

**Mechanisms of Neutrophil Recruitment and Immunopathology During Acute
Clostridium difficile Colitis**

by

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To Mom, Dad, and Daniel

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Chapter 1

Background

Portions of this chapter have been previously published

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Kingdom: Eubacteria(1)
Phylum: Firmicutes(2)
Class: Clostridia(2)
Order: Clostridiales(2)
Family: Peptostreptococcaceae(2)
Genus: <i>Clostridium</i> (2)
Species: <i>difficile</i> (2)
Gram Staining: Gram positive(3)
Morphology: Bacillus(4)
Spore Formation: Yes(3, 5)
Spore Characteristics: Antibiotic-resistant(5, 6), Alcohol-resistant(3, 5, 7), Aero tolerant(5). Heat-resistant (60°C for 24 hours)(7).
Motility: Motile(4), Flagellated(8-11). Flagellar components have been implicated in adherence and colonization in the host(8, 12, 13), but data is conflicting and inconclusive.
Aerotolerance: Obligate Anaerobe(4, 14)
Vegetative Propagation: Grows well at 37°C in the absence of oxygen(14)
Doubling Time: 40-70 minutes(15)
Virulence Factors: Two large clostridial toxins, TcdA(308kDa) and TcdB(270kDa)(3). Binary toxin (CDT) found in a low percentage of strains as well(3, 16).
Genetic Features: Pathogenicity Locus (PaLoc). 19.6 kilobases long. Contains <i>tcdA</i> and <i>tcdB</i> genes (encoding TcdA and TcdB). Also contains <i>tcdE</i> (encodes a holin permitting toxin release), and <i>tcdD</i> and <i>tcdC</i> , positive and negative regulators of the locus respectively(3, 17, 18).
Cdt locus (CdtLoc). Encodes the two subunits of binary toxin, <i>cdtA</i> and <i>cdtB</i> , as well as <i>cdtR</i> , a putative regulator of the locus. Found in only a small percentage of <i>C. difficile</i> stains(3, 19, 20).
Genome Size: 4.29 megabases(21)
Antibiotic Resistance (Reported): Bacitracin, Daunorubicin, Nogalamycin, Erythromycin, Clindamycin, Gentamicin, Tetracycline, Ampicillin, Cefotaxime, Cefoxitin, Cefuroxime(21). Cycloserine(14).
Antibiotic Sensitivity (Reported): Teicoplanin, Vancomycin(21).
Strains Used in This Dissertation: VPI 10463: ATCC 43255 630: ATCC BAA-1382
Representative Genomes: VPI 10463: GenBank Accession Number: NZ_ABKJ00000000.2 630: GenBank Accession Number: AM180355

Table 1: Microbiological Characteristics of *Clostridium difficile*

Clinical Significance of *Clostridium difficile*

Clostridium difficile (*C. difficile*) is a Gram-positive spore-forming obligate anaerobic bacterium (Table 1) and is a causative agent of antibiotic-associated diarrhea and the major causative agent of antibiotic associated pseudomembranous colitis(22-24). Though *C. difficile* was first described in 1935 after its isolation from the feces of healthy infants(22-24), it was not until the late 1970s when a series of experiments with clindamycin-treated hamsters identified *C. difficile* as the causative agent of antibiotic-associated pseudomembranous colitis(22, 25, 26). Subsequent studies have revealed that colonization with *C. difficile* was associated with a broad array of clinical outcomes in patients: from asymptomatic colonization to diarrhea to severe outcomes including pseudomembranous colitis and fulminant colitis(23, 27, 28). Indeed, despite *C. difficile* being first described as a human pathogen in relation to pseudomembranous colitis, less than half of all patients infected with *C. difficile* actually develop pseudomembranous colitis(23, 29, 30).

The prevalence and severity of *C. difficile* infection in patients has increased considerably in recent years(23, 31, 32). The incidence of *C. difficile* infection in the US has drastically increased in recent years from less than 150,000 cases in 2000 to nearly 350,000 cases reported in 2010(31). The higher incidence of disease has also been associated with an increase in mortality attributable to *C. difficile* infection: while *C. difficile* was associated with less than 6 deaths per one million population in 1999, by 2004 that number had climbed to nearly 24 deaths per one million population(23, 32). All told, *C. difficile* infection is estimated to be responsible for at

least 14,000 deaths and \$1 billion in healthcare-associated costs annually in the United States(33-35), underscoring the clinical importance of this disease.

In recent years, it has been suggested that the emergence of so-called “hypervirulent” B1/NAP1/027 strains of *C. difficile* may be at least partly responsible for the increased frequency of *C. difficile* infection(36, 37). In addition to resistance to fluoroquinolones(36, 37), preliminary studies suggested that these “hypervirulent” isolates produced much higher levels of both TcdA and TcdB as compared to other clinical isolates(37, 38). Furthermore, NAP1/027 strains were also reported to sporulate at a faster rate and produce more spores overall than other *C. difficile* strains(37, 39, 40). Additionally, a recent study by Carlson Jr. and colleagues using a large collection of ribotype 027 strains found that in aggregate, ribotype 027 strains did not produce more spores than other *C. difficile* strains *in vitro*(41). However, *C. difficile* isolates from cases of severe disease produced significantly higher numbers of spores than all other strains assayed, suggesting that spore production, independent of ribotype, may contribute to the severity of *C. difficile* infection(41).

The main virulence factors of *C. difficile* are two large clostridial toxins, named TcdA and TcdB(18, 23, 27, 42). Both of these toxins are glycosyltransferases, which glucosylate and irrevocably inactivate small GTPases including Rho, Rac, and Cdc42 within target cells(18, 42). Upon binding to a target cell, both toxins are endocytosed and undergo a conformational change within the endosome(42-45). Though the process is better understood for TcdB, the internalization toxin ultimately results in the release of the N-terminal glycosyltransferase domain of the

toxin into the host cytosol(42, 46-48). Intoxication of eukaryotic cells with *C. difficile* toxin results in cell rounding and loss of cell membrane integrity, as well as cell death(18, 49, 50).

Pathogenesis of *C. difficile*

C. difficile was first identified as a causative agent of pseudomembranous colitis in the hamster model(22, 25, 26), and many investigations into the pathogenesis of *C. difficile* have been performed using this same model(51-56). As infection of hamsters(57, 58) or mice(59) with non-toxigenic (TcdA and TcdB negative) strains of *C. difficile* does not result in disease, and indeed precolonization of hamsters with non-toxin producing strains of *C. difficile* prevents the development disease upon challenge with toxigenic *C. difficile* strains(53, 57), many studies have focused on the role of *C. difficile* toxins in disease(51, 52, 56, 58, 60). However, many of these investigations have produced conflicting results. In one study genetic deletion of TcdB, but not TcdA, resulted a drastic decrease in mortality following infection with TcdB deficient mutants in an acutely fatal hamster model in one study(52). Additionally, numerous studies have demonstrated that *C. difficile* strains producing only TcdB are still capable of producing high levels of morbidity and mortality in clindamycin treated hamsters(51, 61). A subsequent study using TcdA or TcdB deficient mutants reported near identical mortality following infection of hamsters with strains expressing each toxin alone(58). While initial studies using strains of *C. difficile* deficient in TcdA and TcdB but positive for binary toxin indicated no role for binary toxin in promoting morbidity or mortality in

hamsters(56), a recent study has reported mortality following infection of hamsters with *C. difficile* expressing binary toxin but not TcdA and TcdB (60). Thus, while disease as a result of *C. difficile* infection is most certainly toxin-mediated, the relative importance of each individual toxin in driving disease development is unclear.

Colonization Resistance, the Microbiome, and Antibiotics

The microbiome provides numerous nutritional benefits to the host, including synthesizing vitamins(62) and short chain-fatty acids (SCFAs)(63), and the presence of the microbiome is also vitally important for the development and functionality of the intestinal immune system(64, 65). Additionally, the presence of the microbiome within the gastrointestinal tract limits the ability of pathogens, including *C. difficile*, to persist within the gut and cause disease, a phenomenon known as colonization resistance(66, 67).

Alteration of the intestinal microbiome through the use of antibiotics is commonly associated with increased susceptibility to intestinal pathogens(68-70). Metronidazole treatment markedly alters the composition of the colonic microbiota and is associated with increased disease severity during *C. rodentium* colitis(70). Antibiotic treatment also permits efficient *Campylobacter jejuni* infection in mice(69), as well as the development of acute typhlocolitis following *Salmonella typhimurium* infection(68). Furthermore, disruption of the intestinal microbiota by host inflammatory responses also permits the expansion of members of the Family

Enterobacteriaceae(71), highlighting the potential for unwanted bacterial overgrowth following disruption of the normal microbiota.

The intestinal microbiome controls the susceptibility of experimental animals to *C. difficile* colonization and infection. Under normal conditions mice are refractory to *C. difficile* infection(66, 72), however, antibiotic administration permits subsequent *C. difficile* colonization and the development of intestinal disease(59, 66, 72-82). Antibiotic treatments that permit *C. difficile* infection are associated with marked alterations in the composition and diversity, but not overall bacterial density, of the intestinal microbiome(66, 70, 73, 80, 83). Alterations in the structure of the microbiome are also associated with increased levels of certain metabolites, including taurocholate, succinate, and fructose, which can be utilized by *C. difficile* for outgrowth(83, 84), suggesting a potential mechanism of colonization resistance to *C. difficile*.

Structure and Cellular Composition of The Intestines

The gastrointestinal tract is the largest environment-exposed surface area in the body, and is in direct contact with a large and varied microbial community(85). Fortunately, the gastrointestinal tract is also home to a large variety of immune cells and structures that help maintain intestinal homeostasis in the face of microbial challenge(86-88). Intestinal epithelial cells physically separate underlying tissues from the intestinal lumen(89, 90), while goblet cells maintain a mucus layer to prevent microbial contact with epithelial cells(91, 92). Leukocytes beneath the

epithelial cell layer can both promote or inhibit inflammatory responses(93-96), and are efficiently organized into effector and inductive sites(97-99). This organization largely prevents unwanted inflammation while retaining the ability to respond rapidly to a wide array of perturbations.

