MicroRNAs

Citation for published version:

Digital Object Identifier (DOI):
10.1136/gutjnl-2014-307891

Link:
Link to publication record in Edinburgh Research Explorer

Document Version:
Publisher’s PDF, also known as Version of record

Published In:
Gut

Publisher Rights Statement:
This is an Open Access article distributed in accordance with the Creative Commons Attribution Non Commercial (CC BY-NC 4.0) license, which permits others to distribute, remix, adapt, build upon this work non-commercially, and license their derivative works on different terms, provided the original work is properly cited and the use is non-commercial. See: http://creativecommons.org/licenses/by-nc/4.0/

General rights
Copyright for the publications made accessible via the Edinburgh Research Explorer is retained by the author(s) and / or other copyright owners and it is a condition of accessing these publications that users recognise and abide by the legal requirements associated with these rights.

Take down policy
The University of Edinburgh has made every reasonable effort to ensure that Edinburgh Research Explorer content complies with UK legislation. If you believe that the public display of this file breaches copyright please contact openaccess@ed.ac.uk providing details, and we will remove access to the work immediately and investigate your claim.
MicroRNAs: new players in IBD

R Kalla,1 N T Ventham,1 N A Kennedy,1 J F Quintana,2 E R Nimmo,1 A H Buck,2 J Satsangi1

ABSTRACT

MicroRNAs (miRNAs) are small non-coding RNAs, 18–23 nucleotides long, which act as post-transcriptional regulators of gene expression. miRNAs are strongly implicated in the pathogenesis of many common diseases, including IBDs. This review aims to outline the history, biogenesis and regulation of miRNAs. The role of miRNAs in the development and regulation of the innate and adaptive immune system is discussed, with a particular focus on mechanisms pertinent to IBD and the potential translational applications.

INTRODUCTION

The IBDs, Crohn’s disease (CD) and UC affect an estimated 2.5–3 million people in Europe, with the associated annual healthcare costs amounting to approximately €4.6–5.6 billion.1 The increasing incidence of early onset disease in the developed world and of disease in all ages in the developing world has catalysed studies attempting to characterise pathogenic mechanisms. In the last two decades, international collaborations have been successful in identifying susceptibility genes for IBD through genome-wide association studies (GWAS) and subsequently meta-analysis of GWAS and Immunochip data (http://www.ibdgenetics.org).2 These studies have been important in highlighting mechanistic pathways, notably autophagy and innate immunity in CD and epithelial barrier dysfunction in UC and have provided clues into new therapeutic strategies.

There is now increasing interest in exploring epi-genetic mechanisms in common diseases, with notable progress in studies of DNA methylation, histone modifications, long intergenic non-coding RNAs and in characterising the contribution of microRNAs (miRNAs). miRNAs are short strands of non-coding RNA (~22 nt long) encoded in genomic DNA which post-transcriptionally regulate expression. The field of miRNA research is expanding rapidly with the number of miRNA-related citations increasing almost exponentially (figure 1) and miRNAs have been implicated in neurological diseases, cardiovascular diseases, autoimmune diseases and cancer.3 With such a wealth of data now available, reviews have been published on individual miRNAs in health and disease. miR-21 is perhaps the most compelling miRNA involved in IBD, with associations between miR-21 and IBD being replicated in several studies, functional relevance in mouse models, as well as being highly expressed in other diseases including cancer. Key miRNAs, such as miR-21, are the focus of anti-miR therapeutic development.4–8

Well-designed high-impact publications have established functional interactions between miRNAs and key mechanisms implicated by GWAS in IBD, notably T helper cell (Th)17 mediated inflammation and autophagy.9 10 The review aims to outline the history, biogenesis and regulation of miRNAs. The important role of miRNAs in the development and regulation of an innate and adaptive immune system is discussed, with a particular focus on IBD pathogenesis and other immune-mediated diseases. The review will also provide an insight into the translational applications of miRNAs as biomarkers and the potential therapeutic miRNA application.

