Bacterial proteases in IBD and IBS

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ABSTRACT

Proteases play a decisive role in health and disease. They fulfil diverse functions and have been associated with the pathology of gastrointestinal disorders such as inflammatory bowel disease (IBD) and irritable bowel syndrome (IBS). The current knowledge focuses on host-derived proteases including matrix metalloproteinases, various serine proteases and cathepsins. The possible contribution of bacterial proteases has been largely ignored in the pathogenesis of IBD and IBS, although there is increasing evidence, especially demonstrated for proteases from pathogenic bacteria. The underlying mechanisms extend to proteases from commensal bacteria which may be relevant for disease susceptibility. The intestinal microbiota and its proteolytic capacity exhibit the potential to contribute to the pathogenesis of IBD and IBS. This review highlights the relevance of host- and bacteria-derived proteases and their signalling mechanisms.

INTRODUCTION

Inflammatory bowel disease (IBD)—including the two main distinct pathologies ulcerative colitis (UC) and Crohn's disease (CD)—and irritable bowel syndrome (IBS) are chronically relapsing diseases with an accelerating incidence, especially in developed countries.[1] It is noteworthy that IBS-like symptoms such as diarrhoea or visceral pain are frequently observed in some patients with IBD in remission. Although IBD and IBS are two distinct entities, their complex pathogenesis involves common features including alterations in immune responses, altered microbiota composition with an impact on microbiota–host interactions, impaired intestinal barrier functions, altered bowel habits and changes in visceral sensitivity.[2 3] There is increasing evidence that all of the above factors are influenced by proteases, although the particular protease involved and the pathways influenced by proteases may be different in IBD and IBS. This review focuses on the involvement of host- or bacterial-derived proteases in IBD or IBS and highlights those protease-activated pathways that may be relevant in the pathogenesis of IBD and IBS.

Host-derived proteases in IBD and IBS

The large group of zinc-dependent matrix metalloproteinases (MMPs) plays a central role in extracellular matrix turnover. Furthermore, MMPs proteolytically activate a variety of non-matrix substrates such as cytokines, chemokines, growth factors and junction proteins. The deregulated expression or activity of host-derived MMPs has been implicated in several diseases including arthritis, atherosclerosis and colon cancer.[4 5] Increasing evidence suggests that MMPs are the predominant proteases involved in the pathogenesis of IBD.[6 7] MMPs influence the disease progression in multiple ways involving the function and migration of inflammatory cells as well as matrix deposition and degradation. The expression and activity of certain MMPs is increased during acute inflammation,[8] but also an imbalance between MMPs and their natural tissue inhibitors (TIMPs) has been reported for IBD.[9] Besides MMPs, other proteases including trypsin, neutrophil elastase,[10] mast cell tryptase,[11] cathepsins[12] and thrombin[13] have been implicated in IBD. Supernatants of mucosal biopsy specimens from patients with IBS evoked activation of visceral nociceptive neurons[14] as well as enteric neurons[15] and induced hyperalgesia,[16] a key feature of IBS. The responses could be attributed to serine proteases.

Intestinal microbiota in IBD and IBS

Changes in diversity and composition as well as functionality of the intestinal microbiota were associated with IBD[17 18] and IBS.[19] Pathogenic infections are suggested as the starting point for IBD[20] and IBS,[21] but further work is needed to understand the role of commensal bacteria and their possible contribution to the pathogenesis of intestinal disorders. In the context of intestinal inflammatory disease, it has to be considered that commensalism changes into a harmful situation for the host which then becomes a continuous inflammatory trigger.[22]

Protease activity in the gut lumen

Excessive concentrations of proteases have been found in the faeces of patients with UC or IBS.[23–26] Consistent with these findings, secreted factors of colonic biopsy samples from patients with IBD and IBS showed increased proteolytic activity.[16] Although the origin of the proteolytic activity was not elucidated, it is conceivable that proteases released from biopsy specimens are derived from the host. However, increased faecal proteolytic activity might result from colonic luminal bacteria which release serine, cysteine and metalloproteases.[27] Oral antibiotic treatment of mice resulted in reduced numbers of colonic microbiota and reduced colonic luminal serine protease activity, which provides further evidence for the bacterial origin of the proteases.[23] Bacterial proteolytic activity could be demonstrated even in the absence of inflammation, supporting the hypothesis that bacterial proteases are ubiquitously present in the gut lumen but only have an impact in a susceptible situation.[28]