The **intestinal epithelium** is actually a single layer of cells, all of which are derived from multipotent stem cells located within the intestinal crypts(86, 90). Collectively, these cells are responsible for nutrient absorption, physical exclusion of luminal contents from underlying tissues, antimicrobial peptide production, and maintenance of the intestinal mucus layer(86, 90).

Columnar epithelial cells constitute the majority of cells present in the intestinal epithelium(90, 100). Enterocytes provide a physical barrier separating the luminal contents of the GI tract from underlying tissues, as well as participating in the absorption of materials from lumen(89, 90). Epithelial cells directly participate in immunological surveillance and direction of host responses in the gut. Epithelial cells can express numerous Pattern Recognition Receptors (PRRS), including TLR5(101), TLR1, TLR2, TLR3, TLR9(86), and NOD2(89), and can produce chemotactic factors for both myeloid and lymphoid cells following inflammatory stimulation(102). IL-17 stimulation of intestinal epithelial cells can drive the expression of neutrophil chemokines(103). Epithelial cells can produce anti-microbial peptides, such as CRAMP, to directly influence microbial populations in the lumen of the gut(104). Additionally, epithelial cells can interact with leukocyte populations through the expression of both MHCII(105) and MHCI(106). Therefore, enterocytes play a key role in not only preventing microbes and microbial products

from penetrating to underlying tissues, but also initiating and directing inflammatory responses.

Goblet cells are another class of specialized epithelial cells found in the intestinal epithelium(100, 107). While goblet cells can be found in both the small and large intestines, they represent approximately 15 percent of the cells found in the large intestine epithelium(100, 107). Goblet cells contain large mucus-laden vacuoles(107), and express high levels of the MUC2 gene(91). MUC2 is the major structural component of both intestinal mucus layers(108). The lower mucus layer makes direct contact with the intestinal epithelium and is rarely contaminated with bacteria, while the outer layer contacts the intestinal lumen and the intestinal microbiome(92). Goblet cells have also recently been found to produce the antimicrobial peptides Ang4, RegIII γ and RegIII β (109, 110). RegIII γ activity is especially important in preventing microbial contact with the underlying epithelium(111). Goblet cells may also transfer antigens acquired in the intestinal lumen to dendritic cells in the lamina propria(112). These studies have demonstrated a potential role for goblet cells beyond mucus production by participating directly in the uptake of antigen and influencing the development of inflammatory responses.

Within the intestinal epithelium resides a population of lymphocytes referred to as **Intraepithelial lymphocytes** (IEL)(113). Almost all IELs are T cells, with both $\alpha\beta^+$ and $\gamma\delta^+$ populations represented(113, 114). Adherence of IELs to epithelial cells is mediated by interactions between CD103 expressed on IELS, and E-cadherin expressed on epithelial cells(115). Many IELs at baseline display a mixed

phenotype, with expression of some activation markers but not others(116). However, following stimulation, IELs become activated and express effector cytokines including IFN γ and KGF(116-118). IELs can exert both protective and pathogenic roles during inflammation: while IEL-derived KGF is believed to protect the epithelium from damage during chemically induced colitis(119), IELs producing IFN γ and TNF α have been associated with the development of inflammatory bowel disease(120). The proximity of IELs to the lumen of the gut, and their ability to rapidly produce both inflammatory and epithelial-protective signals, make them key “first line” defenders in the intestinal tract.

Underlying the intestinal epithelium is the **lamina propria**, an area rich in B and T lymphocytes(86). In contrast to Peyer’s patches, which are inductive sites for the priming of lymphocytes, the lamina propria is an effector site where activated lymphocytes respond to appropriate stimulation(97-99). $\alpha\beta$ TCR $^+$ T-cells are the most common lymphocyte within the small intestinal lamina propria(114). In keeping with the effector function of the lamina propria, T-cells found within the lamina propria express markers indicative of activation, including high levels of CD69 and CD25 (121), as well as spontaneously secreting of IL-4 and IFN γ (122). Subsets within this population have drastically different activities: while CD4 $^+$ CD25 $^+$ regulatory T-cells in the lamina propria can inhibit T-cell proliferation, cytokine production and the development of colitis(94, 95), lamina propria CD4 $^+$ T-cells can secrete both IL-17 and IL-22 and are associated with the development of intestinal inflammation(93, 96). Therefore, lamina propria T-cells have the ability to

rapidly react to signals received from the luminal environment and initiate both inflammatory and anti-inflammatory responses.

In contrast to the small intestine, **B-cells** are the predominant lymphocyte present in the lamina propria of the large intestine(114). Lamina propria B-cells secrete dimeric IgA, which is transcytosed through epithelial cells to the lumen of the gut through the action of the polymeric immunoglobulin receptor (pIgR)(123, 124). While antigen-specific IgA can be generated during intestinal infection(125), intestinal IgA secretion also plays a key role at baseline by inhibiting the penetration of commensal microbes through the epithelium and enhancing the uptake of luminal bacterial by M-cells(123). Intestinal IgA can also directly modulate the composition of the intestinal microbiome(126), highlighting the key role of IgA and lamina propria B-cells in shaping both the membership and location of the microbiome.

Lamina propria dendritic cells (LPDCs) play a large role in determining whether the response to a particular antigen will be inflammatory or anti-inflammatory. LPDCs capture luminal antigen by extending their processes through the epithelial cell layer, a process dependent on CX3CR1(127). There are two broad classifications of LPDCs to consider: CD103⁺ and CD103⁻. CD103⁺ LPDCs promote the generation of Foxp3⁺ regulatory T-cells through the secretion of retinoic acid and in combination with TGF- β (87, 88). In contrast, CD103⁻ LPDCs support the development of inflammation, and increase expression of inflammatory mediators such as TNF α and IL-6 following stimulation with TLR ligands(128). The presence of CD103⁺ LPDC is particularly important in preventing unnecessary inflammation, as

the absence of CD103⁺ CX3CR1⁻ LPDCs enhances epithelial damage during colitis (129).

Innate Lymphoid Cells (ILCs) are another cellular population found in the lamina propria(130, 131). ILCs morphologically resemble lymphocytes, but do not possess recombination activating gene-dependent antigen receptors(132). ILCs can be broken down into three broad groups(132). The defining characteristic of group 1 ILCs, such as NK cells, is the production of IFN γ (132). Many group 1 ILCs are also T-bet⁺(132, 133), and group 1 ILCs can be found at sites of mucosal inflammation(133). In contrast, generation of group 2 ILCs requires GATA3 and ROR α (132), and IL-5 and IL-13 are the signature cytokines of this group(132). Group 2 ILCs are important in responding to nematode infections(132).

Particularly relevant to the intestinal tract are **group 3 ILCs**, which are primarily defined by their ability to produce IL-22 and IL-17(132). Additionally, the generation and activity of group 3 ILCs is dependent on ROR γ t(132). Recent evidence has strongly suggested that IL-17 positive group 3 ILCs drive colonic inflammation during *Helicobacter hepaticus* infection(131). In contrast, during *Citrobacter rodentium* (*C. rodentium*) colitis group 3 ILCs are known to produce IL-22(130). IL-22 drives antimicrobial peptide expression and is required to prevent severe intestinal pathology and mortality during *C. rodentium* colitis(134). Thus, group 3 ILCs are important intestinal sources of IL-17 and IL-22, and can both promote and protect against intestinal pathology during insult(131, 132, 134).

Innate Inflammation in the Large Bowel

The host response to a wide range of bacterial and chemical perturbations within the large intestine is characterized by conserved immunological phenomena. Inflammatory cytokines, including IL-23, IFN γ , and TNF α are induced locally in response to the challenge(82, 135-137). Leukocyte recruiting chemokines, including CXCL1, CXCL2, and CCL2 are also induced, and are associated with an influx of monocytes and neutrophils into the mucosa(78, 80, 82, 135, 138, 139). Finally, intestinal histopathology characterized by epithelial damage and/or edema develops, as a result of either the perturbing agent directly or by the resulting immune response(49, 72, 80, 134, 138, 140).

Neutrophils, defined by high levels of Gr-1 (Ly6G) and CD11b expression, are myeloid cells that are rapidly recruited to the colonic epithelium during colitis(78, 80, 82, 139). Neutrophil recruitment is often beneficial to the host, as neutrophils are capable of phagocytosing pathogens(141, 142), and interference with neutrophil recruitment is associated with decreased host survival during acute large bowel infections(74, 76, 78, 143). Neutrophils are also capable of supporting inflammatory responses directly by producing inflammatory cytokines directly including IL-1 β , TNF α , and IL-8(141, 144). However, neutrophil recruitment is commonly associated with the development of colonic histopathology(82, 138), and neutrophil elastase is partially responsible for intestinal histopathology during DSS colitis(140). Thus, neutrophil recruitment can both reduce pathogen burden and protect against mortality as well as drive tissue damage during innate colitis.

IL-23 is a critical driver of the host response during acute inflammation at mucosal sites, including in the large bowel(135, 138, 145-147). IL-23 promotes neutrophil recruitment during acute pulmonary inflammation(145-147), and the recruitment of neutrophils is largely dependent on IL-23 in both infectious and chemically induced models of large bowel inflammation(135, 138). The expression of the neutrophil chemotactic factor KC (CXCL1) is also driven by IL-23 during *S. typhimurium* typhlocolitis(135). Additionally, expression of the antimicrobial peptide RegIII γ is almost entirely dependent on IL-23 during *S. typhimurium* typhlocolitis as well as DSS colitis(135, 138).

