RELM α may play a critical role in wound healing and tissue remodeling following nematode infection. Indeed, this repair response may also have a protective anti-parasitic effect, functioning to encapsulate nematode parasites or to alter the tissue, making it less permissive to chronic nematode infections. Nair et al. recently suggested an immuno-regulatory role for RELMs. In addition to expression in macrophages within the GI tract, RELM α is also expressed in B cells, dendritic cells and macrophages in the lymph nodes following exposure to *B. malayi* (Nair et al., 2005). Furthermore, in vitro activation with IL-4 induced RELM α expression in B cells, bone marrow-derived DC and bone marrow-derived macrophages (Nair et al., 2005). Therefore, in addition to potential anti-parasite activity and influencing tissue remodeling in the GI micro-environment, these studies highlight a possible role for RELM α in regulating innate and adaptive immune responses in secondary lymphoid tissues. The ability of RELMs to activate mitogen-activated protein kinases and suppressor-of-cytokine-signalling pathways (Kushiyama et al., 2005; Stepan et al., 2005) is consistent with their ability to influence host immune response genes. Supporting a broader regulatory role for this family of proteins, recent studies have highlighted that expression of RELMs is not restricted to nematode infection. For example, RELM α is highly expressed during chronic murine trypanosomiasis and in *Schistosoma mansoni* egg-induced granulomas (Raes et al., 2002a,b; Sandler et al., 2003; Noel et al., 2004). In addition to other infectious diseases, expression of RELM α and RELM β has been reported in other inflammatory diseases including airway inflammation and cystic fibrosis (Stutz et al., 2003; Liu et al., 2004b; Norkina et al., 2004; Zimmermann et al., 2004). A dominant type 2 cytokine response characterises these conditions and although the function of each RELM family member is likely to be dictated by the infectious/inflammatory stimuli and tissue-specific location, these studies collectively implicate RELM proteins as effector and/or regulatory molecules in type 2 inflammation. The development of new reagents to block or overexpress the RELM proteins should provide important new insights into their biological functions.

4. Cytokine regulation of epithelial cell turnover: the 'epithelial escalator' model

In addition to profound changes in gene expression following exposure to nematode infection (Li et al., 1998; Knight et al., 2004; Datta et al., 2005; and Table 1), host intestinal epithelial cells also exhibit dramatic alterations in their proliferative behaviour, at least some of which

are regulated by the immune system. The mammalian intestinal epithelium undergoes continuous and rapid homeostatic renewal and within each crypt unit forms a highly polarised proliferative hierarchy (Li et al., 1994; Potten, 1998; Marshman et al., 2002). Anchored pluripotent stem cells are found at the base of the crypts and following asymmetric division give rise to transit daughter cells that undergo continuous linear migration lumenally from the base of the crypts to the extrusion zone at the luminal surface. In the process of migration, epithelial cells undergo maturation and differentiation into a number of lineages including absorptive enterocytes, endocrine cells, M cells and goblet cells (Marshman et al., 2002). Proliferative indices suggest epithelial cells lose their ability to proliferate as they migrate with the bulk of mature differentiated cells undergoing apoptosis at the luminal surface. The balance of cell proliferation, migration and death is critical in maintaining epithelial integrity and tissue morphology in the gut.

A number of studies have demonstrated that epithelial cell proliferation can be severely disrupted following infection with parasitic nematodes such as *N. brasiliensis*, *S. stercoralis*, and *Trichostrongylus colubriformis*, implicating this dysregulated epithelial response in the crypt hyperplasia and villous atrophy commonly reported following nematode infection (Symons, 1978; Hoste, 1989; Hoste and Mariana, 1989; Artis et al., 1999). In the case of *T. muris*, cell position-linked proliferation analysis demonstrated that chronic infection of susceptible mouse strains was associated with a significant increase in the frequency of proliferating stem cells and transit cells in each crypt (Artis et al., 1999). The accumulation of proliferating epithelial cells during chronic infection suggested that either the epithelium was undergoing elevated proliferation or that proliferating cells were impaired in their migration up the crypt column, resulting in a build-up of proliferating epithelial cells in the crypt column. Critically, IFN- γ was found to play a critical role in the accumulation of proliferating epithelial cells during chronic infection, suggesting the anti-nematode immune response plays an important role in regulating epithelial cell turnover in the inflamed intestine (Artis et al., 1999).