IMPLICATIONS FOR BACTERIAL PROTEASES IN THE PATHOLOGY OF IBD

Role of pathogen-derived proteases

It has been suggested that alterations in microbial diversity and composition in disease-susceptible populations may alter innate defence mechanisms leading to chronic immune-mediated activation in active IBD.[29 30] Pathogens can be considered as the initiation step at the beginning of the disease development or during disease progression.[18 20 31] Many attempts have been made to identify the bacterial structures or molecules responsible for the pathogenicity of microbes. Besides the mechanism of type-specific secretion systems which allow the infiltration of bacterial material or whole bacteria into host cells, proteases have been shown to be involved in the infectious process of pathogens. However, the pattern of different types of proteases and their expression, regulation, activation and substrate specificity is very diverse. Host tissue provides different target points for bacterial proteases. In addition to the activation of specific types of host receptors, which will be discussed later, the degradation of extracellular matrix and the disruption of epithelial barrier function exhibits the most frequently described consequence of bacterial proteases. Targeting host epithelial barrier function is a central mechanism to be considered in the complex pathogenesis of IBD. Impaired intestinal barrier function has been associated with IBD,[32–34] although it is still uncertain whether the loss of barrier integrity is the cause or a consequence of chronic inflammation. Table 1 the proteases from pathogens targeting epithelial or endothelial barrier function in different organs and summarises the general mechanisms attributed to bacterial proteases which might be relevant in IBD.

Role of commensal-derived proteases

The adherence junction protein E-cadherin is the best described target for bacterial proteases derived from pathogens. This might be surprising as E-cadherin provides cell—cell contact on the lateral site of epithelial cells and it remains unclear how bacterial proteases in the gut lumen get access to their cleavage sites. We have demonstrated for the first time that a commensal-derived protease plays a role in intestinal inflammation. Gelatinase (GelE), a zinc-dependent metalloproteinase from *Enterococcus faecalis*, disrupted the integrity of the intestinal epithelial barrier by targeting the junction proteins occludin and E-cadherin.[44] The presence of disease susceptibility, but not tissue inflammation, is required for *E faecalis* GelE-mediated disruption of colonic barrier function (figure 1), supporting the hypothesis that commensal-derived proteases remain harmless in the healthy host. Similar to pathogens, commensal bacteria also possess a variety of virulence genes which are expressed under certain environmental conditions. *E faecalis* GelE can be regarded as an example in which a commensal-derived protease that has been associated with bacterial virulence plays a role in the development of intestinal inflammation. Further analysis of the structure/function interplay between bacteria and the host, including the

Table 1 Bacterial proteases target epithelial cell barrier function

Species	Classification	Protease	Host target structure/proposed mechanism	Reference
Bacillus anthracis	Pathogen	Metalloproteinase lethal toxin (LT) M4 metalloproteinase neutral protease (Npr599) M6 metalloproteinase immune inhibitor A metalloproteinase (InhA)	LT impairs barrier function in primary human endothelial cells (altered VE-cadherin distribution) Npr599 and InhA reduce endothelial barrier function through increased syndecan-1 ectodomain shedding in cultivated murine mammary gland cells	35
Citrobacter rodentium	Pathogen	Lymphostatin: virulence factor consisting of a glycosyltransferase, a protease and an aminotransferase	Disruption of epithelial barrier function via modulation of the small GTPase Rho and Cdc42	36
Clostridium difficile, *Clostridium sordellii*, *Clostridium novyi*	Pathogen	Large clostridial toxins (glycosyltransferases)	Inactivation of GTPases Rho, Rac and Cdc42 in intestinal epithelial cells	37
Clostridium perfringens	Opportunistic pathogen	Collagenase A	Intestinal barrier function, basal type-IV-collagen, mucus	28
Enterohaemorrhagic *Escherichia coli*	Pathogen	Metalloproteinase StcE	Cleavage of mucin 7 and glycoprotein 340, facilitation of adherence to epithelial-like HEp-2 cells	38
Enterotoxigenic *Bacteroidis fragilis*	Opportunistic pathogen	Metalloproteinase fragylisin or *B fragilis* toxin (BFT)	Induction of γ-secretase dependent shedding of E-cadherin ectodomain in HT29 cells	39
Helicobacter pylori	Pathogen	Serine protease *Helicobacter pylori* high temperature requirement A (HpHtrA)	Reduction of epithelial barrier integrity through targeting E-cadherin	40
Pseudomonas aeroginosa	Pathogen	*Pseudomonas* elastase	Reduction of barrier function in MDCK cells, altered ZO-1 expression and disturbed microfilaments	41
Staphylococcus aureus	Opportunistic pathogen	Serine proteases	Modulation of chemokine expression through NF-κB activation	42
Vibrio cholerae	Pathogen	Metalloproteinase haemagglutinin/ protease	Reduction of barrier integrity through actin and tight junction rearrangement	43