IL-22 is a pleiotropic cytokine that is induced in response to mucosal inflammation, including innate colitis(80, 82, 135, 138, 148). The induction of IL-22 at mucosal sites is driven by IL-23(134, 135, 138, 146), and several studies have demonstrated an epithelial-protective role for IL-22 during mucosal inflammation(134, 149). IL-22 limits the severity of intestinal histopathology during infectious and chemically induced colitis(134, 149). Furthermore, IL-22 both promotes RegIII γ induction and limits mortality during *C. rodentium* colitis(134). However, IL-22 also promotes neutrophil recruitment during chemically induced pulmonary inflammation(148), and stimulation of colonic epithelial cells and colonic subepithelial myofibroblasts with IL-22 results in the production of neutrophil chemotactic factors(150, 151). As such, IL-22 can potentiate a wide array of host responses at mucosal sites.

IL-17 is a proinflammatory cytokine that is commonly and rapidly induced at sites of mucosal inflammation(80, 135, 136, 138, 146, 148). IL-17 promotes

neutrophil recruitment in models of pulmonary inflammation including *K. pneumoniae* infections(152) and bleomycin challenge(148), as well as intestinal inflammation models including *S. typhimurium* infection(153) and TNBS(154) and DSS(155) colitis. IL-17 also contributes to epithelial damage during colonic inflammation as well(154, 155). Recent studies have demonstrated that IL-23 can drive the expression of IL-17 during mucosal inflammation(135, 138).

Previous studies have reported a role for **TNF α** signaling in promoting myeloid cell recruitment during mucosal inflammation (156, 157). TNF α can enhance the expression of CCL3 during chemically-induced pulmonary inflammation (157), and interference with TNF α signaling reduces neutrophil recruitment in response to acute allergic airway inflammation (156). TNF α can contribute to inflammatory cytokine expression and tissue damage during mucosal inflammation(158, 159). Directly applicable to gastrointestinal inflammation, during 2,4,6-Trinitrobenzenesulfonic acid (TNBS) colitis, TNF α signaling promotes both IL-18 and TNF α expression as well as the development of intestinal histopathology (159). Furthermore, TNF α also protects against immunopathology in response to *C. rodentium* colitis(137), highlighting the pleiotropic nature of TNF α signaling during mucosal inflammation.

Likewise, **GM-CSF** is a potent driver of mucosal inflammation in numerous settings, including the intestinal tract(160-162). GM-CSF can play a role in neutrophil recruitment during acute pulmonary inflammation (both chemical and microbial)(163-166) and drive maximal production of TNF α and CXCL2 in response to pulmonary LPS challenge(163). Colonic IL-6 production during chemically-

induced colitis has also been shown to be GM-CSF-dependent(167). However, GM-CSF signaling also serves to protect the epithelium from damage during mucosal inflammation(167-170). Ablation of GM-CSF signaling can result in a significant increase in colonic histopathology, including colonic ulceration, during dextran sulfate sodium (DSS)-induced colitis(167, 169). Furthermore, treatment of afflicted animals with exogenous GM-CSF is capable of reducing colonic ulceration in the same model(168). Thus, the host response to innate colitis is characterized by the induction of pleiotropic cytokines, capable of potentiating inflammatory responses such as neutrophil recruitment as well as epithelial protective responses(134).

Innate Inflammatory Responses to *C. difficile* TcdA and TcdB

Many studies have focused on the innate inflammatory responses of cultured myeloid cell populations to *C. difficile* TcdA and TcdB; the two best characterized virulence factors in *C. difficile*. Stimulation of human monocytes with TcdA or TcdB induces high levels of IL-8 production, and TcdA stimulation alone is sufficient to elicit significant production of both IL-1 β and TNF α (171). A more recent study has demonstrated that IL-1 β production in THP-1 monocyte-like cells in response to TcdA and TcdB is associated with caspase 1 activation, and that IL-1 β production was drastically reduced in peritoneal macrophages isolated from ASC-deficient mice(172). Dendritic cells also react rapidly to *C. difficile* stimulation: treatment of bone marrow derived immature dendritic cells with TcdA results in maturation,

characterized by increased expression of CD80, CD86, and MHCII, within 24 hours of stimulation(173). Dendritic cells under these conditions also express high levels of CXCL2 transcript within 12 hours of treatment with TcdA(173). Bone marrow derived dendritic cell maturation and activation can also be driven by stimulation with *C. difficile* surface layer proteins in a TLR4-dependent manner(174). Additionally, mast cells release high levels of TNF α following treatment with TcdA(175).

Though intoxication of intestinal epithelial cells with *C. difficile* toxins results in cell rounding and death(49, 176, 177), these cells also mount innate inflammatory responses following exposure to *C. difficile* toxins(176, 178-180). One of the most commonly reported responses of epithelial cells *in vitro* is increased expression of IL-8, which has been reported from both colonocyte and goblet cell-like cell lines(176, 178, 180). The secretion of these chemokines also appears to be directed, as treatment of polarized epithelial cells with TcdA *in vitro* results in primarily basolateral secretion of IL-8(180). Furthermore, epithelial cells isolated from *in vivo* ileal loops injected with TcdA show increased expression of CXCL2(179).

As mice are refractory to *C. difficile* colonization without antibiotic pretreatment(72), many early animal studies were performed by delivering purified *C. difficile* toxins directly to the gastrointestinal tract(172, 181-183). *in vitro* experiments using excised rabbit ileum revealed that treatment with *C. difficile* toxins promotes intestinal fluid secretion(184). Treatment of intestinal epithelial cell monolayers *in vitro* with purified TcdA results in rapid loss of transepithelial resistance and enhances tight junction permeability(185), suggesting the fluid

secretion seen in toxin-treated animals was due to loss of epithelial integrity caused by TcdA intoxication. Subsequent studies utilizing ileal loops instilled with *C. difficile* toxin also demonstrated high levels of fluid secretion in response to toxins, as well as marked disruption of intestinal architecture and neutrophil recruitment (172, 182, 183, 186, 187).

The ileal loop model has also been used to investigate the immunological drivers of inflammation in response to *C. difficile* toxins, especially those mechanisms underlying neutrophil recruitment(172, 179, 181, 186, 188). Studies using the ileal loop model reported decreased CXCL1 expression and decreased MPO levels in the absence of IFN γ (188). The depletion of mast cells also impairs neutrophil recruitment in response to TcdA(187), as does the chemical inhibition p38 MAP kinase activation(189). Rat ileum epithelial cells have also a cellular source of CXCL2 following TcdA administration to the rat ileum(179). Furthermore, neutrophils have also been suggested to promote intestinal histopathology in response to *C. difficile* toxins, as interference with neutrophil recruitment using an anti-CD18 antibody is also associated with decreased fluid secretion and epithelial damage in the rabbit ileum(186). Finally, Ng and colleagues demonstrated that IL-1 β , IL-18, and CXCL1 production as well as intestinal histopathology, in the ileum in response to TcdA and TcdB was largely dependent upon the NLRP3 inflammasome(172). Many of these results, including the requirement for NLRP3 inflammasome activity for IL-1 β production and neutrophil recruitment (as assessed by MPO activity), were later confirmed in the colon by administering *C. difficile* toxin intrarectally(181).

Mouse Modeling of *Clostridium difficile* Colitis

While the work by Hirota and colleagues and others demonstrate that toxin-based models can provide mechanistic insight into the initial inflammatory response to *C. difficile* toxins(172, 179, 181, 186, 188), such models are not without limitations. In addition to potential differences in the host response to purified bacterial toxins as opposed to a metabolically active infectious organism, toxin based models often offer a very limited timeframe before which samples must be collected (often four hours or less)(172, 179, 181, 188).

In recent years numerous murine models of *C. difficile* infection, relying on antibiotic pretreatment to permit infection, have been developed. The first published model, developed by Chen and colleagues, relied on the administration of a cocktail of kanamycin, gentamicin, colistin, metronidazole, and vancomycin in the drinking water as well as a subsequent intraperitoneal injection of clindamycin to permit *C. difficile* colonization and infection(72). This particular model has been utilized in several studies to infect mice with *C. difficile* and investigate the host response to infection(66, 77, 82, 190). Subsequent studies have utilized modified versions of the aforementioned protocol with the addition of ampicillin to the cocktail(74-76), while other groups have developed models using solely intraperitoneal clindamycin injections(73, 78), or the use of broad-spectrum third-generation cephalosporins in drinking water(59, 79-81, 83, 191, 192) to permit *C. difficile* colonization.

Two strains of *C. difficile*, VPI 10463 and 630, are commonly used in mouse models of *C. difficile* colitis(59, 66, 74-76, 78-83). Both VPI 10463(17, 193) and

630(21) contain the pathogenicity locus, which encodes genes for TcdA and TcdB production, release, and regulation(18). However, *in vivo* infection with *C. difficile* strain 630 is associated with less cytotoxicity (per gram of cecal content) than VPI 10463 infection(59). Consistently, 630 infection is associated with less mortality and less severe intestinal histopathology as compared to VPI 10463 infection(59). However, infection of susceptible animals with either strain results in a conserved host response characterized by inflammatory cell recruitment, the induction of inflammatory cytokines and chemokines, and the development of intestinal histopathology in the large bowel (59, 66, 74-76, 78-82). Thus, while the overall severity of disease differs between the two strains of *C. difficile*, the host inflammatory responses to both strains are conserved, and infection with either strain serves as an appropriate context in which to investigate the mechanisms underlying inflammatory responses during *C. difficile* colitis.

The Host Response to *Clostridium difficile* Colitis *in vivo*

Utilizing the mouse models mentioned above, numerous groups have begun to investigate the mechanisms underlying inflammation, microbial recognition, and immunopathology during *C. difficile* infection(74-82, 174, 190, 191, 194). Initial studies, using vegetative *C. difficile* as the infectious challenge, reported marked myeloid cell recruitment to the large bowel(59, 72, 74, 76, 80, 82, 195). For example, Sadighi Akha and colleagues reported significant neutrophil recruitment to the colon in association with marked intestinal histopathology and increased expression

of inflammatory cytokines including TNF α , GM-CSF, and CXCL1(82). Subsequent studies inoculating with *C. difficile* spores likewise reported marked neutrophil recruitment to the large bowel associated with the activation of numerous inflammatory pathways(78, 79, 81, 191, 194). Collectively, these studies demonstrate that infection with viable *C. difficile*, either vegetative cells or *C. difficile* spores, results in a conserved host response highlighted by robust neutrophil recruitment, marked intestinal histopathology, and the induction of inflammatory cytokines and chemokines including CXCL1(59, 72, 74-82, 191, 194).

