Degradation of the extracellular matrix is part of the pathology of ulcerative colitis

Kirov, Stefan; Sasson, Ariella; Zhang, Clarence; Chasalow, Scott; Dongre, Ashok; Steen, Hanno; Stensballe, Allan; Andersen, Vibeke; Birkelund, Svend; Bennike, Tue Bjerg

Published in:
Molecular Omics

DOI:
10.1039/c8mo00239h

Publication date:
2019

Document version:
Final published version

Document license:
CC BY-NC

Citation for published version (APA):
Kirov, S., Sasson, A., Zhang, C., Chasalow, S., Dongre, A., Steen, H., Stensballe, A., Andersen, V., Birkelund, S., & Bennike, T. B. (2019). Degradation of the extracellular matrix is part of the pathology of ulcerative colitis. Molecular Omics, 15(1), 67-76. https://doi.org/10.1039/c8mo00239h

Go to publication entry in University of Southern Denmark's Research Portal
Degradation of the extracellular matrix is part of the pathology of ulcerative colitis†

Stefan Kirov, Ariella Sasson, Clarence Zhang, Scott Chasalow, Ashok Dongre, Hanno Steen, Allan Stensballe, Vibeke Andersen, Svend Birkelund and Tue Bjerg Bennike

Introduction

Ulcerative colitis (UC) is a chronic relapsing inflammatory disorder of the gastrointestinal tract. The prevalence of UC is increasing worldwide. In Europe, for example, the incidence has reached almost 24 cases per 100,000 person-years. The disease manifests itself at all ages and it severely affects the quality of life of the patients and their families. In addition, UC has a large impact on society, due to interrupted education, sick leave, and the significant strain it places on the healthcare system.

The underlying cause of UC is not completely understood, but both genetics and the environment have been found to be factors in the disease etiology. More than 230 genetic loci have been identified as being associated with the inflammatory bowel diseases (IBD) which, in addition to UC, include Crohn’s disease (CD). Identified genes have been found to be involved in the epithelial barrier function and both the innate and adaptive immune response. Additionally, a westernized lifestyle and environmental impact is associated with increased risk of IBD, which may be linked to changes in the gut microbiome. Accordingly, the prevalence in the West is increasing. Cigarette smoking also affects the risk of IBD and gene-smoking interactions have been identified.

An early diagnosis and individualized management of the disease are critical in avoiding irreversible damage to the intestinal tract. However, finding good treatments remains a challenge due to the heterogeneous nature of the disease. Hence, despite the introduction of biological treatments for UC, colectomy still is required in 25–30% of the patients at some point during their lifetime due to the development of colitis refractory to other treatments. The intestinal mucosa is critical to inflammatory processes and regulates immune responses at the interface between the host and the environment. It has been previously hypothesized that initial damage to the intestinal mucosal barrier results in a misdirected immune response which ultimately leads to the manifestation of IBD. An in-depth characterization of the intestinal mucosa via molecular profiling technologies would therefore help to understand the molecular pathophysiology.

Using a comparative analysis of the proteome in IBD and healthy...
Research Article

Materials and methods

Proteomics data acquisition

For the original study, colon biopsies were taken from ten UC patients and 10 gastrointestinal healthy controls with sigmoidoscopy from macroscopically healthy-looking (non-inflamed) tissue at the Regional Hospital Silkeborg in Denmark. The samples were immediately snap-frozen in liquid nitrogen and stored at −80 °C until time of processing within one year. The samples were prepared for bottom-up proteomics analysis using a label-free quantitation strategy. Briefly explained, the samples were homogenized using steel beads and digested using a filter-aided sample preparation protocol with the protease trypsin. The samples were analyzed by high-throughput bottom-up proteomics using a label-free quantitation strategy. This study lead to the identification and quantification of 5711 different proteins and proteomics using a label-free quantitation strategy. This study lead to the identification and quantification of 5711 different proteins and found an increased abundance of neutrophils and neutrophil extracellular traps (NETs) in the biopsy samples from UC patients.

Proteomics data are inherently complex and can be analyzed at many levels, and statistical analysis of proteomics datasets can be confounded by a number of factors. We present here our re-examination of our proteomics dataset comparing UC samples to gastrointestinal healthy controls, using a different statistical approach compared to the original study. Employing a linear mixed-effects regression model, rather than t-tests, and analyzing the data on the protein and peptide level, we obtained a higher statistical sensitivity. In this study we confirmed the findings of the initial publication. In addition, the expanded findings allowed us to hypothesize that the degradation of the colon mucosa extracellular matrix (ECM) may play a critical role in the pathology of UC, in addition to neutrophil extracellular traps (NETs).
level more than log2 RMA of 3.5 in at least 10 samples were considered. Fold change values were determined for the control subjects vs. the UC patients (Table 1).

Fold change values for probesets were collapsed to a gene level by taking the median. Pearson pairwise correlations were then calculated for all microarray sets and the proteomics data.

The list of proteins with significant disagreement between RNA expression and protein levels was compiled by thresholding for mass spec fold change and microarray median fold change and sorting by the mass spec fold change. The directionality and downregulation of proteins was stored as a Boolean vector.

Pathway analysis. Differentially regulated peptides were converted to protein identifiers using the peptides.txt file. Protein identifiers were converted to EntrezGene identifiers using a combination of conversion techniques according to the source of the originating protein ID (Refseq, Ensembl and Uniprot).

We split the lists into up- and down-regulated sublists and examined each list separately with WebGestalt and GSEA. Webgestalt was used to explore GO enrichment and GSEA was used to explore other ontologies and gene lists, such as MSIGDB, Reactome (www.reactome.org) and Pubmed (www.ncbi.nlm.nih.gov/pubmed/).