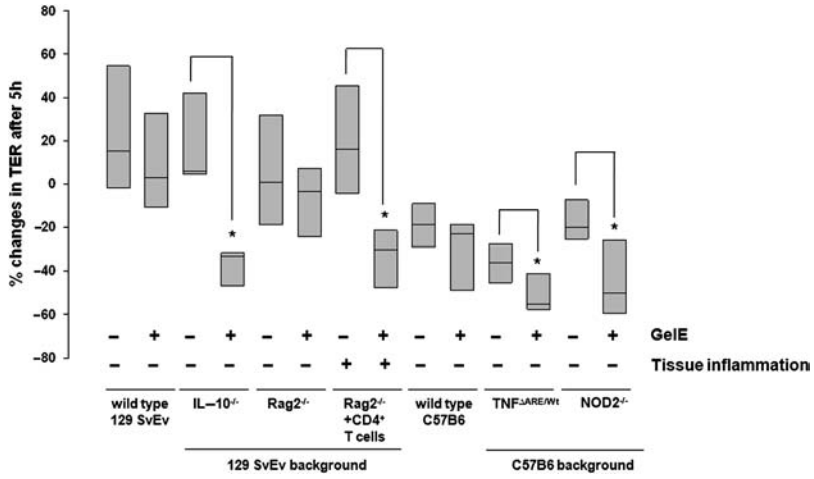

Figure 1 *Enterococcus faecalis* GelE impairs barrier function in the susceptible host. To assess the impact of GelE on colonic barrier function, different susceptibility models were used for intestinal inflammation. Interleukin-10-deficient (IL-10$^{-/-}$) and TNF$^{\Delta ARE/Wt}$ mice are genetically-driven spontaneous mouse models for the development of chronic inflammation in the colon and ileum, respectively. Rag2-deficient (Rag2$^{-/-}$) mice lack B and T cells and develop colitis after transfer of CD4+ T cells. NOD2-deficient (NOD2$^{-/-}$) mice lack the intracellular pattern recognition receptor NOD2 (nucleotide-binding oligomerisation domain 2) and are susceptible to certain bacterial infections. Appropriate wild type (Wt) counterparts 129SvEv and C57B6 were used as controls. Except for T cell transferred Rag2$^{-/-}$ mice, all other models did not develop histological changes with respect to inflammation in the colon after 8 weeks. Distal colon segments of the mice were apically stimulated with purified GelE (10 μg/ml) for 5 h in Ussing chamber systems. The results are expressed as the percentage change in transepithelial electrical resistance (TER) compared with the initial value of the tissue. Data are partially published[44] and represent median with 25th and 75th percentiles from five animals per group; *p≤0.05.

putative role of various bacterial virulence factors in commensal bacteria, will provide important insights into the pathogenesis of IBD.

Bacterial mucolytic activity: an underestimated potential

The question of how and when commensal-derived proteases are involved in IBD is clinically of great importance. Patients with IBD have an increased number of mucosa-associated bacteria and the thickness of the intestinal mucus layer is diminished.[45 46] Mucolytic activities allow bacteria to use mucus as a carbohydrate source and enable them to survive in the niche of the intestinal outer mucus layer. Over 20 years ago, Rhodes and colleagues hypothesised that bacterial mucus degradation could be associated with IBD, but they could not correlate bacterial glycosidase activity with disease activity in patients with IBD.[47] However, a recent study demonstrated a shift in the mucolytic consortium of bacteria in IBD patients. The most abundant mucolytic species in healthy controls, *Akkermansia muciniphila*, is reduced in IBD whereas *Ruminococcus* species are disproportionally increased under conditions of chronic inflammation. *Ruminococcus* α- and β-glycosidases remove terminal sugars from the mucus matrix that subsequently become accessible for other bacteria, providing a possible explanation for the increase in total mucosa-associated bacteria in IBD.[48] Pathogens have evolved several strategies to disrupt and avoid mucosal barriers. The enzymatic degradation of mucins and the downregulation of mucin production are two of the most common mechanisms.[49] The substrate specificity of bacterial proteases is often not restricted to one molecule. Proteases that have been demonstrated to digest mucins have also been shown to facilitate adherence to host cells[38] or to disrupt epithelial barrier function.[28] Alterations in microbial composition and mucus structure under disease-susceptible conditions might allow commensal-derived proteases to gain access to the epithelium, targeting protein substrates that would not be accessible to them under physiological conditions.