Recent studies have focused on the host signals required for full recruitment of neutrophils in response to infection(74-76, 78, 79, 81). For example, Hasegawa and colleagues demonstrated a key role for NOD1 in supporting CXCL1 expression and neutrophil recruitment to the large bowel following *C. difficile* infection(76). Furthermore, Jarchum and colleagues also reported decreased neutrophil recruitment and CXCL1 expression in MyD88-deficient mice(78). Additional studies have suggested roles for ASC(74) and the combined signaling of IL-22 and CD160(81) in driving neutrophil recruitment to the large intestine in response to *C. difficile* infection.

These investigations into the host mechanisms promoting neutrophil recruitment have also revealed an association between reduced neutrophil recruitment and increased mortality during *C. difficile* infection(74, 76, 78). For example, in the study mentioned above by Hasegawa et al, the deficiency in neutrophil recruitment seen in NOD1-deficient mice was also associated with a significant increase in mortality following *C. difficile* challenge(76). Furthermore,

elimination of neutrophils through the use of a depleting mAb was also associated with decreased survival(78), seeming to suggest a protective role for neutrophil recruitment in response to *C. difficile* infection.

Other studies, however, have reported interventions that reduce neutrophil recruitment without increased mortality(79-81). For example, Sadighi Akha and colleagues reported decreased CXCL1 expression and reduced neutrophil recruitment following treatment with a combination of anti-IL-22 and anti-CD160 mAb, without any increase in mortality(81). Additionally, while El-Zaatari et al reported increased neutrophil recruitment in association with decreased *C. difficile* colonization in IDO-deficient mice, the increase in neutrophil recruitment was also associated with more severe intestinal histopathology(191). Thus, the host inflammatory signals that drive neutrophil recruitment to the colon, as well as the role of neutrophils themselves in promoting inflammatory responses in the colon, in response to *C. difficile* infection is poorly understood.

Central Hypothesis:

***C. difficile* infection results in induction of interleukin-23, interleukin-17, and interleukin-22, which drives increased chemokine and inflammatory cytokine production, neutrophil recruitment, and immunopathology in the colon**

Aims:

- 1. To determine the role of GM-CSF in promoting neutrophil recruitment and inflammatory cytokine expression during acute *C. difficile* colitis.**

Induction of GM-CSF in response to *C. difficile* infection has been previously reported(79, 82), and GM-CSF is known to promote neutrophil recruitment and inflammatory cytokine expression during inflammation at numerous mucosal sites(160-167). However, the role of GM-CSF in driving neutrophil recruitment and the induction of inflammatory cytokines during *C. difficile* infection has never been directly investigated.

2. To determine the role of neutrophils in driving intestinal histopathology and inflammatory cytokine expression, and the role of TNF α in promoting neutrophil recruitment and inflammatory cytokine expression, in response to *C. difficile* infection.

Neutrophil recruitment, in association with inflammatory cytokine expression including TNF α , is one of the most prominent host responses to *C. difficile* infection(74, 76, 78-82, 191). Neutrophils are known to produce inflammatory cytokines(141, 144) and their recruitment is often associated with host tissue damage during inflammation(82, 138, 140). However, the role of neutrophils in driving epithelial damage and inflammatory cytokine expression has not been extensively studied. Additionally, TNF α promotes neutrophil recruitment in numerous models of mucosal inflammation(156, 157), and is induced in response to *C. difficile* infection(80, 82), yet the role of TNF α in supporting neutrophil recruitment and inflammatory cytokine expression during *C. difficile* colitis is unknown.

3. To determine the roles of IL-23, IL-22, and IL-17a in driving CXC chemokine expression and neutrophil recruitment during *C. difficile* colitis.

IL-23 promotes neutrophil recruitment and neutrophil-recruiting chemokine expression in numerous models of mucosal inflammation in both the lungs and the intestinal tract(135, 138, 145-147). Furthermore, IL-23 controls the expression of both IL-22 and IL-17a, two cytokines capable of controlling neutrophil recruitment(148, 150-154), during inflammation at mucosal sites(134, 135, 138). Though a recent study has suggested a role for IL-23 in driving morbidity and mortality during *C. difficile* infection(190), the role of IL-23 in promoting neutrophil influx during *C. difficile* colitis has not been explicitly examined.

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Chapter 2

Materials and Methods

Animals and Housing:

Male C57BL/6, mice aged 5-11 weeks were used in all studies. All mice were either obtained directly from Jackson labs, or acquired from a breeding colony maintained at the University of Michigan founded by Jackson breeders.

Chapter 5: Male and female IL-17^{-/-} (IL-17KO) and p19^{-/-} (IL-23KO) mice aged 5-14 weeks were used as well. IL-17KO and IL-23KO mice on a C57BL/6 background were likewise obtained from breeding colonies maintained at the University of Michigan. IL-23KO breeders were a kind gift from Dr. Benjamin Segal, University of Michigan.

All mice were maintained under specific pathogen-free conditions, and autoclaved food, water, and bedding was provided *ad libitum*. All animal manipulations were carried out in laminar flow hood. All experiments were conducted in accordance with a protocol approved by the University Committee on Use and Care of Animals (UCUCA) at the University of Michigan.

***Clostridium difficile* Spore Preparation:**

C. difficile spore stocks, both VPI 10463 and 630, were generated by plating an earlier spore preparation on Taurocholate Cefoxitin Cycloserine Fructose Agar (TCCFA) plates anaerobically. Single colonies were isolated, and grown overnight in Columbia broth. 2ml of the overnight culture was inoculated into 40ml of Clospore broth(1), and the culture was allowed to grow for seven days. Spores were collected by centrifugation, and washed to remove vegetative cell debris. All spore stocks were stored in water at 4⁰C until used.

***Clostridium difficile* Vegetative Cell Preparation:**

C. difficile was prepared for infection as described previously(2, 3). Briefly, an overnight culture of *C. difficile* strain VPI 10463 (ATCC 43255) was back-diluted 1:10 in fresh brain-heart infusion (BHIS) broth and grown for 4-6 hours. The culture was then collected, washed in deoxygenated PBS (x3), and diluted to the desired dose. Mice were challenged via oral gavage. The inoculum was serially diluted and plated on BHIS plates to confirm dosage. *C. difficile* was grown and prepared for gavage in a Coy anaerobic chamber (Coy Industries).

***Clostridium difficile* Infection**

Chapter 3: Mice were treated with cefoperazone (0.5g/L) in their drinking water for five days in order to permit *C. difficile* infection. Following a 2-day recovery period, animals were challenged with $4.73 \pm 0.59 \log_{10}$ 630 spores as described previously(2). Following challenge, the inoculum was serially diluted and

plated on Taurocholate Cefoxitin Cycloserine Fructose Agar (TCCFA) plates anaerobically in order to confirm the dosage. All animals were monitored for weight change during the course of the experiment, and were monitored for signs of severe *C. difficile* infection (lethargy, hunched posture, >20% weight loss) and were euthanized if meeting any of these criteria. Uninfected animals received neither antibiotic treatment, nor *C. difficile* challenge. Samples were collected at four days post-infection.

Chapter 4: For ceftriaxone and *C. difficile* infection studies, mice were treated with ceftriaxone (0.5g/L) (Sigma) given *ad libitum* in their drinking water for 4 days. Antibiotic water was replaced every other day. Mice were then given a two-day recovery period on drinking water without antibiotic prior to infection with *C. difficile* as described previously(2, 3). Ceftriaxone treated mice were given the antibiotic regimen only, and untreated animals were not manipulated at all.

For *C. difficile* infection studies, mice received $5.06 \pm 0.31 \text{ Log}_{10} \text{ CFU}$ vegetative *C. difficile* via oral gavage on. *C. difficile*-infected animals were monitored for signs of severe disease (hunched posture, lethargy, weight loss exceeding 20% of baseline body weight) and were humanely euthanized if moribund. All surviving animals were euthanized two days post infection for subsequent analysis.

Chapter 5: Mice were given a 5 day course of cefoperazone (0.5g/L) in their drinking water in order to permit *C. difficile* infection as described previously(2, 4). After a two-day recovery period, mice were challenged with $5.70 \pm 0.25 \log_{10} C. difficile$ spores from strain VPI 10463. Animals were followed for an additional two days, and all samples were collected at two days post infection. Inoculum dosage

was confirmed by serially diluting and plating the inoculum on TCCFA plates anaerobically. Animals were monitored following infection for signs of severe disease, including lethargy, hunched posture, >20% weight loss, and any animals found moribund were humanely euthanized. Untreated animals did not receive antibiotics or *C. difficile* challenge.

Neutralizing Antibody Treatments:

Chapter 3 Anti-GM-CSF Treatment: Animals were given three intraperitoneal injections of anti-GM-CSF mAb (clone MP1-22E9). Each mouse received 250µg per injection, and injections were given every 48 hours beginning 24 hours prior to infection(5, 6).

Chapter 4 Anti-Gr-1 and anti-TNFα Treatment: Mice were given intraperitoneal injections of 250µg of anti-TNFα mAb (clone MP6-XT3) one day prior to infection with *C. difficile* or injections of 250µg of anti-Gr-1 mAb (clone RB6-8C5) one-day prior and one-day post infection. Mouse serum (Sigma) injections were administered to control mice.