Both tools allowed lists of genes to be uploaded and to serve as background models and we used all identified proteins to define the background reference.

Reproducibility

Most results from this analysis (hits lists, graphs, etc.) can be reproduced on a Linux system with R 3.3.1, perl and several R packages (listed available in the downloadable Supplementary Materials file, ESI†). Once all input datasets are downloaded along with the scripts, executing reproduce.sh would generate identical results to those we communicate in this paper. All datasets and scripts necessary to reproduce these findings are downloadable from http://pubd.web.bms.com/.

Immunohistochemistry

Formalin-fixed colon biopsies were paraffin embedded, cut in 10 μm sections, mounted on Superfrost Plus slides (Thermo Scientific) and deparaffinized. Sections were blocked with 0.1% bovine serum albumin (BSA) in phosphate-buffered saline (PBS) for 1 hour. Thereafter, the sections were incubated for one hour with the primary antibody in 0.1% BSA in PBS using either 2 μg ml⁻¹ rabbit anti-Protein S100-A9 (Abcam, Cambridge, UK), 2 μg ml⁻¹ mouse IgG1 anti-Protein S100-A12 (Abcam), 2 μg ml⁻¹ rabbit anti-myeloperoxidase (ab9535, Abcam), 2 μg ml⁻¹ isotype control mouse monoclonal IgG1, or 2 μg ml⁻¹ rabbit IgG. Sections were washed 3 times with PBS. The samples were then incubated for 1 hour in PBS with the secondary antibody using either TRITC conjugated goat anti-rabbit IgG or TRITC conjugated goat anti-mouse IgG (Jackson ImmunoResearch, Bar Harbor, ME). The samples were then diluted 1:200 in PBS with 0.1% BSA. To stain for DNA, the sections were washed in PBS and incubated for 30 minutes with 1 μM ToPro-3 (Thermo Scientific) in PBS. The slides were analyzed with an SP5-confocal microscope (Leica, Wetzlar, Germany) using an HC PL APO 63×/1.40 Oil objective (Leica) and the data was analyzed in ImageJ.³⁵

To provide a semi-quantitative addition to the proteomics data, the stain intensity surrounding the 10 cells with the highest staining intensity was averaged for each confocal microscopy image using ImageJ 1.48v. The intensities between the samples was compared by two sample t-tests in R.

Results

Quality control

We have established an R-based pipeline to comprehensively evaluate the quality of proteomics data (manuscript in preparation). A full quality report is available in the (available in the downloadable Supplementary Materials file, ESI†).

We used the quantro R package to evaluate global effects and observed no statistically significant change in protein intensities between the UC and control groups (p = 0.11, 10,000 simulations). We therefore applied median centering as a global normalization method.

Protein level analysis

This study aimed to identify proteins differing in abundance on average between the UC and control groups. For this purpose we performed linear regression analysis based on the protein groups generated by MaxQuant.

We identified a similar number of protein groups – 6399 – compared to the original study where 6268 were identified. After rigorous filtering, 5093 proteins were considered to be quantifiable, versus 5711 in the original publication. However, our statistical model allowed us to identify substantially more differentially regulated proteins: 251 versus 49 in the previous study. This difference reflects two methodological differences: different filtering and imputation strategies, and the linear mixed effects model we used that allowed us to take advantage of the technical replicates, which had been averaged in the original study. Including a random donor effect to allow for intra-donor correlations between technical replicates allowed the assessment of technical variability and increased statistical power of hypothesis tests.

As with the original study we were able to establish statistically significant overlap with NETs (hypergeometric test, p < 0.001), most significantly with NET granules.⁵⁵ We were able to confirm the presence of a neutrophil immune cell signature also based on MSIGDB.¹⁶

Of the differentially regulated proteins, 90 had increased and 161 had decreased abundance in the UC samples. However, 9 of the top 10 proteins with the largest absolute expression difference (Table 2) were upregulated, signifying the larger
Table 2  The top 10 differentially regulated proteins when comparing the UC and control groups. The list is filtered by FDR adjusted p-value (p < 0.05) and sorted by effect size (log2 ratio). Complete table of the differentially regulated proteins is available as Supplementary File 1 and the non-filtered data is available in Supplementary File 2 (ESI).

| Protein acc. | p-value | FDR | Entrez gene | log2 ratio | Description                          | Gene     | NETs protein |
|--------------|---------|-----|-------------|------------|--------------------------------------|----------|--------------|
| NP_002334    | 8.57 × 10⁻¹² | 4.37 × 10⁻⁸ | 4057 | 7.45       | Lactotransferrin                      | LTF      | Yes          |
| NP_001532124 | 2.02 × 10⁻¹³ | 1.03 × 10⁻⁹ | 4353 | 6.76       | Myeloperoxidase                      | MPO      | Yes          |
| NP_004985    | 1.87 × 10⁻¹² | 9.52 × 10⁻⁹ | 4318 | 6.06       | Matrix metalloproteinase 9           | MMP9     | Yes          |
| XP_011545190 | 2.93 × 10⁻⁷  | 1.49 × 10⁻³ | 1991 | 5.02       | Elastase, neutrophil expressed       | ELA2     | Yes          |
| NP_001691    | 1.28 × 10⁻⁸  | 6.50 × 10⁻⁵ | 566  | 4.92       | Azurocidin 1                         | AZU1     | Yes          |
| XP_011514177 | 5.16 × 10⁻¹³ | 2.63 × 10⁻⁹ | 2006 | -4.88      | Elastin                              | ELN      | No           |
| NP_002956    | 2.13 × 10⁻⁹  | 1.09 × 10⁻³ | 6280 | 4.67       | S100 calcium binding protein A9      | S100A9   | Yes          |
| NP_006623    | 2.02 × 10⁻¹⁰ | 1.03 × 10⁻⁶ | 3684 | 4.53       | Integrin subunit alpha M             | ITGAM    | No           |
| NP_002768    | 6.37 × 10⁻⁷  | 3.24 × 10⁻³ | 5657 | 4.49       | Proteinase 3                         | PRTN3    | Yes          |
| XP_005260579 | 8.75 × 10⁻¹⁰ | 4.46 × 10⁻³ | 671  | 4.45       | Bactericidal/permeability-increasing protein | BPI      | No           |