PROTEOLYTIC ACTIVATION OF NEURONS

The functional relevance of the elevated protease levels in patients with IBD and IBS has been demonstrated. In a rodent model, faecal supernatants of diarrhoea-predominant IBS patients with elevated serine protease contents induced visceral hypersensitivity and increased paracellular permeability via the protease-activated receptor (PAR) 2.[26] However, faecal supernatants of patients with UC generated hyposensitivity to rectal distension, which was a result of PAR4 activation by cathepsin G. This anti-nociceptive action overpowered the pro-nociceptive effects of PAR2 activating proteases in the faecal supernatants.[24] This study suggested that even though patients with IBD and IBS have increased faecal protease levels, the functionally active proteases must be different and, in addition, signal through distinct mechanisms. Supernatants of colonic biopsy samples of patients with IBS released proteolytic mediators that directly sensitised murine sensory neurons and generated visceral and somatic hypersensitivity through the activation of PAR2.[16] Further studies showed that mucosal biopsy supernatants from patients with IBS also activated human enteric neurons[15] as well as rat visceral nociceptive neurons.[14] In both studies proteases have been identified as the main mediator responsible for neural excitation. Serine proteases such as thrombin, trypsin or mast cell tryptase, which are released by epithelial cells, immune cells, blood cells or even neurons, activate enteric and visceral sensory neurons as well as enteric glia by targeting PARs.[50 51] There are four PARs (PAR1, PAR2, PAR3, PAR4), all of which are G-protein coupled tethered ligand receptors. They are activated by the proteolytic cleavage of the N-terminus which allows the tethered ligand to bind to the receptor. PAR1, PAR2 and PAR4 activate enteric neurons (see below for further details). However, PAR4 inhibits excitability of dorsal root ganglion neurons which supply the sensory innervation of the gut.[52] This effect may explain the finding that PAR4 exerts analgesic effects by suppressing somatic and visceral hyperalgesia and pain.[53 54] The functional expression of PARs in different cells may have a clinical impact in that it may open new ways to specifically target protease actions. In this context, it is important to realise

that the contribution of PARs is different between rodent and human enteric neurons. While submucous neurons in the guinea pig have strong responses to PAR2 activation, PAR1 seems to be the dominant receptor in human submucous neurons.[55] It needs to be considered that PARs are present on muscle cells, epithelial cells and immune cells as well as on neurons. For example, human tissue resident macrophages are activated by PAR2 ligands.[55] Therefore, the disease relevant PAR signalling is a combination of several neuronal and non-neuronal pathways. It is not known whether the neural- and glia-mediated actions of proteases are part of the cascades initiating or maintaining inflammatory processes or whether they serve protective functions. In principle, bacterial proteases may also be able to activate nerves in the gastrointestinal tract but this has not yet been demonstrated. For the purpose of this review, we therefore addressed this open issue and found that the metalloproteinase GelE from commensal *E faecalis* activated about 20% of guinea-pig enteric neurons (figure 2). Interestingly, pretreatment of the tissue with GelE negatively influenced the ability of a selective PAR2-activating peptide to excite neurons. This suggests that GelE may signal through PAR2-expressing or dependent pathways, but further evidence for such a route is needed.

HOST RECEPTORS FOR BACTERIAL PROTEASES

Protease-activated receptors

The potential of different bacterial proteases to target PAR as well as other host receptors has been shown for respiratory and oral epithelial cells as well as for platelets and neutrophils (table 2). However, the mode of action of bacterial proteases in the gastrointestinal tract, except for *E faecalis* GelE,[44] is still largely unknown. In general, proteases target the G-protein coupled PAR receptors and induce activation by proteolytic cleavage of the N-terminal ligand or inactivation by disarming the receptor due to alternative cleavage of the N-terminus. The bacterial arginine-specific cysteine protease gingipain-R of the periodontitis pathogen *Porphyromonas gingivalis* has been shown to cleave and activate PAR2 on human neutrophils, PAR1 and PAR4 on platelets to induce platelet aggregation and PAR1 and PAR2 on an oral epithelial cell line to induce secretion of the pro-inflammatory cytokine interleukin 6 (IL-6).[56–58] In addition to PARs, several other cell surface proteins such as occludin and E-cadherin were targets of gingipain in Madin-Darby canine kidney cells[65] and CD14 human monocytes.[66] The lung opportunistic pathogen *Pseudomonas aeruginosa* secreted the elastolytic metalloproteinase *P aeruginosa* elastase/LasB which disarmed PAR2 by proteolysis, made the receptor unresponsive to activating proteases and avoided receptor internalisation and mobilisation of intracellular pools. However, *P aeruginosa* elastase has also been shown to increase respiratory epithelial permeability by cleavage of tight junction proteins zonula occludens 1 and 2. Furthermore *P aeruginosa* released the exoprotease LepA which induced the activation of the transcription factor NF-κB via PAR1, PAR2 and PAR4 activation.[60 61 67] *Serratia marcescens*, which is an opportunistic pathogen of the respiratory and urinary tract,