MicroRNAs: a historical perspective

miRNAs were first identified in 1993 in the nema-tode model organism (Caenorhabditis elegans) using a genetic screen to identify defects in postembryonic development.11–13 It became evident that lin-4, which emerged as the first described miRNA, was able to downregulate a nuclear protein called lin-14, thereby initiating the second stage in larval development.14 15 By the turn of the century a second miRNA, let-7, was identified in C. elegans that appeared to be highly conserved among species including humans.15 16 At the time of writing 35 828 mature miRNAs occurring across all species have been registered in miRBase (http://mirbase.org).17

Biogenesis of microRNAs

miRNA genes are located throughout the genome, either within intronic sequences of protein-coding genes, within intronic or exonic regions of non-coding RNAs, or set between independent transcription units (intergenic).18 Some miRNAs have their own promoters and are transcribed independently, some share promoters with host genes,19 while others are co-transcribed as a single primary miRNA transcript.20 The biogenesis of miRNAs from transcription in the nucleus to generation of the mature miRNA in the cytoplasm is described in figure 2.

In plants, fully complementary binding occurs when the ‘seed’ region (located near the 5’end) of the miRNA binds to the 3’ untranslated region (UTR) of the target mRNA and this is sufficient for mRNA degradation to occur. In contrast, in humans, miRNAs bind to mRNA targets with incomplete complementarity, which results in mRNA destabilisation and translational inhibition.53 Other regions of the mRNA can also contain functional miRNA binding sites, including the 5’UTR and the amino acid coding sequence. Furthermore, beyond seed site pairing, the centre and the 3’end of the miRNA sequence can contribute to target recognition.54–56 Under certain conditions such as cell cycle arrest, miRNAs can alter their regulatory role from translational inhibition to upregulation of translation of target miRNAs.57 Studies have also shown that
miRNAs affect gene expression

It is estimated that miRNAs regulate more than 60% of protein coding mRNAs. Each miRNA can target hundreds of mRNAs resulting in mRNA destabilisation and/or inhibition of translation. Generally, the overall effect on target protein levels is subtle and can be thought of as ‘fine-tuning’ of cellular mRNA expression within a cell. The combinatorial targeting of genes by miRNAs in this fashion makes them interesting therapeutic candidates that in theory may reduce resistance in diseases such as cancer.

miRNAs regulate important cellular functions such as differentiation, proliferation, signal transduction and apoptosis and exhibit highly specific regulated patterns of gene expression.

A number of applications have been developed to predict miRNA/miRNA interactions and aid in understanding specific miRNA targets.

miRNA regulation

At various stages in miRNA biogenesis, several factors can influence the development of the mature miRNA. Figure 2 depicts the various steps of biogenesis that are subject to regulation. These include regulation of transcription, cleavage of the stem loop structures by Drosha and Dicer enzymes, editing as well as regulation of miRNA turnover. The regulatory mechanisms occurring at each stage have been reviewed elsewhere. Each of these mechanisms acts as part of a signalling network that modulates gene expression in response to cellular or environmental changes.

miRNA gene regulatory networks

Over 5400 miRNAs have now been identified with each miRNA possessing the ability to target multiple gene transcripts. miRNAs are members of complex gene regulatory networks (GRNs) and figure 3 summarises these GRNs, comprising of feedback and feed-forward loops. Certain subcircuits are evolutionarily favoured and are termed network motifs. Coordinated transcriptional and miRNA-mediated gene regulation is a recurrent network motif and fortifies gene regulation in mammalian genomes. Inflammation driven miRNA circuits are described in the literature and examples include nuclear factor-xB (NFxB) and hepatocyte nuclear factor-4α circuits. Within the NFxB circuitry, transient activation of Src oncprotein triggers an NFxB mediated inflammatory response by downregulating let-7a and upregulating its direct target interleukin (IL)-6. This forms a stable positive feedback circuit across many cell divisions. Similarly, the hepatocyte nuclear factor-4α circuit consists of miR-124, IL6R, STAT3, miR-24 and miR-629 and is essential for liver development and hepatocyte function. Several other examples of miRNAs involved in GRNs are summarised in a recent review.