Chapter 5 Anti-IL-22 Treatment: Animals were given two intraperitoneal injections of anti-IL-22 mAb (clone 8E11). Each mouse received 150µg antibody one day prior and one day post infection(7). The anti-IL-22 mAB was a kind gift from Dr. Wenjun Ouyang(7).

Histology:

Colonic tissue was fixed in 10% formalin for at least 24 hours, and then transferred to 70% ethanol. Tissue was processed, paraffin embedded, sectioned, and used to prepare haematoxylin and eosin stained slides by McClinchey Histology Labs Inc. Representative images were acquired using an Olympus BX40 light microscope (Olympus Corporation) and a QImaging MicroPublisher RTV 5.0 5 megapixel camera. All images were acquired at a total magnification of 400X. Panels were assembled in Adobe Photoshop CS5, version 12.0. Image processing was restricted to global adjustments of brightness, contrast, and image size.

Histological Scoring:

Chapter 4: Histological sections were coded, randomized, and scored in a blinded manner. The slides were first scored categorically on a 0-5 scale for epithelium damage and for inflammation, using defined criteria. Epithelium damage was scored as follows: 0, intact epithelium; 1, minimal, scattered goblet cell loss with no significant epithelium destruction and no histologically defined loss of surface integrity; 2, widespread moderate goblet cell loss with no significant epithelium destruction and no histologically defined loss of surface integrity; 3, moderate to extensive widespread goblet cell loss with scattered epithelium destruction and histologically defined loss of surface integrity; 4, extensive epithelium and goblet cell destruction with histologically defined loss of surface integrity; 5, severe epithelium destruction and goblet cell destruction with widespread histologically apparent loss of surface integrity. Inflammation was

scored as follows: 0, no inflammation; 1, minimal multifocal leukocytic infiltrates; 2, moderate multifocal leukocytic infiltrates and low level edema (greater submucosal involvement); 3, significant multifocal leukocytic infiltrates, edema, submucosal involvement; 4, extensive multifocal leukocytic infiltrates, edema, extensive submucosal involvement; 5, severe multifocal leukocytic infiltrates, extensive edema and submucosal involvement with luminal involvement and/or abscess formation. The slides were then assigned an overall score using a rank-order scoring system. The total of both categorical scores (epithelium damage and inflammation) were used to rank all the slides in the study in order of increasing severity of histopathological changes (1=least, 16=most). This method offers significant advantages over straight categorical scoring systems for comparing histological changes between groups and has been previously reported for scoring *C. difficile*-induced intestinal pathology(2, 8, 9).

Chapter 5: Light microscopic evaluation of H&E stained colonic sections was performed by a board-certified veterinary pathologist (ILB). The pathologist was blinded to experimental groupings at the time of the evaluation, and sections were scored using a previously established system(2). Edema: 0 no edema, 1 mild, focal or multifocal edema with minimal submucosal expansion (<2X), 2 moderate multifocal edema with moderate submucosal expansion (2-3X), 3 severe multifocal to coalescing edema with severe submucosal expansion (>3X), 4 same as 3 with diffuse submucosal expansion. Inflammation: 0 no inflammation, 1 minimal, multifocal neutrophilic infiltration, 2 moderate, multifocal neutrophilic infiltration (greater submucosal involvement), 3 severe multifocal to coalescing neutrophilic

infiltration (greater submucosal +/- mural involvement), 4 same as 3 with abscesses or extensive transmural involvement. Epithelial damage: 0 no epithelial damage, 1 mild multifocal, superficial damage (vacuolation, increased apoptosis, villus tip attenuation/necrosis), 2 moderate, multifocal superficial damage (same qualitative changes as above), 3 severe multifocal to coalescing mucosal damage +/- pseudomembrane formation (intraluminal aggregate of neutrophils and sloughed epithelium in a fibrinous matrix covering eroded or ulcerated mucosa), 4 same as 3 with extensive pseudomembrane or ulcer formation.

Quantification of *C. difficile* colonization

Mucosal *C. difficile* colonization was determined using a species-specific qPCR of DNA isolated from colonic tissue. The *C. difficile*-specific qPCR was performed as described previously(3, 10). All reactions were carried out in a total volume of 10 μ l. Each reaction contained 2 μ l of template primers, 6.25pmol forward and reverse tcdB primers, and 1pmol tcdB probe. The cycling conditions and probe and primer sequences are identical to those used previously(3). Raw Ct values were normalized to signal from a single-copy host internal control gene to generate dCt values(3, 11). dCt values were then converted to "*C. difficile* genomes/g tissue" using a standard curve generated with known amounts of vegetative *C. difficile* and colonic tissue(4, 12).

Microbiome Analysis

Chapter 3: The DNeasy blood and tissue kit (Qiagen, Valencia, CA) was used to extract genomic DNA from colonic tissue samples. The extraction was performed according to the manufacturer's instructions except for the following modifications: adding a bead-beating step using UltraClean fecal DNA bead tubes (Mo Bio Laboratories, Carlsbad, CA); doubling the amount of ATL buffer and the proteinase K used in the protocol; and decreasing by half the amount of the AE buffer used to elute the DNA. Subsequently, the V3, V4 and V5 hyper-variable regions of the 16S ribosomal RNA gene in each of the samples were targeted for amplification with the 357F and 929R primer sets(13). Amplicons were purified with the Agencourt AMPure XP PCR purification system (Beckman Coulter, Indianapolis, IN), and quantified with the Quant-iT PicoGreen dsDNA kit (Life Technologies, Grand Island, NY) to obtain an equal pool for pyrosequencing. They were then sequenced on a Roche 454 GS Junior Titanium platform according to the manufacturer's specifications. Bacterial 16S sequences were first processed using the microbial ecology software suite *mothur*(14) to generate operational taxonomic units (OTUs) at a 3%, i.e. species level of difference. These data, in the form of the *.shared* file, were then imported into the R software and analyzed using the R-package *vegan*. The inverse Simpson diversity measure was calculated using the function *diversity()*.

Chapter 4: All procedures and analyses were performed as previously described(15). Briefly, DNA was isolated from rinsed colonic tissue and V3-V5 16S ribosomal RNA gene amplicon libraries generated. They were then sequenced on a Roche 454 GS Junior Titanium platform according to the manufacturer's

specifications. Bacterial 16S rRNA gene sequences were processed using the microbial ecology software suite *mothur*(14) to generate operational taxonomic units (OTUs) at a 3% level of difference (approximating species-level differences). These data were then imported into the software package R and analyzed using the R add on-package *vegan*(16). Rank abundance plots were generated by selecting for the OTUs that contributed to >0.5% of the population. The content of each treated tissue was ordered according to the average rank order of its untreated counterpart. Taxonomic classification of an OTU was assigned within *mothur* by identifying the consensus sequence of the OTU and assigning taxonomy using a Bayesian classifier trained on an RDP training set (*classify.otu*).

RNA Isolation and Expression Analysis:

Colonic tissue snips (1cm²) were collected from the center of the colon and stored in RNAlater (Ambion). RNA isolation and purification from colonic tissue was performed as described previously(4, 12, 15, 17). Tissue was homogenized in TRIzol reagent (Life Technologies) and the resulting RNA was purified using the RNeasy Mini kit (Qiagen) according to the manufacturer's instructions. The concentration of the purified RNA was determined using a Nanodrop instrument (Thermo Fisher). cDNA synthesis, using the purified RNA as a template, was performed using the RT² First Strand kit (Qiagen), and colonic gene expression was assessed using RT² Profiler PCR arrays (Qiagen). All reactions were run on a Roche Lightcycler 480. In order to correct for variation between RT² Profiler PCR arrays, cross card normalization was performed as described previously(15, 18). ΔCt (dCt) values

were calculated by subtracting the geometric mean of two internal control genes from the Ct value of the gene of interest.(19) The $2^{-\Delta\Delta Ct}$ method was utilized to calculate fold change gene expression in treatment groups as compared to untreated animals for all comparisons(11).

Leukocyte Isolation:

Leukocytes were isolated from colonic tissue as described previously(12). Isolated colonic tissue was minced with serrated scissors to physically disrupt the tissue, and was subsequently incubated in 20ml Hank's Balanced Salt Solution (HBSS) supplemented with 2.5% fetal bovine serum, 5mM EDTA, and 1 mM DTT for 20 minutes at 37°C. Tissue was then incubated in 20ml of a digest solution consisting of HBSS supplemented with 2.5% fetal bovine serum, 400U/ml collagenase type 3 (Worthington Biochemical) and 0.5mg/ml DNase I (Roche) for 60 minutes at 37°C. Samples were then resuspended in 20% Percoll (Sigma) in PBS, and centrifuged at 900f for 30 minutes at room temperature without brake. The resulting single cell suspensions were stained for flow cytometric analysis.

Flow Staining and Analysis:

Single cell suspensions were plated at a concentration of approximately 10^6 cells per well in a 96 well plate. Cells were blocked with unlabeled FC RIII/II, and then stained fluorescently labeled antibodies for 30 minutes. Cells were washed to remove excess antibody, and were resuspended in stabilizing fixative (BD

Biosciences). Data was collected on a three-laser Canto II using FACSDiva software (BD biosciences). All data analysis was performed in FlowJo (Treestar).

Chapter 4: The following antibodies were used for flow cytometric analysis of intestinal leukocytes. CD11c (clone HL3), CD45 (clone 30-F11), CD11b (clone M1/70), Gr-1 (clone RB6-8C5), and Ly6C (clone AL-21) as well as Fc RIII/II (clone 2.4G2). All antibodies were purchased from BD Biosciences (San Diego, CA) and Biolegend (San Diego, CA).

Chapter 5: Isolated colonic cells were stained with the following antibodies: CD45 (clone 30-F11), CD11b (clone M1/70) and Ly6G (clone IA8) as well as Fc RIII/II (clone 2.4G2). All antibodies were purchased from eBioscience, BD Pharmingen, and Biolegend.