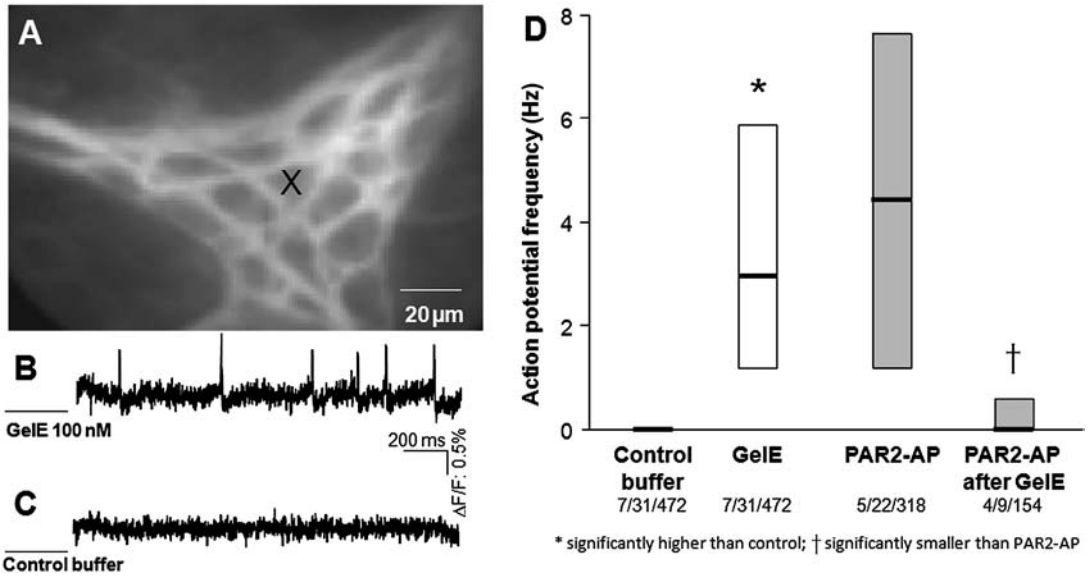

Figure 2 Effect of the bacterial protease GelE from *Enterococcus faecalis* on guinea-pig submucous neurons. (A) A submucous ganglion. Individual neurons were labelled with the voltage sensitive dye Di-8-ANEPPS which allowed direct detection of action potentials. (B) Application of GelE (100 nM) for 30 s induced action potential discharge (sharp upward deflections) whereas the control buffer solution alone had no effect (C).The traces are from the neuron marked by a black cross in (A). GelE and buffer were applied shortly before the recording period as indicated by the horizontal bars. GelE significantly increased action potential discharge (D). The ability of the PAR2-AP SLIGRL-NH_2 (100 µM) to evoke action potential discharge was significantly impaired by predisposing the neurons to GelE (100 nM). Symbols mark significant differences as explained in the figure. The numbers indicate numbers of tissues/ganglia/neurons studied.

Table 2 Protease-activated receptors (PARs) as targets for bacterial and mite proteases

Species	Classification	Protease	Host target structure/proposed mechanism	Reference
Porphyromonas gingivalis	Pathogen in periodontitis	Cysteine protease gingipain-R	Activation of PAR2 on neutrophils	56
			Activation of PAR1 and PAR2 induced release of pro-inflammatory cytokine IL-6 from oral epithelial cells	57
			Activation of PAR1 and PAR4 on platelets mediated induction of platelet aggregation	58
Treponema denticola	Pathogen in periodontitis	Released peptidases	Inhibitory effect on proteolysis-mediated PAR2 activation	59
Pseudomonas aeroginosa	Opportunistic lung pathogen	Metalloproteinase *P aeroginosa* elastase/LasB	Inactivation of PAR2 in respiratory epithelial cells led to unresponsiveness to activating proteases	60
		ExoproteaseLepA	Activation of PAR1, PAR2 and PAR4 induced activation of NF-κB	61
Serratia marcescens	Opportunistic pathogen of the respiratory and urinary tract	Metalloproteinase serralysin	Activation of PAR2 induced expression of IL-6 and IL-8 transcripts	62
House dust mite		Cysteine protease allergen Der p1	Inactivation of PAR1, activation of PAR2 mediated release of pro-inflammatory cytokines in respiratory epithelial cells	63
		Serine protease Der p3 and Der p9	Activation of PAR2 induced release of pro-inflammatory cytokines in lung epithelial cells	64