Regulation of miRNAs through epigenetic mechanisms

Emerging evidence suggests miRNA expression can be regulated by epigenetic mechanisms such as DNA methylation, histone modifications and circular RNAs (circRNAs). DNA methylation, the addition of methyl groups at CpG islands by DNA methyltransferases (DNMTs), is associated with transcriptional repression. Similarly, acetylation or deacetylation of histones may alter transcriptional activity. The recently established EpimiR database has collected 1974 regulations between 19 categories and 617 miRNAs across seven species.

The aberrant DNA methylation of miRNAs has been demonstrated in various cancers, including lymphoid, gastric...
and colorectal malignancies. Up to 10% of miRNAs are tightly controlled by DNA methylation as seen in cell lines deficient in DNMT1 and DNMT3b. Time-dependent miRNA regulation has also been described. In murine models, partial hepatectomy results in downregulation of miR-127 as early as 3 h post partial hepatectomy with significantly different levels in treatment-naïve children with CD and healthy controls using the Illumina 450 K platform.

DNA damage - DNA damage can promote post-transcriptional processing of primary and precursor miRNAs which play a role in the initiation, activation and maintenance of the DNA damage response. DNA damage accelerates nuclear export of pre-miRNAs via Exp5-nucleopore-Nup153 interaction. miRNA binding proteins - miRNA binding proteins bind to the 3′-UTR elements of the target miRNA and can either enhance or reverse translational repression by influencing miRNA-miRNA complex interaction.

Figure 2 miRNA biogenesis and regulation. (A) Processing begins in the nucleus where primary miRNA transcripts (pri-miR) are transcribed by RNA polymerase II or RNA polymerase III. (B) Nuclear cleavage of pri-miRNA is performed by a protein complex consisting of the RNase III-type enzyme Drosha and DGCR8 (DiGeorge critical region 8), which generates a 60–70 nucleotide sequence called pre-miRNA. Drosha cleavage generates a 2 nucleotide 3′ overhang which appears to be a key biogenesis step. DGCR8 acts as an anchor on the stem loops of the target miRNA, allowing Drosha to correctly position on the pri-miRNA. MiRtrons are similar in structure but do not undergo Drosha/DGCR8 processing. (C) pre-miRNA is transported from the nucleus to the cytoplasm by the Exportin-5 (Exp5) complex. Correct binding of the double stranded stem and 3′ regions to the RanGTP structure stabilises the miRNA, preventing degradation and facilitating the correct transport of pre-miRNA. Following 3 hours of endurance exercise in an untrained male, there is upregulation of Drosha, Dicer and Exp5 mRNA levels.

RNA editing occurs in miRNA gene- and tissue-specific regions to the RanGTP structure stabilising the miRNA, preventing degradation and facilitating the correct transport of pre-miRNA. Once transcribed, miRNAs can undergo editing, which can influence miRNA target specificity. RNA editing occurs in ~6% of human miRNAs with some studies reporting higher levels of RNA editing (50%). RNA editing is miRNA gene- and tissue-specific (e.g. A to I edited members of the miR-376 family specifically within the human cortex). Dicer/DGCR8 The Drosha-DGCR8 complex can undergo post-transcription self-regulation, which allows circulatory negative feedback once sufficient microprocessor activity is available. Cross-regulation between Drosha and DGCR8 may assist in homeostatic control of miRNA biogenesis. miRNA processing factors Specific proteins can either directly or indirectly up-regulate or downregulate the maturation of select miRNAs. A nucleo-cytoplasmic protein with dual functionality is heterogeneous nuclear ribonucleoprotein A1 (hnRNP-A1) which facilitates nuclear RNA polymerase II or RNA polymerase III.