Total number of neutrophils per colon was calculated by multiplying the frequency of CD45^{High} CD11b^{High} Ly6G^{High} neutrophils as defined by flow cytometry by the total number of cells in the colon in question.

Statistical Analysis:

Chapter 3: For the initial assessment of GM-CSF expression during *C. difficile* colitis, statistical significance was determined via an unpaired two-tailed t-test comparing dCt values from uninfected and *C. difficile* infected mice. For all other analyses of colonic gene expression, datasets were first checked by outlier analysis and then statistically significant changes were identified using a One-Way ANOVA with a Tukey post hoc test comparing normalized dCt values from uninfected, *C. difficile* infected, and anti-GM-CSF treated and *C. difficile* infected animals.

Statistically significant changes in the Inverse Simpson Index were also determined using One-Way ANOVA with a Tukey post hoc test. Significance was set at $p < 0.05$ in all analyses.

Chapter 4: Unpaired two-tailed t-tests were used to identify statistically significant differences in gene expression between untreated and ceftriaxone-treated mice. For all other analyses, statistically significant changes were identified using a One-Way ANOVA with Tukey's *post hoc* test for multiple comparisons. For all qPCR data (colonic gene expression and *C. difficile* colonization), statistical analysis was performed on normalized dCt values. Significance was set at $p \leq 0.05$ in all analyses.

Chapter 5: Statistically significant differences in gene expression were determined using a One-Way ANOVA with Tukey's *post hoc* test for multiple comparisons. For all qPCR data, statistical tests were performed on normalized dCt values (4, 12). A One-Way ANOVA with Tukey's *post hoc* test was also used to identify significant differences in the number of neutrophils per colon. Significant differences in histopathological scoring were determined using the Kruskal-Wallis test with followed by Dunn's multiple comparisons test. For all analyses, significance was set at $p \leq 0.05$.

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Chapter 3

Role of GM-CSF in the Inflammatory Cytokine Network that Regulates Neutrophil Influx into the Colonic Mucosa during *Clostridium difficile* Infection in Mice

Portions of this chapter have been previously published

McDermott AJ, Frank CR, Falkowski NR, McDonald RA, Young VB, Huffnagle GB.

2014. Role of GM-CSF in the inflammatory cytokine network that regulates neutrophil influx into the colonic mucosa during *Clostridium difficile* infection in mice. *Gut Microbes* 5:476-484.

Introduction

Clostridium difficile infection is associated with robust neutrophil recruitment, increased expression of inflammatory cytokines and chemokines, and marked damage to the intestinal epithelium(1-7). GM-CSF promotes myeloid cell recruitment(8-12) and inflammatory cytokine production during mucosal inflammation(10, 13), as well protecting against epithelial damage during colonic inflammation(13-15). While recent studies in our lab have reported increased expression of GM-CSF in response to *C. difficile* infection(5), the role of GM-CSF during *C. difficile* colitis has not been directly investigated. In this chapter, we assessed the role of GM-CSF in promoting inflammatory cytokine expression, neutrophil recruitment, and epithelial damage during *C. difficile* colitis.

Results

Expression of GM-CSF during *C. difficile* infection

We used a *C. difficile* infection model adapted from a previously described mouse model of acute *C. difficile* infection.⁽⁶⁾ Briefly, mice received the broad-spectrum antibiotic cefoperazone in their drinking water for 5 days, were infected with spores from *C. difficile* strain 630 by oral gavage 2 days after the cessation of antibiotics and then followed for 4 days (Figure 3-1). *C. difficile* 630 infection causes relatively mild disease, and this strain was chosen to permit investigation of both proinflammatory and epithelial-protective functions of GM-CSF. Cefoperazone treatment and *C. difficile* challenge resulted in a significant decrease in total bacterial diversity in the colon that persisted for at least one week post-antibiotic treatment (Figure 3-2) and the establishment of *C. difficile* colonization in the colon (Figure 3-2). Beginning at one-day post-infection, *C. difficile*-infected mice began to lose body weight (Figure 3-2). Additionally, there was a statistically significant increase in GM-CSF expression in the colon of *C. difficile*-infected mice compared to uninfected mice (Figure 3-2), which was not seen in mice treated only with cefoperazone (data not shown).

Effect of anti-GM-CSF treatment on *C. difficile* infection and the intestinal epithelium

To begin to investigate the role of GM-CSF in the pathogenesis of *C. difficile* infection, mice were treated with a neutralizing anti-GM-CSF monoclonal antibody (MP1-22E9), every other day beginning one day prior to infection (Figure 3-1). This treatment did not affect the low bacterial diversity in these mice (Figure 3-2), nor did it significantly alter the composition of the bacterial microbiome (data not shown). Although not statistically significant, there was a trend toward lower *C. difficile* colonization levels and more modest weight loss during the course of disease in mice treated with anti-GM-CSF mAb (Figure 3-2). *C. difficile* infection induced robust expression of the IL-22 pathway in the colonic mucosa, including induction of RegIII γ (Figure 3-3). There was a trend toward lower IL-22 expression levels in anti-GM-CSF treated mice, but neither IL-22 nor RegIII γ expression was significantly lower in these mice (Figure 3-3). Thus, treatment with anti-GM-CSF did not exacerbate disease; rather, *C. difficile* colonization levels, weight loss and induction of the IL-22 pathway remained the same, if not slightly improved.

One of the other salient features of *C. difficile* infection in the colon is the destruction of goblet cells in the epithelium. This loss was observed in both levels angiogenin-4 expression (Figure 3-3) and histologically evident changes (Figure 3-4). In the colon, angiogenin-4 is expressed solely by goblet cells in the crypts(41), and the expression of angiogenin-4 was significantly reduced in *C. difficile*-infected mice. Loss of goblet cells from colonic crypts was evident in histology sections, with a marked reduction in these cells (denoted by their vacuoles) observed in both transverse and oblique sections (Figure 3-4). Treatment with anti-GM-CSF mAb did

not significantly protect against loss of angiogenin-4 expression (Figure 3-3) or goblet cells (Figure 3-4) that occurred during *C. difficile* infection.

Effect of anti-GM-CSF treatment on inflammation and neutrophil recruitment during *C. difficile* infection

However, investigation into some of the specific inflammatory pathways associated with *C. difficile* infection revealed a role for GM-CSF in driving inflammatory cell recruitment, most notably neutrophils. *C. difficile* 630 infection induced significant expression of the inflammatory cytokines IFN γ , IL-1 β , IL-6 and TNF α in the colon mucosa at four days post-infection (Figure 3-5). Treatment of *C. difficile* infected mice with anti-GM-CSF mAb resulted in significantly lower expression of IL-1 β and TNF α (Figure 3-5). There was no significant induction of IL-12, IL-23, IL-17, IL-10 or TGF- β in either group of infected mice (data not shown). Consistent with the leukocytic infiltrates evident in histological sections of *C. difficile* 630 infected mice (Figure 3-4), there was a significant increase in expression of the CC chemokines CCL2 (MCP-1) and CCL4 (MIP-1 α) and the IFN γ -inducible non-ELR CXC chemokines CXCL9 (MIG) and CXCL10 (IP10) (Figure 3-6). Anti-GM-CSF treatment had no effect on expression of these chemokines. In contrast to CCL2, CCL4, CXCL9 and CXCL10, anti-GM-CSF treatment significantly reduced expression of the ELR+ CXC chemokines CXCL1 (KC) and CXCL2 (MIP-2) (Figure 3-6). ELR+ CXC chemokines are predominantly neutrophil chemotactic factors and contain a conserved amino acid sequence motif (glutamic acid-leucine-arginine, i.e. E-L-R)

that immediately precedes the first cysteine residue near the amino-terminal end and confers binding specificity to specific CXC chemokine receptors. Expression of both of these ELR+ CXC chemokines in the colon following *C. difficile* infection was also associated with the influx of neutrophils into the parenchyma (Figure 3-4). Consistent with the lower, but still significant, expression of CXCL1 and CXCL2 in anti-GM-CSF treated mice, neutrophils were still evident in colonic mucosal sections, but their numbers were reduced (Figure 3-4).

Inducible nitric oxide synthase (iNOS) is often associated with host antimicrobial responses, and can be expressed by a variety of cells including neutrophils(42, 43) and intestinal epithelial cells.(44) iNOS was expressed in colonic tissue following *C. difficile* infection concomitant with the development of inflammation and neutrophil influx (Figure 3-4). Anti-GM-CSF treatment also resulted in a significant decrease in iNOS expression (Figure 3-6).

Secretory leukocyte protease inhibitor (SLPI) is a well-documented inhibitor of neutrophil elastase, and other serine proteases, is produced by epithelial cells and can protect against neutrophil-mediated protease damage.(45-49) Following *C. difficile* infection, SLPI expression is significantly upregulated in the colonic mucosa (Figure 3-6). However, treatment with anti-GM-CSF significantly reduced expression of SLPI, concomitant with the reduced neutrophil influx in these mice (Figure 3-6).

Infectious Inoculum: $4.73 \pm 0.59 \log_{10}$ *C. difficile* strain 630 spores

Anti-GMCSF mAb: Clone MP1-22E9 (250 μ g/dose)

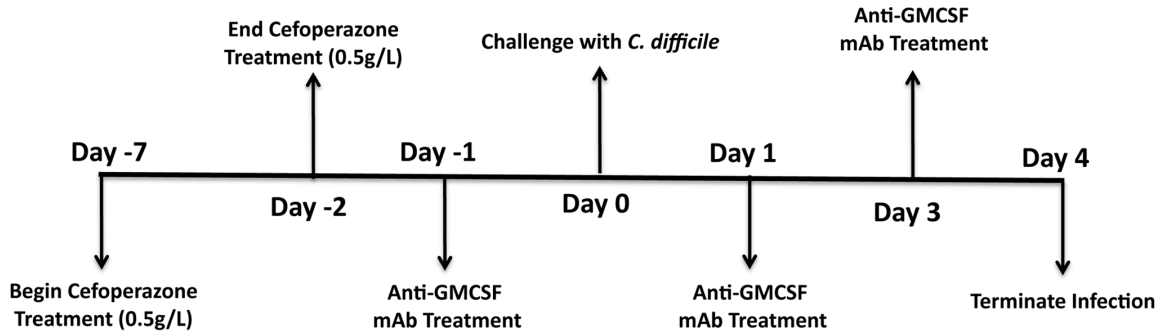


Figure 3-1. Experimental Timeline for Investigating the Role of GM-CSF During *C. difficile* Colitis.