In addition to comparing the epithelial cell proliferation between resistant and susceptible mouse strains following *T. muris* infection, a recent study by Cliffe et al. compared the rate of epithelial cell migration and turnover in mouse strains that develop type 2 cytokine responses and expel infection versus those that express type 1 cytokine responses and develop chronic infection. In striking contrast to genetically susceptible AKR mice, resistant mouse strains exhibited a much more rapid rate of epithelial cell migration up the crypt column around the period of worm expulsion (Cliffe et al., 2005). Critically, the protective type 2 cytokine, IL-13, was implicated in driving rapid migration and turnover of the epithelium, essentially creating an 'epithelial escalator' proposed to dislodge *T. muris* from its epithelial niche. IFN- γ -induced expression of the chemokine CXCL10 was found to reduce epithelial cell turnover in susceptible animals and blockade of this chemokine in infected AKR mice reversed the accumulation of proliferating epithelial cells and resulted in enhanced epithelial cell migration and turnover coupled with expulsion of *T. muris* (Cliffe et al., 2005). In addition, the same treatment strategy resulted in enhanced epithelial cell turnover and worm expulsion in infected severe combined immunodeficient mice (that lack T and B cells), providing the first demonstration that immunity to this nematode infection can occur in the absence of an adaptive immune response. Moreover, this finding suggests that regulation of epithelial cell turnover alone is sufficient to control worm expulsion (Cliffe et al., 2005). These studies suggest that earlier reports of elevated frequencies of proliferating cells during chronic nematode infection were not indicative of increased proliferation but rather the result of reduced migration of epithelial cells up the crypt column. Indeed, slowing the rate of epithelial cell turnover may be a strategy employed by parasitic nematodes to promote their own survival. The existence of nematode-derived factors that can influence host intestinal epithelial cell proliferation support this hypothesis (Rikihisa et al., 1984; Huby et al., 1999). Based on these new findings discussed

above, it will be interesting to determine whether the ‘epithelial escalator’ model contributes to expulsion of other GI nematode parasites and whether chemicals known to influence epithelial turnover will prove effective in eradicating infection in chronically infected hosts. Based on the discussion above, it will also be interesting to determine whether blockade of CXCL10, in addition to altering epithelial cell turnover, also results in altered epithelial cell differentiation and gene expression including the intelectins and/or RELM family members. It is tempting to speculate that a combination of type 2 cytokine-driven dysregulation of epithelial cell turnover, coupled with profound changes in gene expression, provide an arsenal of host epithelial cell-intrinsic anti-nematode responses that precipitate worm expulsion and resistance to infection.

5. Concluding remarks

The molecules and pathways discussed in this review, and their potential functions in contributing to expulsion of intestinal nematode parasites, are areas of intense research and the development of new tools to deplete or enhance these pathways offer promise for future discoveries. Challenges that lie ahead include identifying how expression of these host molecules is regulated and the identification of nematode gene products that are targeted by the host response. Defining how different lifecycle stages of parasitic nematodes are influenced by these molecules and whether these pathways play distinct roles in primary versus secondary infection, will also be important. An additional task will be to determine whether the novel cytokine-induced epithelial genes identified in micro-arrays perform unique roles following infection with individual nematode species or if certain epithelial gene products exhibit a common protective role against multiple GI nematodes; identification of a single anti-nematode factor that acts against all nematode species would have important implications, particularly given the polyparasitism often reported in individuals exposed to nematode parasites. As we look forward, it will be important to extend these studies to humans and veterinary species that suffer the debilitating consequences of parasitic nematode infections. Notwithstanding these challenges, the recent data accumulated on cytokine regulation of gene expression in intestinal epithelial cells and the influence of cytokines on enterocyte function indicate these pathways are a critical component in host control of intestinal nematode infection. Harnessing these discoveries offers the potential to instruct the design of a new generation of intervention strategies.