IL, interleukin.

produced the zinc metalloproteinase, serralysin, which has been shown to induce IL-6 and IL-8 mRNA expression in a respiratory cell line and transactivation of AP-1, C/EBP- and NF-κB-driven promotors via PAR2.[62] A house dust mite cysteine protease allergen (Der p1) has been shown to target PAR2 but to inactivate PAR1 in respiratory epithelial cells and to induce release of pro-inflammatory cytokines.[63] The mite allergens Der p3 and Der p9, which are serine proteases, activated lung epithelial cells by interaction with PAR2 and induced the release of pro-inflammatory cytokines.[64]

Pattern recognition receptors

Toll-like receptors (TLR) are part of the innate immune system and belong to the pattern recognition receptor family that identifies microbial pathogens through the recognition of pathogen- or microbial-associated molecular patterns (carbohydrates, nucleic acids, peptidoglycans, lipoteichoic acids, lipoproteins). Direct proteolytic activation of a full-length TLR has recently been described for the avian TLR15. Virulence-associated microbial-derived proteases from the fungi *Candida guilliermondii*, *Trichosporon* spp., *Penecillium* spp. and *Mucor* spp. and the Gram-negative opportunistic pathogen *P aeruginosa* have been shown to activate TLR15, which is a unique type of receptor that combines TLR characteristics with an activation mechanism typical of the evolutionary distinct PARs.[68] Although it is still unknown which proteases activate TLR15, one could speculate that these are serine proteases as the receptor activation could be inhibited by the serine protease inhibitor phenylmethanesulfonylfluoride (PMSF). Mammalians seem to lack a TLR that is able to sense proteolytic activity, although mammalian TLR4 can be activated by elastase-activated compounds from the extracellular matrix.[69] Furthermore, lipopolysaccharide (LPS) recognition by TLR4 was indirectly influenced by trypsin which is augmented in ileal inflammation and cleaved MD-2, an accessory glycoprotein essential for TLR4 signalling. The proteolysis of MD-2 provided a mechanism for intestinal epithelial LPS tolerance that helped to regulate immune responses to commensal bacteria-derived ligands.[70] Recent work connected TLR and PAR signalling and described distinct features of the TLR–PAR interaction which contribute to signal diversity in inflammation and host antimicrobial responses.[71] The cross-talk between different receptor signalling cascades and the recognition of diverse microbial signals provide homeostasis, but further investigations are needed to understand this complex network more fully.

E-cadherin

The adherence junction protein E-cadherin is a calcium-dependent single-pass transmembrane protein generally expressed in the lateral plasma membrane of epithelial cells. E-cadherin provides contact to adjacent cells and plays a major role in epithelial cell differentiation. The intracellular domain is highly conserved and signals through cytoplasmic proteins from the catenin family.[72] The extracellular domain could act as a receptor for bacterial or fungal entry into epithelial cells, which so far has only been demonstrated for surface proteins. Internalin A from *Listeria monocytogenes*[73] and invasion Als3 from *Candida albicans*[74 75] interact with E-cadherin and mediate the internalisation of the respective microorganisms. E-cadherin is also targeted by bacterial proteases; the metalloproteinase toxin BFT from *Bacteroidis fragilis* was shown to induce the shedding of the E-cadherin ectodomain through an unknown intestinal epithelial cell receptor-mediated induction of γ-secretase.[39] A direct E-cadherin cleavage could be demonstrated for the trypsin-like serine protease HpHtrA from *Helicobacter pylori*.[40] We demonstrated that a commensal-derived metalloproteinase, GelE from *E faecalis*, was able to degrade the extracellular domain of E-cadherin in the susceptible host, suggesting that proteases from the commensal gut microbiota might play a role in the disease pathogenesis of chronic intestinal inflammation, but only if they get access to the target tissue under predisposed conditions.[44] The proteolytic cleavage of E-cadherin, either direct or

indirect, reflects an important mechanism for bacteria—especially pathogens—to reach the intercellular space and to translocate across the epithelium. Furthermore, E-cadherin is targeted by a number of endogenous metalloproteinases including stromelysin-1, matrilysin,[76] ADAM-10[77] and meprin-β.[78]