Experimental approach and timeline. Briefly, mice were treated with cefoperazone (0.5g/L) in their drinking water for five days in order to permit *C. difficile* infection. Following a 2-day recovery period, animals were challenged with $4.73 \pm 0.59 \log_{10}$ 630 spores. All samples were collected four days post infection.

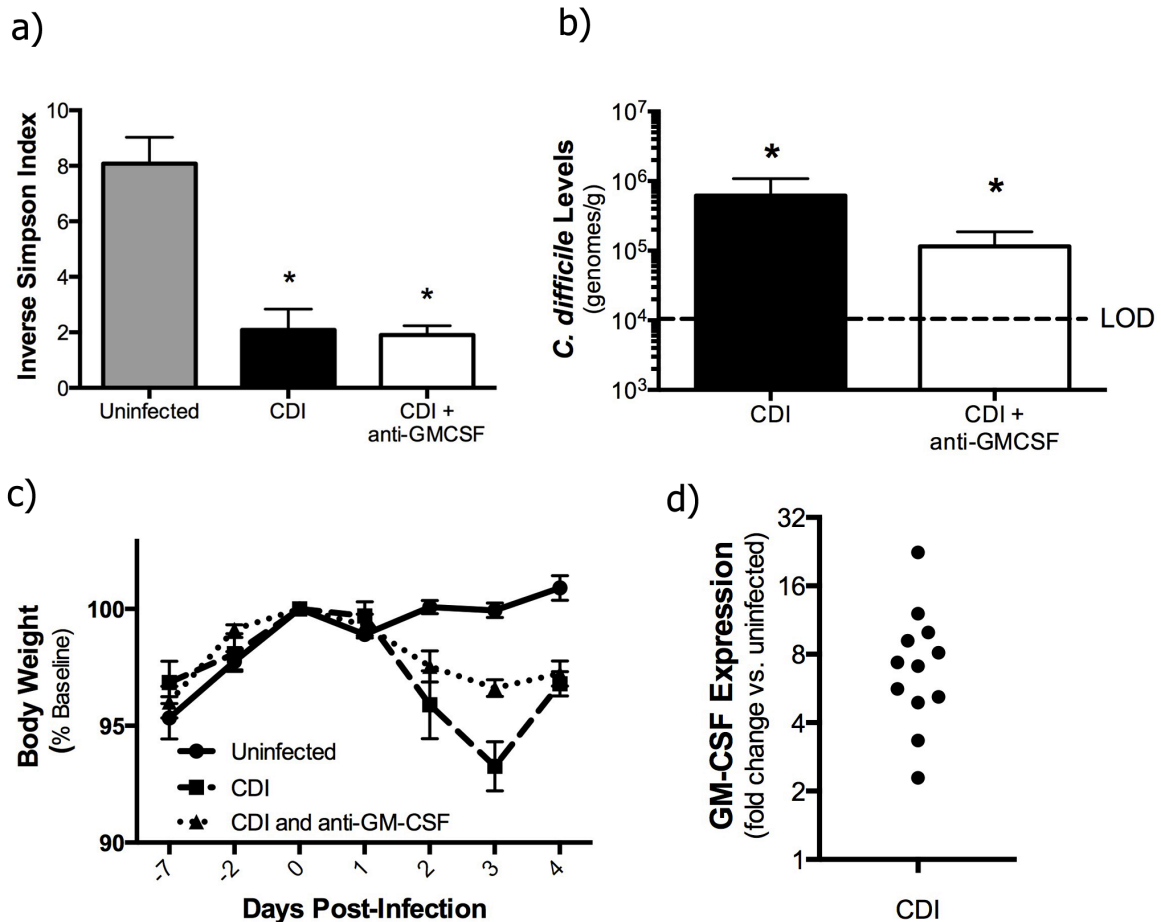


Figure 3-2. Impact of Anti-GM-CSF Treatment on *Clostridium difficile*-Induced Disease.

(a) Colonic microbiota diversity during *C. difficile* 630 infection (Day 4). (b) *C. difficile* 630 colonization of the colonic mucosa, as determined by *C. difficile*-specific qPCR (Day 4). LOD = Limit of Detection (c) Change in body weight during *C. difficile* infection, expressed as percent of baseline body weight at start of experiment. (d) Change in expression of GM-CSF following *C. difficile* 630 infection (Day 4) compared to uninfected mice. (A-C) Mice were treated as outlined in Figure 3-1. CDI= *C. difficile* infected. n= 8 mice per group. Data are the mean ± SEM. *p<0.05 compared to uninfected. (d) Mice were treated as outlined in Figure 3-1. n=12 per group (infected & uninfected). p<0.05 for dCt values of infected vs. uninfected.

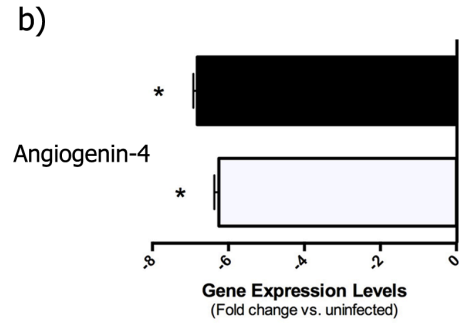
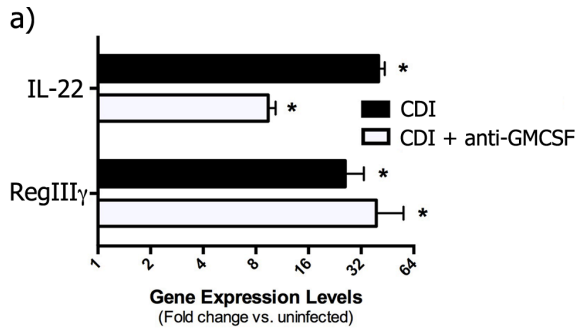


Figure 3-3. Effect of anti-GM-CSF Treatment on IL-22, RegIIIγ, and Angiogenin-4 Expression in the Colonic Mucosa.

Mice were treated as outlined in Figure 3-1. CDI= *C. difficile* infected. Expression was measured by qPCR as outlined in the methods. n ≥ 8 mice per group. Data are the mean ± SEM. *p<0.05 compared to uninfected.

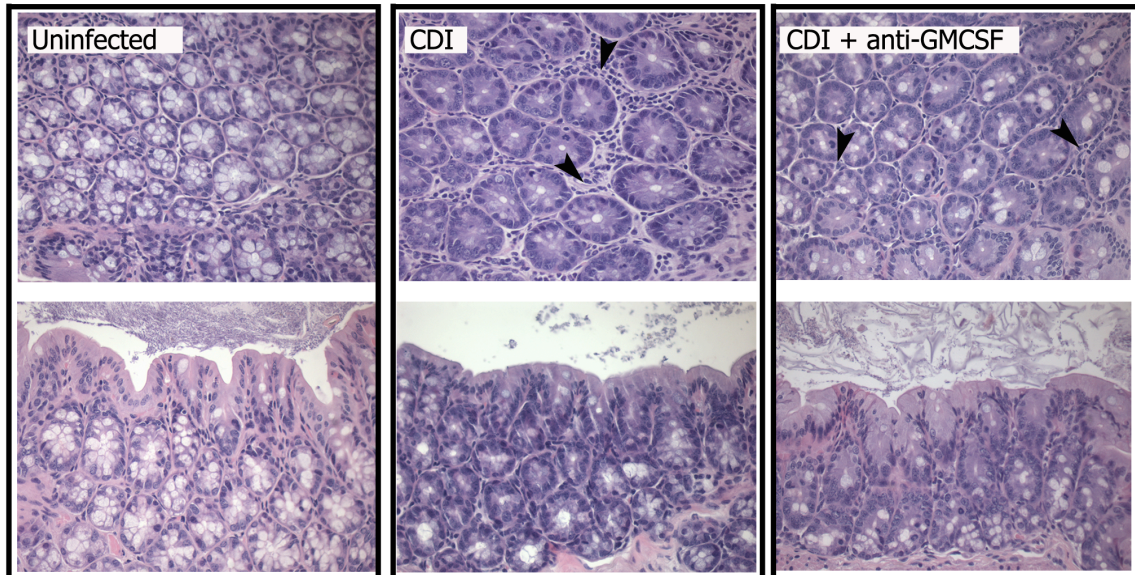


Figure 3-4. Colonic Histopathology Following anti-GM-CSF Treatment.

Photomicrographs of representative H&E-stained oblique and transverse sections of colonic crypts from uninfected (untreated), *C. difficile* 630 infected (Day 4) and *C. difficile* 630 infected, anti-GM-CSF treated (Day 4) mice. CDI= *C. difficile* infected. Mice were treated as outlined in Figure 3-1. Black arrows indicate infiltrating neutrophils. 400X.

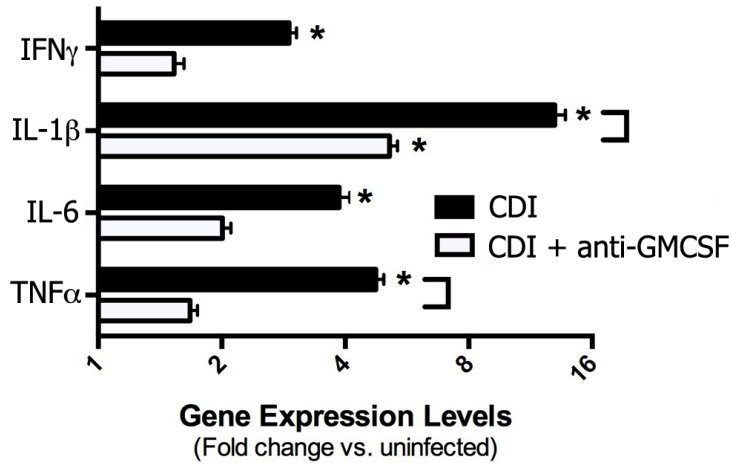


Figure 3-5. Inflammatory Cytokine Expression in the Colonic Mucosa Following anti-GM-CSF Treatment.