Table 3  Top 10 of the proteins where significant disagreement between protein log2 ratios and transcriptional profiling ratios were observed, ranked by mass spec log2 fold change.

| Protein acc. | MassSpec Olsen | MassSpec Planell | MassSpec Kugathasan | Planell Olsen | Planell Planell | Planell Kugathasan | Kugathasan Olsen | Kugathasan Planell | Kugathasan Kugathasan | Mean of all arrays | Symbol |
|--------------|----------------|------------------|---------------------|--------------|----------------|--------------------|------------------|-------------------|----------------------|-------------------|--------|
| NP_002469    | -3.25          | -0.55            | 0.19                | 1.06        | 0.60           | INS15               |                   |                   |                      |                   |        |
| NP_005223935 | -2.42          | 0.26             | 0.02                | 1.53        | 0.60           | OLFM1               |                   |                   |                      |                   |        |
| NP_011508876 | -2.37          | 1.57             | 1.94                | 2.41        | 1.97           | COL6A3              |                   |                   |                      |                   |        |
| NP_001034438 | -2.15          | -0.24            | 0.39                | 0.92        | 0.69           | EFEMP1              |                   |                   |                      |                   |        |
| NP_060150    | -1.71          | 0.26             | 0.27                | 1.29        | 0.60           | ASPN                |                   |                   |                      |                   |        |
| NP_01129408  | -1.41          | 0.92             | 0.64                | 1.08        | 0.88           | POSTN               |                   |                   |                      |                   |        |
| XP_011519350 | -1.34          | 1.41             | 1.67                | 1.86        | 1.65           | COL4A1              |                   |                   |                      |                   |        |
| NP_002014    | -1.13          | 0.36             | 0.44                | 1.48        | 0.76           | FMOD                |                   |                   |                      |                   |        |
| NP_001275908 | -1.09          | 1.70             | 0.48                | 1.69        | 1.29           | LIPA                |                   |                   |                      |                   |        |
| NP_000129    | -1.02          | 0.95             | 0.60                | 2.01        | 1.19           | FBN1                |                   |                   |                      |                   |        |
| NP_000080    | -1.00          | 1.44             | 1.43                | 1.86        | 1.58           | COL1A2              |                   |                   |                      |                   |        |
| NP_001837    | -0.95          | 0.94             | 0.64                | 1.26        | 0.94           | COL1A2              |                   |                   |                      |                   |        |
| NP_004376    | -0.84          | 1.20             | 0.77                | 2.18        | 1.38           | VCAN                |                   |                   |                      |                   |        |
| XP_006713333 | -0.66          | 1.14             | 0.71                | 2.23        | 1.36           | DCN                 |                   |                   |                      |                   |        |
| NP_001702    | -0.64          | 0.75             | 0.72                | 0.52        | 0.66           | BGN                 |                   |                   |                      |                   |        |
| XP_011327754 | -0.61          | 0.38             | 0.77                | 0.38        | 0.58           | COL6A2              |                   |                   |                      |                   |        |

In bold-**bona fide** components of the extracellular matrix (ECM).
Anecdotal reports of similar phenomena have been recorded in the past. For example, collagen protein is known to be lost due to degradation in models of IBD, and PGP fragments are subsequently increased.42 This degradation of collagen could trigger compensation at a transcriptional regulation level and would explain the upregulation seen in the microarray studies29–31 we examined. In a recently published RNA-Seq dataset,43 3 of the genes we found to be upregulated as transcripts, but at decreased protein levels were confirmed to be increased as transcripts as well (Table S2, ESI†).

Chromogranin A

In addition to the protein level analysis, we also looked at differential expression at the peptide level (available in the downloadable Supplementary Materials file, ESI†). This analysis may occasionally highlight differences in protein processing and secretion. We decided to look specifically at chromogranin A, as the log2 ratio for the identified peptides originating from this protein showed substantial dispersion. The variability of most peptides is higher in the UC group because of more imputed values.

Chromogranin A (CHGA) is a protein that is post-translationally processed to multiple hormones and functional peptides.44,45 While chromogranin A was one of the differentially regulated proteins, it was not a top hit. CHGA ranked in the top 28.17% of all hits (71/252) in terms of fold change (log2 FC = −1.77, FDR = 0.0015). At the peptide level, differential regulation was more pronounced with fold changes ranging from –3.7 to –5.7, and the top peptide ranked at the top 6.54% of all hits (42/642). The reason for this discrepancy is that some of the peptides were significantly downregulated in UC (Fig. 2), while others were only marginally higher in controls. For all peptides, the characteristics and fold change differences between tissues from healthy controls and UC patients are given in the (Supplementary File 3, ESI†).

Identification of CHGA sub-regions as some of the most significant peptide hits (available in the downloadable Supplementary Materials file, ESI†) allowed us to describe EA-92, chromofungin, serpinin, and pancreastatin as potential biomarkers and perhaps targets in the context of UC. In addition, we can now speculate on the involvement of EA-92 in inflammation.