Protease-dependent receptor activation

The release of tumour necrosis factor α (TNFα) is associated with an increased permeability of the gut epithelial barrier. The blockade of TNF with anti-TNF antibodies is an established strategy in the treatment of IBD. The increase of soluble biologically active TNF arises from the conversion of membrane-bound TNF by TNF-converting enzyme (TACE).[79 80] TACE or ADAM17 belong to the ADAM (a disintegrin and a metalloprotease) family of metal-dependent proteases and has been additionally implicated in the shedding of other membrane-bound precursors of cytokines and growth factors.[81] One of these factors is transforming growth factor-α which in turn activates the epidermal growth factor receptor (EGFR). Phosphorylated EGFR induces the activation of mitogen activated protein kinases and mediates changes in intestinal permeability.[82] Many of these processes and receptor activation mechanisms are described in the context of carcinogenesis,[83] a frequent IBD-associated complication. In particular, the fact that numerous cytokines and growth factors are membrane-associated as precursors and require proteolytic conversion may represent a novel mechanism for bacterial-derived proteases.

CLINICAL IMPLICATIONS

The inhibition of host-derived proteases has been discussed as a therapeutic option in IBD but there are only limited reports with inconsistent results. Studies in animal models showed that inhibition of cathepsins[12] and tryptase[84] ameliorates chemical-induced colitis. Furthermore, the serine protease inhibitor camostat has been reported to induce and maintain remission in patients with UC.[85] Various MMP inhibitors have been shown to improve inflammation, particularly in rat models of IBD[86–88] but also in dextran sodium sulfate (DSS)-induced colitis in mice. Despite the fact that MMP inhibitors showed beneficial therapeutic effects in