Mice were treated as outlined in Figure 3-1. Expression was measured by qPCR as outlined in the methods. CDI= *C. difficile* infected. n= 8 mice per group. Data are the mean \pm SEM. *p<0.05 compared to uninfected.]Brackets p<0.05 in comparing CDI vs. CDI+anti-GMCSF.

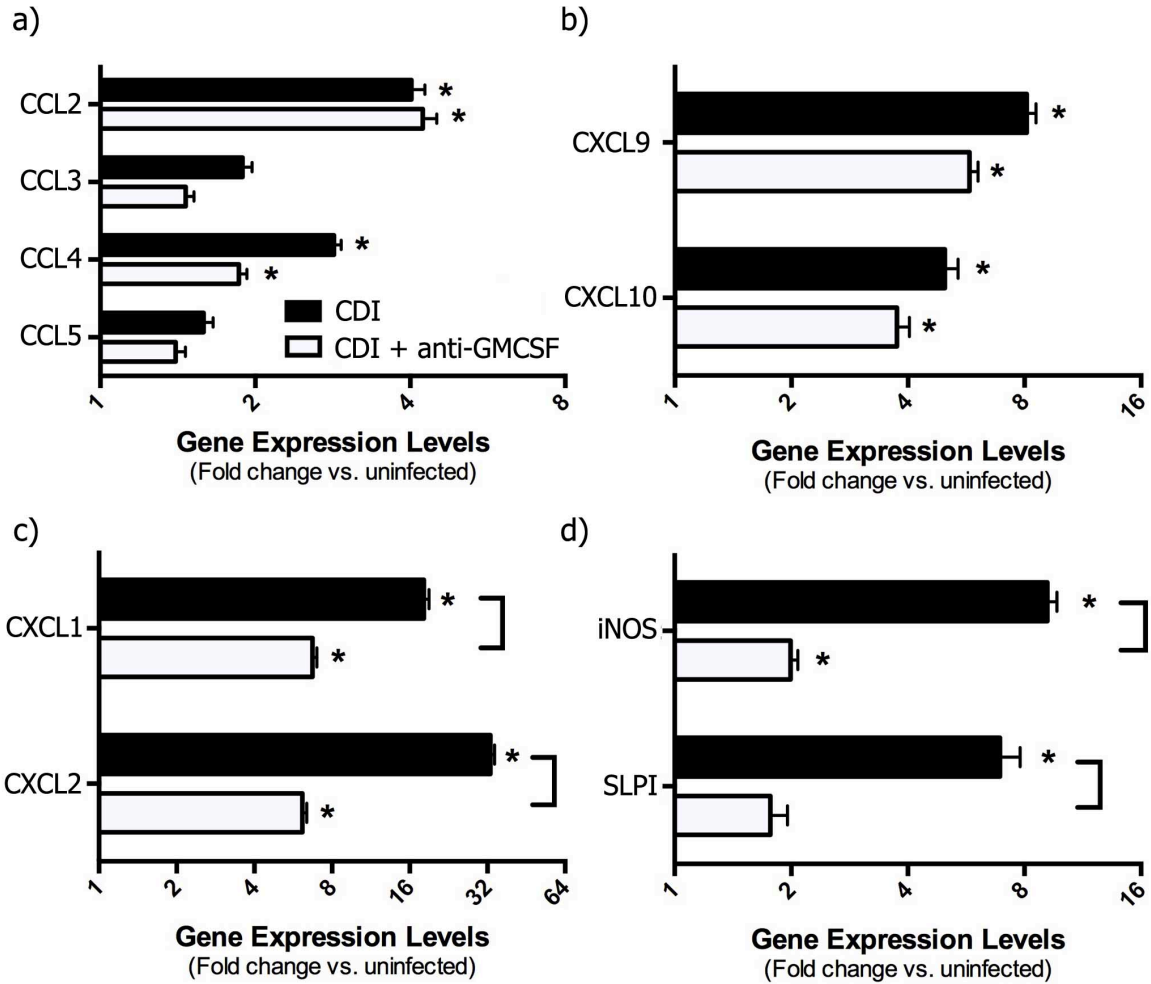


Figure 3-6. Effect of anti-GM-CSF Treatment on Colonic Chemokine Expression. (a-c) Effect of anti-GM-CSF treatment on chemokine expression in the colonic mucosa during *C. difficile* infection (Day 4). (d) Effect of anti-GM-CSF treatment on iNOS and SLPI expression in the colonic mucosa during *C. difficile* infection (Day 4). (A-D) Mice were treated as outlined in Figure 3-1. Expression was measured by qPCR as outlined in the methods. CDI= *C. difficile* infected. n= 8 mice per group. Data are the mean \pm SEM. *p<0.05 compared to uninfected.]Brackets p<0.05 in comparing CDI vs. CDI+anti-GMCSF.

Discussion

This is the first reported investigation of the role of GM-CSF in the cytokine network that regulates inflammation following *C. difficile* infection. In the current study, we observed reduced ELR+ CXC chemokine expression in addition to evidence of decreased neutrophil recruitment following anti-GM-CSF treatment. GM-CSF is a potent driver of mucosal inflammation in other disease settings, including the intestinal tract(25-27), but has not been investigated for the pathogenesis of *C. difficile*, a toxin-producing bacteria with distinct virulence mechanisms from attaching and effacing enteric bacteria. GM-CSF has been reported to promote neutrophil recruitment during acute pulmonary inflammation(8-11) and is also required for full recruitment of neutrophils and production of CXCL1 (KC) in an experimental model of otitis media(50). Within the gut, GM-CSF has also been shown to promote neutrophil recruitment during 2,4,6-trinitrobenzenesulfonic acid (TNBS)-colitis(12). Additionally, one study suggests that GM-CSF can function directly as a chemoattractant for neutrophils(12). While we have demonstrated that GM-CSF is expressed in the colon, and previous studies have demonstrated colon-localized effects following intraperitoneal injection of the anti-GM-CSF mAb used in the current study(51), we have no evidence in this study that the site of activity of our anti-GM-CSF mAb is the colon itself. GM-CSF is a critical factor for the survival of infiltrating neutrophils in a tissue, protecting them against apoptosis, but it also plays a role in the differentiation of neutrophils from bone marrow-derived precursors. Thus, an important site of GM-CSF activity during *C. difficile* infection may be the bone marrow. Altogether, our data strongly support the concept that

GM-CSF can regulate neutrophil chemokine expression and neutrophil recruitment during *C. difficile* colitis although its activity may include extra-intestinal regulation of neutrophil biology.

In addition to reduced ELR+ CXC chemokine expression, we also observed decreased expression of inflammatory cytokines, most notably TNF α , during *C. difficile* colitis following treatment with anti-GM-CSF. TNF α expression has been demonstrated to be largely dependent upon GM-CSF signaling in chemical(11) and microbial(10) models of acute pulmonary inflammation. GM-CSF also promotes TNF α production during middle-ear inflammation(50). Inflammatory cytokine expression during chemically-induced colitis is also dependent upon GM-CSF(13). Consistent with other reports, our data strongly suggest that GM-CSF promotes inflammatory cytokine expression during *C. difficile* colitis.

Numerous studies have reported an epithelial-protective function for GM-CSF during mucosal inflammation(13-15, 28, 29). In the absence of GM-CSF, colonic ulceration and overall intestinal pathology in response to DSS is significantly increased(13, 14). Additionally, during *Citrobacter rodentium* infection, GM-CSF serves to protect against the development of severe intestinal pathology(15). In the current study, however, we did not observe increased epithelial damage during *C. difficile* infection following anti-GM-CSF treatment or further reduction in expression of the goblet cell-associated antimicrobial peptide angiogenin-4(41), suggesting colonic goblet cells were not under additional stress following anti-GM-CSF treatment. Altogether, this may reflect a difference in the nature of the primary

source of epithelial damage during infection, *C. difficile* toxins(21-23), compared to other mechanisms of epithelial damage.

One model that could explain the association between reduced neutrophil recruitment and reduced cytokine and chemokine expression seen following anti-GM-CSF treatment is that neutrophils may also be a cellular source of inflammatory cytokines during *C. difficile* infection. Neutrophil recruitment into the colonic mucosa and production of a "storm" of inflammatory cytokines are key features of the pathogenesis of the disease(1-7, 24, 30). *C. difficile* toxins TcdA and TcdB, as well as other factors from *C. difficile*, can elicit IL-1 β , TNF α , CC and CXC chemokine production from macrophages and epithelial cells in vitro, but neutrophils have not been investigated as a cellular source(31-37). Neutrophils are capable of producing IL-1 β and TNF α , as well as chemokines(52, 53). Additionally, GM-CSF not only serves to prevent neutrophil apoptosis, but also modifies neutrophil behavior and can promote the production of neutrophil chemokines(52, 54). However, other studies in our laboratory, using anti-Gr1 to deplete Gr1+ cells during *C. difficile* VPI 10463 infection in mice, found no change in the levels of IL-1 β , TNF α or CXCL1 expression following anti-Gr-1 treatment(55). One caveat of this observation is that this strain of *C. difficile* produces higher levels of toxins, resulting in a more severe disease with more extensive epithelial damage(6, 7, 24). Thus, additional cellular pathways of IL-1 β , TNF α or CXCL1 expression may be induced when toxin levels are higher.

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