Significant changes occurred in four peptide regions. These regions overlap with the biologically active peptides serpinin, vasostatin and chromofungin that are known to have antimicrobial activity.46,47

As we did not intend to explore bioactive peptide expression, it is hard to define exactly which functional regions are differentially regulated. We can speculate, for example, that the CHGA downregulated peptide probably originates from chromofungin, since changes in other vasostatin I and vasostatin II peptides were not statistically significant. We also observed significant changes in EA-92, but some peptides originating from the same region were not consistent with this change. It is possible that EA-92 is further processed into a shorter mature product.

Decreased hydroxyproline in ulcerative colitis

Collagen is a central ECM protein and degradation of it has been associated with IBD.42 Hydroxyproline modifications correlate well with collagen content, collagen protein abundances, and the degree of fibrosis18 which can be found in > 30% of CD patients and about 5% of UC patients.49,50 We therefore decided to include a quantitative analysis of the hydroxyproline PTM content. In addition, ubiquitination has been implicated in IBD and was for that reason also included in the analysis.51

We did not observe differential regulation of any of the individual amino acid sites, either for hydroxyproline or ubiquitinated PTMs. Additionally, we did not observe a statistically significant difference between total or peptide specific ubiquitination (p = 0.146). However, the overall abundance of peptides with a hydroxyproline modification was significantly lower in the UC colon tissue compared to control (Fig. 3), which is consistent with the reduced abundance of collagen proteins determined by proteomics and previously published research of collagen degradation.52
Pathway analysis

We explored the presence of over-represented categories from several different ontologies using lists of upregulated and downregulated features at the peptide and protein levels. When using the GO Biological process ontology and comparing to our protein-level list (available in the downloadable Supplementary Materials file, ESI†), most categories were related to the immune system. The most significant category we observed was “Response to bacteria”. We also observed the enrichment of leukocyte migration, which is a hallmark feature of IBD.53 At the same time, downregulated proteins significantly overlapped with extracellular structure organization as well as mitochondrial respiratory complex assembly and glycosylation (available in the downloadable Supplementary Materials file, ESI†). While mitochondrial changes have been previously implicated in the pathogenesis of IBD,54 the association of ECM categories with downregulated proteins was largely unexpected. This observation was consistent with the decreased hydroxyproline levels and the data we obtained by comparing transcriptional profiling data with the list of differentially regulated proteins.

Next, we explored additional ontologies and gene lists, including MSigDB and Pubmed (available in the downloadable Supplementary Materials file, ESI†). Most lists we identified as significantly overlapping with our list of upregulated proteins were related to immune function, and further reinforce the neutrophil association. One category also of interest is Reactome’s “Degradation of extracellular matrix”, which is consistent with decreased hydroxyproline levels and collagen protein, supporting our hypothesis. In addition, it appears that lists associated with cell line proliferation (stem cells, cancer) overlap significantly with our downregulated list of proteins.

In the GO Component ontology, only one category was enriched in the list of upregulated peptides: “Blood microparticles” (Fig. S6, ESI†). Blood microparticles (MPs) have been associated previously with inflammation and infection, including Crohn’s disease.55 Secreted MPs or secreted Microvesicles (sEV) are a diverse range of lipid vesicles containing a cargo of protein and RNA/DNA originating from a range of cell types including neutrophils.56

IHC confirmation

Colon biopsy sections from 4 UC patients and 2 healthy controls were stained for the proteins S100-A9 and S100-A12, or for myeloperoxidase, all of which are present in granulocytes. In Fig. 4, results from one patient with ulcerative colitis and one healthy control are shown. No reaction with antibodies to S100-A9 and S100-A12 was observed in sections of the healthy control (Fig. 4, A and D) or in immunoglobulin controls (Fig. 4F and I), showing that granulocytes are not present in healthy intestinal mucosa (mucous epithelium and lamina propria). A strong staining was observed for S100-A9 in the UC patients, and, in addition, more cells were observed in lamina propria than in controls (Fig. 4B). By enlarging the image, it can be seen that cells stained for S100-A9 are polymorphonuclear (Segmented nuclei), in agreement with granulocytes, and S100-A9 is located in the cytoplasm of the cells (Fig. 4C). It can also be seen that the S100-A9 contained in polymorphonuclear cells are located between the mucosal epithelial cells (Fig. 4B and C). S100-A12 are also present in the cytoplasm of polymorphonuclear cells in the UC patient (Fig. 4). Myeloperoxidase shows a similar staining pattern as S100-A9 and S100-A12, in agreement with its localization in granulocytes. An analysis of the staining intensity confirmed the statistically significant (t-test p-value < 0.001) increase of S100-A9, S100-A12, and MPO in the UC colonic biopsies compared to controls (Fig. S4, ESI†). The main function of MPO is remodeling of the ECM during degradation, hence the increased abundance of MPO as determined by proteomics and validated by immuno-fluorescence underlines the degradation of the colonic ECM during UC.

Discussion

One of the most unexpected results we report here, supported by several separate findings, is the presence of significantly lower levels of multiple ECM proteins in intestinal biopsies from UC patients. Such downregulation can occur as a result of either modulation of transcriptional and translational activity or degradation and displacement (with the second explanation being more likely based on microscopy findings). The notion that degradation drives the changes we observe is further supported by the increased detection of ECM matrix fragments,
reported in the serum of UC patients vs. controls or CD patients. Of note, the current study is not powered to make definitive conclusion regarding the general population, and the hypotheses we raise require extensive confirmatory studies.