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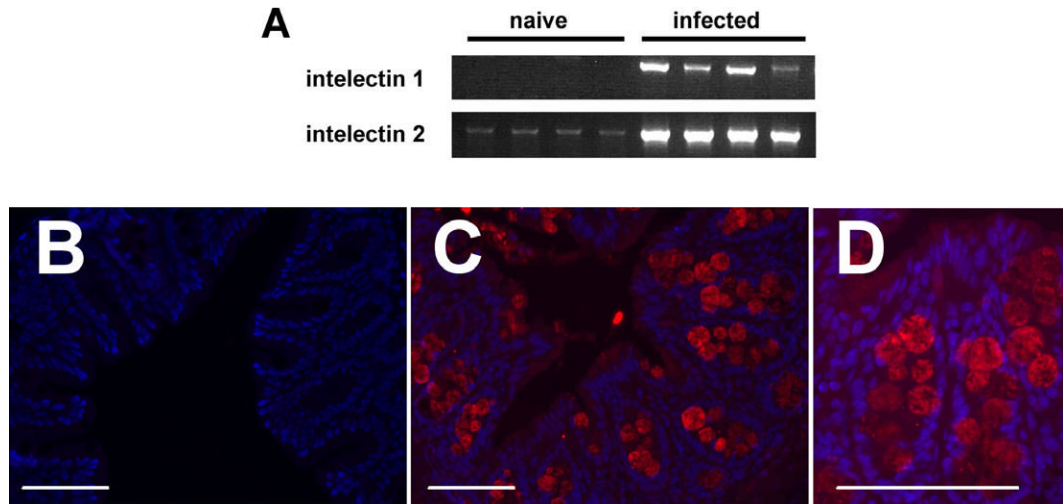


Fig. 1. Intelectins are expressed by intestinal goblet cells following *Trichuris muris* infection. Genetically resistant BALB/c mice were infected with 150 *T. muris* eggs and cecal RNA or histologic sections prepared from naïve or infected animals on day 18 p.i. as previously described (Artis et al., 2002,2004a,b). (A) reverse transcription-PCR analysis demonstrated robust upregulation of intelectin-1 and intelectin-2 in infected animals (details of primer sequences and methodology can be found in (Pemberton et al., 2004a)). (B)-(D) Immunofluorescent staining of intelectins (staining red) in naïve (B) or infected mice (C) and (D). Paraformaldehyde-fixed tissues were wax-embedded and 5 μ m sections stained using a polyclonal rabbit anti-intelectin1/2 antibody (a gift from Hugh Miller, University of Edinburgh, UK) following standard immunofluorescence protocols. Intelectins are expressed within exocrine vesicles of intestinal goblet cells (D). Epithelial cell nuclei are stained in blue with DAPI. Blocking peptide confirmed specificity of staining. Bar, 100 μ m.

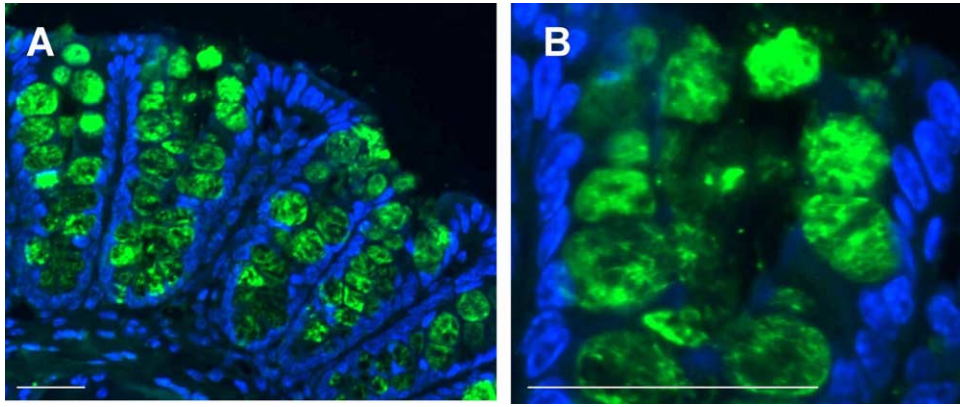


Fig. 2. Resistin-like molecule (RELMB)- β is expressed exclusively in intestinal goblet cells following *T. muris* infection. Genetically resistant BALB/c mice were infected with 150 *T. muris* eggs and histologic sections prepared from naïve or infected animals on day 18 p.i. as previously described (Artis et al., 2002,2004a,b). Paraformaldehyde-fixed tissues were wax-embedded and 5 μ m sections stained using a polyclonal rabbit anti-RELMB antibody (Peprotech, USA) following standard immunofluorescence protocols. (A) Immunofluorescent staining revealed that RELMB (staining green) is localised to intestinal goblet cells. (B) RELMB is expressed exclusively within exocrine vesicles of intestinal goblet cells. Epithelial cell nuclei are stained in blue with DAPI. Blocking peptide confirmed specificity of staining. Bar, 50 μ m.