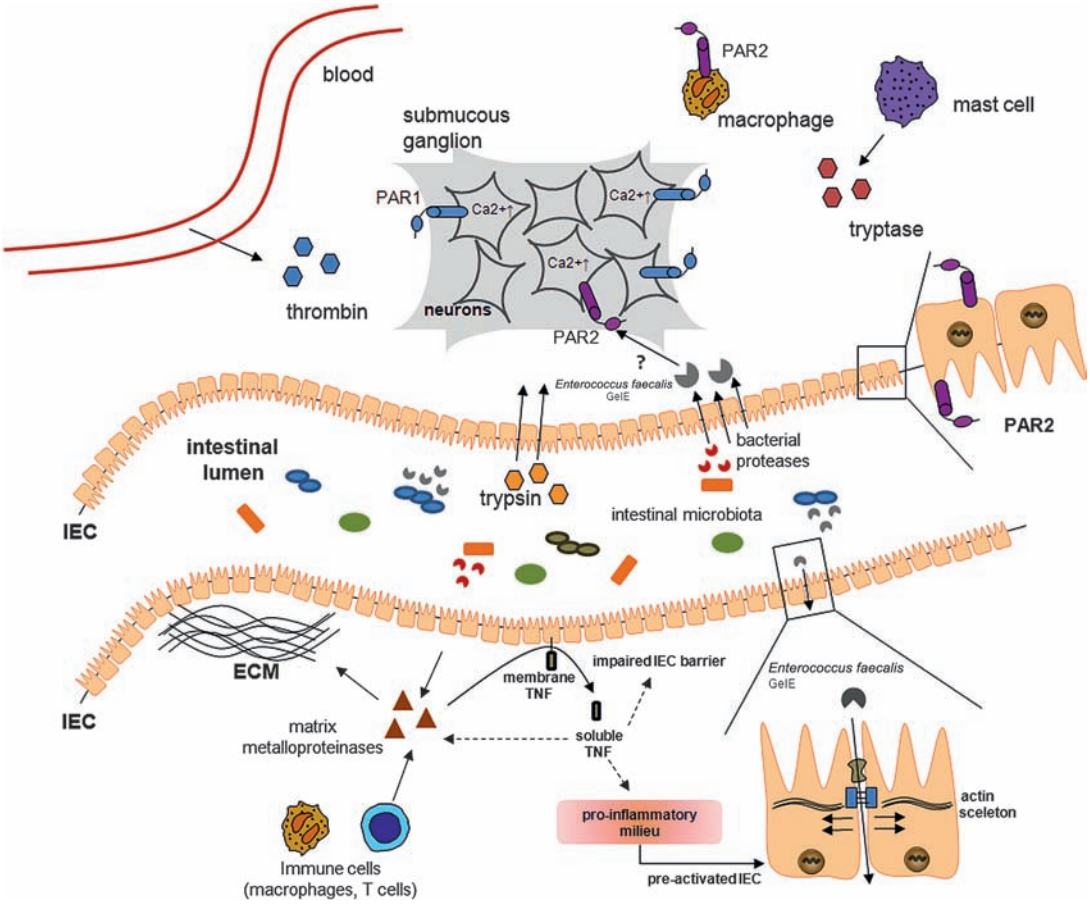

Figure 3 Protease activity in the gut. Illustration of possible involvements of proteases in disease-related mechanisms of inflammatory bowel disease (IBD) and irritable bowel syndrome (IBS). The role of PAR-dependent pathways and the contribution of PARs are based on data from human tissue. PAR2 would play a significant role in rodent enteric neurons. The PAR-related pathways shown in the top part may be primarily relevant in IBS while the bottom pathways prevail in IBD; however, an overlap of some mechanisms is likely. Ca, calcium; ECM, extracellular matrix; GelE, gelatinase from *Enterococcus faecalis*; IEC, intestinal epithelial cells; PAR, protease-activated receptor.

experimental colitis models, a clinical trial investigating the beneficial potential of the MMP inhibitor prinomastat in lung cancer failed because of unacceptable adverse effects.[89] In an animal model, serine protease inhibitors have been shown to be effective in inhibiting the pronociceptive effects induced by the supernatants of mucosal biopsies and faeces samples from patients with IBS.[16 26] These results suggest the use of serine protease inhibitors in the treatment of IBS symptoms. To date, studies that use inhibitors of host-derived proteases have shown rather poor efficacy in the treatment of human IBD. Adverse side effects, presumably resulting from non-specific actions and/or broad spectrum inhibition of host proteases also affecting functions of other organs, need to be addressed before protease inhibitors become a therapeutic option. In addition, the use of endogenous protease inhibitors could be considered as a treatment option in IBD to avoid adverse side effects and to reconstitute the proteolytic balance in the gut. One example is elafin, a serine protease inhibitor, the expression of which is reduced in the gut mucosa of IBD patients.[90] Furthermore, it has been demonstrated that elafin protects against DSS-induced colitis through the inhibition of pro-inflammatory mediators and the strengthening of epithelial barrier function.[91]

The inhibition of PARs by PAR antagonists could be an effective strategy to suppress protease-mediated action, particularly if they specifically target a particular PAR. The use of PAR antagonists as a treatment option for IBD and IBS is supported by their involvement in the generation of pain, inflammation, increased permeability, as well as motor and secretory disorders in the intestine. In this respect it may even be beneficial to develop PAR agonists which would provide the PAR4-mediated anti-nociceptive action in humans.

A few clinical trials have shown that the administration of probiotics such as the probiotic mixture VSL#3 improved IBS symptoms including pain/discomfort, distension/bloating and defecation[92 93] and induced and maintained remission in patients with UC.[94 95] Furthermore, the feeding study conducted by Kunze *et al* provided evidence for the interaction between the probiotic *Lactobacillus reuteri* and colonic enteric neurons.[96] Although probiotic efficacy could be demonstrated in IBD and IBS, the active functional components/structures, the molecular mechanisms or the primary probiotic target still remain to be clarified. It may be speculated that the protective role of probiotics may be related to the release of proteases and/or protease inhibitors. Such a mechanism has recently been reported for the serine protease lactocepin from *Lactobacillus paracasei* which inhibited the recruitment of pro-inflammatory cells to the site of inflammation through degradation of chemokines.[97] The anti-inflammatory effect of lactocepin suggested that bacterial proteases play an important role in the regulation of intestinal homeostasis.

Key messages

- Host-derived proteases are involved in the pathogenesis of IBD and IBS
- Protease-activated receptors are specific targets for host-derived and bacteria-derived proteases
- Proteases belong to virulence factors of intestinal pathogens and commensals
- Mechanistically, bacterial proteases target and impair barrier function of epithelial cells and activates enteric neurons
- Certain susceptibility is necessary for the involvement of commensal-derived proteases in IBD

SUMMARY

We are at the very beginning of understanding the complex intestinal microbial proteolytic capacity which shows significant potential to be involved in the pathogenesis of IBD, IBS and other gastrointestinal disorders. The mechanisms so far described are mostly restricted to proteases from pathogens, whereas proteases from commensal gut bacteria have generally been ignored. As shown in figure 3, the proteolytic activity in the gut is a result of host-derived proteases expressed by a variety of different cell types, as well as bacterial proteases produced by different species. The coordinated interactions of host and bacterial-derived proteases maintain homeostasis but become relevant to disease if deregulated. GelE from *E faecalis* is the first example of a bacteria–host interaction involving a commensal bacterial protease that is implicated in the pathogenesis of IBD and other gut diseases associated with inflammation.

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