Fibrosis is a well described complication of IBD, especially in CD. Therefore, we expected to observe upregulation of collagen proteins and hydroxyproline-containing peptides. Indeed, increases in collagen transcripts were found with all 3 previously published transcriptomics datasets. However, among current proteomics datasets several collagen proteins were found to have lower abundances in the UC group. The discovery of decreased collagen protein abundance in UC was supported by a lower abundance of hydroxyproline-containing peptides, and was in agreement with previous reports of UC colon mucosa. The UC patients in our proteomics study were all medicated and no visible inflammation could be observed on the surface of the colon from which the biopsies were taken. Additionally, the histology analysis of the colon biopsies found that the crypt architecture was preserved and without distinct fibrosis, which is in agreement with the proteomics findings. However, an increased presence of neutrophils, NETs, and pro-inflammatory proteins could be detected with proteomics, and validated by immunofluorescence. We speculate that these seemingly contradictory findings between the collagen protein abundances and the transcript levels are two sides of the same complex process. It is possible that an active process caused by or causing the degradation of the ECM would lead to a compensatory yet insufficient transcriptional response. The comparisons between microarray, RNA-seq, and proteomics data underline the notion that mRNA abundances cannot be directly translated to protein abundances, but rather are a proxy for the protein synthesis-rates. Taken together, the findings indicate the presence of a low-grade inflammation in the tissue, which could trigger the degradation of collagen. It would be interesting to learn the turnover of ECM proteins in the active sites of the disease. Increased rates would support our hypothesis, and increased ECM protein turnover has already been observed in the bleomycin model of pulmonary fibrosis.

Consistent with ECM degradation, we detected increased abundances of ECM degrading enzymes, including myeloblastin, neutrophil collagenase, MMP9, and MMP10. However, our data somewhat surprisingly cannot confirm that MMP9 and MMP10 upregulation is the cause for the ECM protein degradation as we could not detect increased abundance of the activated MMP fragments, suggesting a lack of MMP activation. This observation requires further validation as we are basing this hypothesis on known MMP substrates which may not represent the full diversity, thus potentially skewing the results. In addition, it is possible the current proteomics workflow may not be able to assess the presence of MMP fragments fully. However, the increase in MMP proteins is consistent with the reduced abundance of collagen proteins and hydroxyproline, and by extension the reduction in ECM protein content, thus adding credibility to the potential of ECM degradation as a major event in IBD pathology. We can further speculate that ECM degradation is an initial trigger for both neutrophil infiltration and ECM transcriptional activation which may overcompensate and eventually result in fibrosis. Purely speculatively, ECM degradation could be triggered partially by leaky epithelial tight junctions in intestinal inflammation. Tight junctions are multi-protein complexes that form a seal between adjacent epithelial cells, and thus act as barriers that normally regulate the transport of macromolecules. UC genetic studies have identified susceptibility loci related to defects of the epithelial barrier, and IBD patients often demonstrate a loss of tight junction functions. While not sufficient to cause IBD, the loss of the tight junction function causes an immune activation. Accordingly, epithelial leaks can be detected early in UC, and it has been suggested that these barrier defects allow bacterial antigens to enter the mucosa from the lumen, causing inflammation of the mucosa which could lead to ECM degradation. Degradation of ECM proteins could potentially have an impact on IBD pathology. It has been reported that proteolytic fragments (PGP) of ECM proteins can serve as neutrophil chemoattractants through CXCR1. PGP has also been identified as a potential biomarker in COPD, another disease where inflammation and neutrophil infiltration play a major role. Taken together, emerging evidence of ECM protein degradation and peptidase involvement in the pathology of UC may open new opportunities for biomarker discovery and novel therapeutic options.

We also observed another interesting example of disconnect between protein and mRNA regulation of Chromogranin A (CHGA). CHGA is a great example of a situation where the mRNA and its role in the generation of multiple hormones was characterized decades ago, yet we continue to find novel proteoforms originating from this locus. Chromogranin A upregulated peptides also diverge significantly in terms of differential regulation, potentially due to the different regulation and/or secretion of the many proteoforms that are encoded by this locus. While chromogranin A itself is differentially regulated, specific regions of the protein exhibited much larger differences between UC patients and the control population.

An elevated level of NETs is closely associated with general inflammation by the release of a extracellular lattice, composed of DNA associated with proteins citrullinated by protein-arginine deiminase 4 (PAD4) from neutrophils. The NETosis or NETlysis processes are associated with a range of autoimmune diseases or triggered by inflammatory activation including UC and rheumatoid arthritis. Berthelot et al. have found that NETosis increases the possibility of association between autoantigens and infectious antigens in mucosal biofilms, impairing the clearance of pathogens and possibly triggering autoimmune reactions such as autoantibody formation (ANCAs). These autoantibodies against NET components have been suggested as possible explanations for the breakdown of tolerance to NET autoantigens, such as hypercitrullination. Of the NETs granule proteins identified in this study, LTF, MPO, and PR3 have been associated with autoantibody formation in relation to IBD and ECM-related processes. The release of active PAD2 and PAD4 isoforms into synovial fluid by neutrophil cell death is a plausible explanation for the generation of extracellular autoantigens in RA. The inhibition of PADs by either small molecule drugs or biologies has been
implicated in treatment strategies for autoimmune diseases such as RA but no evidence for such potential has been provided so far.  

Conclusion

One could argue that proteomics data are more complicated than other OMICs data. RNAseq- and DNASeq-data have a single output: variants and/or transcript expression. In contrast, proteomics data can be analyzed in different contexts-expression levels as well as post-translational modifications, and variations. In addition, the field has a much better understanding of splicing isoforms than of proteoforms. All this presents a significant challenge to the community. Therefore, in this work, we re-investigated an existing proteomics dataset, and confirmed and extended the original findings. Some of the differences in the data analysis method included variations in the proteomics identification, filtering, and imputation procedures. However, the largest contributor to the new observations and results can be ascribed to the different statistical test that was applied. In the original dataset, statistically significant proteins were identified mainly using t-tests. In comparison, in this reanalysis, we used tests based on linear mixed effects models, which allowed us to include the replicates in the statistical analysis rather than combining them, thereby increasing the number of significant proteins identified substantially. Combining these findings with an existing microarray and RNAseq-dataset, allowed us to draw novel conclusions, including ECM degradation in UC. In addition to the increased understanding of the pathophysiology of UC, our work demonstrates the significant value in sharing raw data with the community through resources such as PRIDE to enable such cross-OMIC analyses.