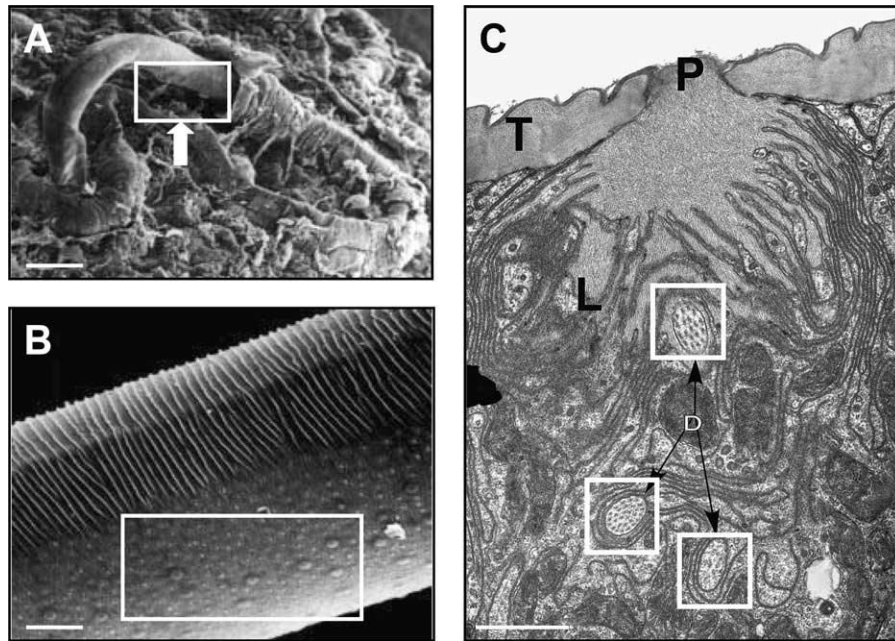


Fig. 3.

Ultrastructural analysis of the bacillary pores of *T. muris*. (A) SEM of *T. muris* entering host intestinal epithelial cells in infected mice. Bar, 100 μm . Genetically resistant BALB/c mice were infected with 150 *T. muris* eggs and tissue sections prepared from naïve or infected animals on day 14 p.i. as previously described (Artis et al., 2004a; Tilney et al., 2005). (B) Higher power analysis revealed the localisation of the bacillary pores to the ventral surface of the parasites (box). Bar, 10 μm . (C) TEM demonstrated that a subset of pores contains numerous dendritic processes (boxes) from adjoining adjacent nerve cells. T, tegument; P, pore opening, L, actin rich plical structures surrounding the pore opening. Bar, 1 μm . (Adapted, with permission, from Tilney et al., 2005.)

Table 1

Global gene profiling of intestinal epithelial gene expression following *Trichuris muris* infection of genetically resistant mice

Gene	Fold induction
Intelectin	83.63 ^a
Mast cell protease 2	35.57
Chloride channel calcium activated 3	10.56 ^a
Pancreatic lipase-related protein 2	9.12 ^a
Serine (or cysteine) proteinase inhibitor, clade F, member 1	9.05
Resistin like beta	8.20 ^a
Colipase, pancreatic	6.07 ^a
Carboxypeptidase A3, mast cell	4.90
Resistin like alpha	4.82
Fanconi anemia, complementation group C	4.29

Genetically resistant BALB/c mice were infected with 150 *T. muris* eggs as previously described (Artis et al., 2002,2004a,b). At day 18 p.i., a time point coincident with maximal type 2 cytokine responses and worm expulsion, RNA was isolated from naïve or infected intestinal tissue and microarray analysis carried out using a Massachusetts General Hospital mouse oligo chip containing 14,611 70-mer oligos. Spots were measured on an Agilent scanner and quantified by GenePix software. Numbers refer to fold induction of gene expression over naïve controls (four animals per group).

^a Denotes known intestinal epithelial gene.