DNA damage - DNA damage can promote post-transcriptional processing of primary and precursor miRNAs which play a role in the initiation, activation and maintenance of the DNA damage response. DNA damage accelerates nuclear export of pre-miRNAs via Exp5-nucleopore-Nup153 interaction. miRNA binding proteins - miRNA binding proteins bind to the 3-UTR elements of the target miRNA and can either enhance or reverse translational repression by influencing miRNA-miRNA complex interaction.
miRNA sponges and are abundant within the human transcriptome. A recent study identified circRNA sponge for miR-17 as a potent inhibitor of miR-7 activity that is abundant in the mouse brain. circRNA sponge for miR-7 contains 70 highly selective miRNA target sites, strongly associated with AGO proteins and is highly resistant to miR-7 mediated destabilisation. They also identified testis specific sex determining region Y (Sry) circRNA as a miR-138 sponge indicating that the sponge effects of circRNAs are a general phenomenon.

miRNA regulation

- miRNAs are an integral part of GRN and modulate gene expression in response to cellular or environmental changes.
- Epigenetic mechanisms such as DNA methylation, histone modifications and circRNAs regulate the expression of miRNAs adding a layer of complexity to the regulation of gene expression.

**Figure 3** Examples of miRNA circuits. Tsang and Milo describe two distinct circuits, Type I and Type II that incorporate miRNAs in their regulatory machinery.

- **Type I circuits** (A) In Type I circuits, upstream transcription factors will positively coregulate miRNA and their target mRNA. One such example is the repression of E2F1 by miR-17-5p, both of which are activated by the transcription factor c-Myc. It has been suggested that the function of such circuits is to define and maintain target-protein homeostasis, especially in cells that are ultrainsensitive to target mRNA abundance.

- **Type II circuits** (B) Type II circuits allow transcriptional activation or repression (positive or negative feedback loop) of a target gene by an upstream factor with associated synergistic miRNA expression. If an mRNA is to be upregulated, this would occur directly by the transcription factor with synergistic miRNA repression.

There appears to be a complex interplay between DNA binding proteins, chromatin modifications and miRNA expression. miR-155 assists in the differentiation and cytokine expression of Th17 cells as miR-155 deficient Th17 cells exhibit increased expression of Jarid2 which actively recruits polycomb repressive complex 2 to chromatin. Binding of polycomb repressive complex 2 to chromatin along with H3K27 histone methylation results in downregulation of cytokines IL-9, IL-10, IL-22 and Araf.

Recently circRNAs have been identified as regulators of miRNA expression. These endogenous RNAs can operate as miRNA sponges and are abundant within the human transcriptome.
Recent advances in basic science

are the most relevant miRNAs in this field and their important regulatory activity is supported by their respective knockout (KO) mice phenotypes. Mice deficient of miR-146a develop autoimmune disorders, myeloid cell proliferation and tumorigenesis while mice deficient of miR-155 display an impaired DC function and are unable to mount an adaptive immune response to pathogens. The induction of the miR-146 family and miR-155 is nuclear factor k light enhancer of activated B cells (xkB) dependent and these miRNAs form negative feedback circuits to fine-tune the inflammatory response upon bacterial infection.

While miR-146 targets MyD88 adaptor proteins: tumour necrosis factor receptor associated factor 6 and IL-1 receptor-associated kinase 1, miR-155 on the other hand targets signalling proteins: suppressor of cytokine signalling 1 and TAK1-binding protein 2. Cells use miR146 to attain tolerance to subinflammatory doses of LPS, however when exposed to proinflammatory doses of LPS, miR-155 is also activated to broadly limit inflammation. The process of miR-146a expression appears dynamic and during early phases of the inflammatory response in macrophages, there is transient reversal of miRNA mediated repression of inflammatory cytokines through AGO2 phosphorylation. LPS stimulation of TLR4 also activates the regulatory PI-3K/Akt circuit which consists of let-7e and miR-155 and its targets TLR4 and suppressor of cytokine signalling 1. Macrophages deficient of Akt suppress let-7e and overexpress miR-155 resulting in a hyper-responsive phenotype to LPS. miRNAs have also been implicated in other infections such as Pseudomonas aeruginosa infection promoting miR-302b expression in order to limit the pulmonary inflammatory response and BCG triggered miR-12 expression.

It must be borne in mind that the implicated miRNAs in the innate immune response are cell-specific. In human monocytes and neutrophils, TLR4 activated NFkB induces the expression of miR-9 however in murine macrophages, the NFkB feedback circuit is governed by miR-210.