Conflicts of interest

There are no conflicts to declare.

Acknowledgements

We would like to acknowledge Thomas Gelsing Carlsen, Torkell Ellingsen, Ole Kristian Bonderup, Henning Glerup, Martin Bøgsted and Gunna Christiansen for their help generating the data that this manuscript is based on and Joseph Szustakowski for helpful comments. We also wish to thank the anonymous reviewers for their help in significantly improving this manuscript.

References

1 D. C. Baumgart and S. R. Carding, Inflammatory bowel disease: cause and immunobiology, *Lancet*, 2007, 369(9573), 1627–1640.
2 D. C. Baumgart and W. J. Sandborn, Inflammatory bowel disease: clinical aspects and established and evolving therapies, *Lancet*, 2007, 369(9573), 1641–1657.
3 W. Strober, I. Fuss and P. Mannon, The fundamental basis of inflammatory bowel disease, *J. Clin. Invest.*, 2007, 117(3), 514–521.
4 N. A. Molodecky, I. S. Soon, D. M. Rabi, W. A. Ghali, M. Ferris and G. Chernoff, et al., Increasing incidence and prevalence of the inflammatory bowel diseases with time, based on systematic review, *Gastroenterology*, 2012, 142(1), 46–54.
5 F. T. Moller, V. Andersen, J. Wohlfahrt and T. Jess, Familial risk of inflammatory bowel disease: a population-based cohort study 1977–2011, *Am. J. Gastroenterol.*, 2015, 110(4), 564–571.
6 J. Z. Liu, S. van Sommeren, H. Huang, S. C. Ng, R. Alberts and A. Takahashi, et al., Association analyses identify 38 susceptibility loci for inflammatory bowel disease and highlight shared genetic risk across populations, *Nat. Genet.*, 2015, 47(9), 979–986.
7 L. Jostins, S. Ripke, R. K. Weersma, R. H. Duerr, D. P. McGovern and K. Y. Hui, et al., Host-microbe interactions have shaped the genetic architecture of inflammatory bowel disease, *Nature*, 2012, 491(7422), 119–124.
8 V. Andersen, A. K. Hansen and A. B. Heitmann, Potential Impact of Diet on Treatment Effect from Anti-TNF Drugs in Inflammatory Bowel Disease, *Nutrients*, 2017, 9(3), E286.
9 G. G. Kaplan, The global burden of IBD: from 2015 to 2025, *Nat. Rev. Gastroenterol. Hepatol.*, 2015, 12(12), 720–727.
10 P. Yadav, D. Ellinghaus, G. Remy, S. Freitag-Wolf, A. Cesaro and F. Degenhardt, et al., Genetic Factors Interact With Tobacco Smoke to Modify Risk for Inflammatory Bowel Disease in Humans and Mice, *Gastroenterology*, 2017, 153(2), 550–565.
11 A. Dignass, J. O. Lindsay, A. Sturm, A. Windsor, J. F. Colombel and M. Allez, et al., Second European evidence-based consensus on the diagnosis and management of ulcerative colitis part 2: current management, *J. Crohns Colitis*, 2012, 6(10), 991–1030.
12 A. Dignass, R. Eliakim, F. Magro, C. Maaser, Y. Chowers and K. Geboes, et al., Second European evidence-based consensus on the diagnosis and management of ulcerative colitis part 1: definitions and diagnosis, *J. Crohns Colitis*, 2012, 6(10), 965–990.
13 A. Dignass, G. Van Assche, J. O. Lindsay, M. Lemann, J. Soderholm and J. F. Colombel, et al., The second European evidence-based Consensus on the diagnosis and management of Crohn’s disease: Current management, *J. Crohns Colitis*, 2010, 4(1), 28–62.
14 G. Van Assche, A. Dignass, B. Bokemeyer, S. Danese, P. Gionchetti and G. Moser, et al., Second European evidence-based consensus on the diagnosis and management of ulcerative colitis part 3: special situations, *J. Crohns Colitis*, 2013, 7(1), 1–33.
15 G. Van Assche, A. Dignass, J. Panes, L. Beaugerie, J. Karagiannis and M. Allez, et al., The second European evidence-based Consensus on the diagnosis and management of Crohn’s disease: Definitions and diagnosis, *J. Crohns Colitis*, 2010, 4(1), 7–27.
16 G. Van Assche, A. Dignass, W. Reinisch, C. J. van der Woude, A. Sturm and M. De Vos, et al., The second European evidence-based Consensus on the diagnosis and management of Crohn’s disease: Special situations, *J. Crohns Colitis*, 2010, 4(1), 63–101.
17 G. Bouguen and L. Peyrin-Biroulet, Increasing incidence and prevalence of the inflammatory bowel diseases with time, based on systematic review, *Gastroenterology*, 2012, 142(1), 46–54.
18 L. Hancock and N. J. Mortensen, How often do IBD patients require resection of their intestine?, *Inflammatory Bowel Dis.*, 2008, 14(Suppl 2), S68–S69.
19 H. Hammad and B. N. Lambrecht, Barrier Epithelial Cells and the Control of Type 2 Immunity, *Immunity*, 2015, 43(1), 29–40.
20. A. Kaser, S. Zeissig and R. S. Blumberg, Inflammatory bowel disease, *Annu. Rev. Immunol.*, 2010, 28, 573–621.
21. J. A. Whitsett and T. Alenghat, Respiratory epithelial cells orchestrate pulmonary innate immunity, *Nat. Immunol.*, 2015, 16(1), 27–35.
22. L. W. Peterson and D. Artis, Intestinal epithelial cells: regulators of barrier function and immune homeostasis, *Nat. Rev. Immunol.*, 2014, 14(3), 141–153.
23. T. Bennike, S. Birkeland, A. Stensballe and V. Andersen, Biomarkers in inflammatory bowel diseases: current status and proteomics identification strategies, *World J. Gastroenterol.*, 2014, 20(12), 3231–3244.
24. T. B. Bennike, T. G. Carllsen, T. Ellingsen, O. K. Bonderup, H. Glerup and M. Bagsted, *et al.*, Neutrophil Extracellular Traps in Ulcerative Colitis: A Proteome Analysis of Intestinal Biopsies, *Inflammatory Bowel Dis.*, 2015, 21(9), 2052–2067.
25. J. Cox and M. Mann, MaxQuant enables high peptide identification rates, individualized p.p.b.-range mass accuracies and proteome-wide protein quantification, *Nat. Biotechnol.*, 2008, 26(12), 1367–1372.
26. RStudio Team. RStudio: Integrated Development for R. 2016, available from: http://www.rstudio.com.
27. R Core Team. R: A language and environment for statistical computing. R Foundation for Statistical Computing. 2017, available from: https://www.R-project.org/.
28. R Core Team, J. Pinheiro, D. Bates, S. DebRoy and D. Sarkar, nlme: Linear and Nonlinear Mixed Effects Models. R package version 3.1-137, 2018, available from: https://CRAN.R-project.org/package=nlme.
29. N. Planell, J. J. Lozano, R. Mora-Buch, M. C. Masamunt, M. Jimeno and I. Ordás, *et al.*, Transcriptional analysis of the intestinal mucosa of patients with ulcerative colitis in remission reveals lasting epithelial cell alterations, *Gut*, 2013, 62(7), 967–976.
30. S. Kugathasan, R. N. Baldassano, J. P. Bradfordfield, P. M. A. Sleiman, M. Imleninski and S. L. Guthery, *et al.*, Loci on 20q13 and 21q22 are associated with pediatric-onset inflammatory bowel disease, *Nat. Genet.*, 2008, 40(10), 1211–1215.
31. J. Olsen, T. A. Gerds, J. B. Seidelin, C. Csillag, J. T. Bjerrum and J. T. Troelsen, *et al.*, Diagnosis of ulcerative colitis before onset of inflammation by multivariate modeling of genome-wide gene expression data, *Inflammatory Bowel Dis.*, 2009, 15(7), 1032–1038.
32. B. Zhang, S. Kirov and J. Snoddy, WebGestalt: an integrated system for exploring gene sets in various biological contexts, *Nucleic Acids Res.*, 2005, 33(Web Server issue), W741–W748.
33. C. A. Schneider, W. S. Rasband and K. W. Eliceiri, NIH Image to ImageJ: 25 years of image analysis, *Nat. Methods*, 2012, 9(7), 671–675.
34. S. C. Hicks and R. A. Irizarry, quarto: a data-driven approach to guide the choice of an appropriate normalization method, *Genome Biol.*, 2015, 16(1), 117.
35. C. F. Urban, D. Ermert, M. Schmid, U. Abu-Abed, C. Goosmann and W. Nacken, *et al.*, Neutrophil extracellular traps contain calprotectin, a cytosolic protein complex involved in host defense against Candida albicans, *PLoS Pathog.*, 2009, 5(10), e1000639.
Research Article
Molecular Omics

50. C. Fiocchi and P. K. Lund, Themes in fibrosis and gastrointestinal inflammation, Am. J. Physiol.: Gastrointest. Liver Physiol., 2011, 300(5), G667–G683.

51. I. Cleynen, E. Vazeille, M. Artieda, H. W. Verspaget, M. Szczypiorska and M.-A. Bringer, et al., Genetic and microbial factors modulating the ubiquitin proteasome system in inflammatory bowel disease, Gut, 2014, 63(8), 1265–1274.

52. M. Rojkind and E. González, An improved method for determining specific radioactivities of proline-14C and hydroxyproline-14C in collagen and in noncollagenous proteins, Anal. Biochem., 1974, 57(1), 1–7.

53. J. Brazil, N. Louis and C. Parkos, The role of polymorphonuclear leukocyte trafficking in the perpetuation of inflammation during inflammatory bowel disease, Inflammatory Bowel Dis., 2013, 19(7), 1556–1565.

54. K. G. Sifroni, C. R. Damiani, C. Stoffel, M. R. Cardoso, G. K. Ferreira and I. C. Jeremias, et al., Mitochondrial respiratory chain in the colonic mucosal of patients with ulcerative colitis, Mol. Cell. Biochem., 2010, 342(1–2), 111–115.

55. J. Suades, T. Padró and L. Badimon, The Role of Blood-Borne Microparticles in Inflammation and Hemostasis, Semin Thromb Hemost., 2015, 41(6), 590–606.

56. A. S. Shet, Characterizing blood microparticles: Technical aspects and challenges, Vasc. Health Risk Manag., 2008, 4(4), 769–774.

57. J. H. Mortensen, T. Manon-Jensen, M. D. Jensen, P. Häggdell, L. G. Klinge and J. Kjeldsen, et al., Ulcerative colitis, Crohn’s disease, and irritable bowel syndrome have different profiles of extracellular matrix turnover, which also reflects disease activity in Crohn’s disease, PLoS One, 2017, 12(10), e0185855.

58. J. H. Mortensen, L. E. Godskesen, M. D. Jensen, W. T. Van Haaften, L. G. Klinge and P. Olinga, et al., Fragments of Citrullinated and MMP-degraded Vimentin and MMP-degraded Type III Collagen Are Novel Serological Biomarkers to Differentiate Crohn’s Disease from Ulcerative Colitis, J. Crohns Colitis, 2015, 9(10), 863–872.

59. F. Rieder and C. Fiocchi, Intestinal fibrosis in IBD—a dynamic, multifactorial process, Nat. Rev. Gastroenterol. Hepatol., 2009, 6(4), 228–235.

60. K. Holgersen, B. Kutlu, B. Fox, K. Serikawa, J. Lord and A. K. Hansen, et al., High-Resolution Gene Expression Profiling Using RNA Sequencing in Patients With Inflammatory Bowel Disease and in Mouse Models of Colitis, J. Crohns Colitis, 2015, 9(6), 492–506.

61. M. F. Graham, R. F. Diegelmann, C. O. Elson, W. J. Lindblad, N. Gotschalk and S. Gay, et al., Collagen content and types in the intestinal strictures of Crohn’s disease, Gastroenterology, 1988, 94(2), 257–265.

62. M. L. Decaris, M. Gmatian, S. FlorCruz, F. Luo, K. Li and W. E. Holmes, et al., Proteomic Analysis of Altered Extracellular Matrix Turnover in Bleomycin-induced Pulmonary Fibrosis, Mol. Cell. Proteomics, 2014, 13(7), 1741–1752.

63. C. A. Anderson, G. Boucher, C. W. Lees, A. Franke, M. D’Amato and K. D. Taylor, et al., Meta-analysis identifies 29 additional ulcerative colitis risk loci, increasing the number of confirmed associations to 47, Nat. Genet., 2011, 43(3), 246–252.

64. UK IBD Genetics Consortium, J. C. Barrett, J. C. Lee, C. W. Lees, N. J. Prescott and C. A. Anderson, et al., Genome-wide association study of ulcerative colitis identifies three new susceptibility loci, including the HNF4A region, Nat. Genet., 2009, 41(12), 1330–1334.

65. K. L. Edelblum and J. R. Turner, The tight junction in inflammatory disease: communication breakdown, Curr. Opin. Pharmacol., 2009, 9(6), 715–720.

66. A. H. Gitter, K. Bendfeldt, J. D. Schulzke and M. Fromm, Leaks in the epithelial barrier caused by spontaneous and TNF-alpha-induced single-cell apoptosis, FASEB J., 2000, 14(12), 1749–1753.

67. J. D. Schulzke, S. Ploeger, M. Amasheh, A. Fromm, S. Zeissig and H. Troeger, et al., Epithelial tight junctions in intestinal inflammation, Ann. N. Y. Acad. Sci., 2009, 1165, 294–300.

68. A. Gagger, P. L. Jackson, B. D. Noerager, P. J. O’Reilly, D. B. McQuaid and S. M. Rowe, et al., A Novel Proteolytic Cascade Generates an Extracellular Matrix-Derived Chemoattractant in Chronic Neuropathic Inflammation, J. Immunol., 2008, 180(8), 5662–5669.

69. M. A. Roda, A. M. Fernstrand, F. A. Redegeld, J. E. Blalock, A. Gagger and G. Folkerts, The matrixine PGP as a potential biomarker in COPD, Am. J. Physiol.: Lung Cell. Mol. Physiol., 2015, 308(11), L1095–L1101.

70. U. M. Benedum, P. A. Baeuerle, D. S. Konecky, R. Frank, J. Powell and J. Mallet, et al., The primary structure of bovine chromogranin A: a representative of a class of acidic secretory proteins common to a variety of peptidergic cells, EMBO J., 1986, 5(7), 1495–1502.

71. A. L. Iacangelo, R. Fischer-Colbrie, K. J. Koller, M. J. Brownstein and L. E. Eiden, The Sequence Of Porcine Chromogranin A Messenger Rna Demonstrates Chromogranin A Can Serve As The Precursor For The Biologically Active Hormone, Pancreas, Endocrinology, 1988, 122(5), 2339–2341.

72. D. N. Nguyen, A. Stensballe, J. C. Lai, P. Jiang, A. Brunse and Y. Li, et al., Elevated levels of circulating cell-free DNA and neutrophil proteins are associated with neonatal sepsis and necrotizing enterocolitis in immature mice, pigs and infants, Innate Immun., 2017, 23(6), 524–536.

73. J. M. Berthelot, B. Le Goff, A. Neel, Y. Maugars and M. Hamidou, NETosis: At the crossroads of rheumatoid arthritis, lupus, and vasculitis, Jt., Bone, Spine, 2017, 84(3), 255–262.

74. D. Wang, L. Yang, P. Zhang, J. LaBaer, H. Hermjakob and D. Li, et al., AAgAtlas 1.0: a human autoantigen database, Nucleic Acids Res., 2017, 45(D1), D769–D776.

75. J. Spengler, B. Lugonja, A. J. Ytterberg, R. A. Zubarev, A. J. Creese and M. J. Pearson, et al., Release of Active Peptidyl Arginine Deiminases by Neutrophils Can Explain Production of Extracellular Citrullinated Autoantigens in Rheumatoid Arthritis Synovial Fluid, Arthritis Rheumatol., 2015, 67(12), 3135–3145.

76. V. C. Willis, N. K. Banda, K. N. Cordova, P. E. Chandra, W. H. Robinson and D. C. Cooper, et al., Protein arginine deiminase 4 inhibition is sufficient for the amelioration of collagen-induced arthritis, Clin. Exp. Immunol., 2017, 188(2), 263–274.