Adaptive immune system

Within the immune system, an intricate network of signalling facilitates maturation of the adaptive immune system. The appropriate development and function of these immune cells (T and B cells) is crucial when distinguishing foreign antigens from self. Recent studies have shown that miRNAs are involved in various stages of T cell and B cell maturation and activation (figure 4).

miRNAs and T cell regulation

The differentiation and maturation of T cells is influenced by miRNAs (figure 4). Specific deletion of Dicer or Drosha in T cell lineages results in aberrant differentiation and cytokine production with a marked bias towards Th1 development and IFN-γ production. During positive and negative selections within the thymus gland, self-reactive T cells are first removed (negative selection) before T cells with functional receptors are selected (positive selection). The miR-181 family plays an important role in this process by altering T cell receptor sensitivity and may also contribute to diminished vaccine responses seen in the elderly.

miRNAs and Th1 and Th2 differentiation

miRNAs contribute to Th1 and Th2 cell differentiation. Several miRNAs including miR-146a, miR-29, miR-155, miR-17-92 cluster, miR-128 and miR-27b have been shown to influence Th1 differentiation and function. Overexpression of miR-155 influences CD4+ T cells to differentiate into Th1 cells while deficiency in miR-155 shows a bias towards Th2 differentiation. Similarly, miR-17-92 promotes Th1 differentiation by upregulating IFN-γ production and suppressing regulatory T cell (Treg) differentiation. Of particular interest is the role of miR-21 expression in T cells. miR-21 has been shown to promote Th2 cell differentiation and as described previously, its dysregulation has been implicated in IBD.

Several miRNAs have been shown to play a regulatory role by targeting transcription factors known to be involved in Th1 cell gene expression. These include miR-29 targeting T-bet and comesodermin, transcription factors known to regulate IFN-γ production and miR-146a that targets signal transducer and activator transcription 1 in Treg cells, a transcription factor that controls Treg mediated regulation of Th1 responses.

miRNAs and Th17 differentiation

The Th17 pathway has been widely researched in the context of IBD. Recent studies determining the effect of miRNAs on the differentiation and function of Th17 pathway have identified direct and indirect regulatory mechanisms. Using murine models with experimental autoimmune encephalomyelitis, studies have shown that miR-326, miR-10a, miR-155 directly regulate Th17 differentiation and/or function while miR-301a is an indirect enhancer of Th17 differentiation. Of these miRNAs, miR-155 seems relevant to IBD as it directly upregulates Th17 differentiation and indirectly influences the regulation of pro-Th17 cytokines from DCs. Furthermore, miR-155 KO mice are protected from dextran sulfate sodium (DSS) induced experimental colitis compared with wild type mice. miRNAs may also regulate hypoxia-induced Th17 differentiation by overexpressing miR-210 and promoting a negative feedback circuit with Hif1a, a key transcription factor of Th17 polarisation.

miRNAs and T regulatory cells

Studies have identified the role of miRNAs in Treg cell development and function by promoting the differentiation of CD4+ T cells into Treg cells in the thymus and maintaining their immune homoeostatic function. It has been shown in vivo that CD4+ T cells that fail to express miRNAs develop spontaneous autoimmunity. Furthermore, conditional Dicer or Drosha deletion in Foxp3+ Treg cells can alter the expression of several Treg specific markers including Foxp3, resulting in early fatal autoimmune disease. Several miRNAs including miR-155, miR146a, miR-10a and miR-17-92 have been shown to maintain Treg cell function by modulating different signalling pathways. miR10a in selective Treg cells assists in maintaining high Foxp3 levels but does not influence the number or phenotype of Treg cells. miR-155 has been shown to regulate mature Treg cell homoeostasis via the IL-2 signalling pathway while miR-146a regulates Treg cell function to limit inflammation. The miR-17-92 cluster has also been implicated in Treg cell function but these studies are conflicting. miR-17-92 Treg cell KO mice develop an exacerbated experimental autoimmune encephalomyelitis, however these studies are conflicting. miR17 and miR-19b inhibit Treg cell differentiation and promote Th1 responses.

miRNAs and other immune cells

miRNAs have been implicated in other immune cell maturation such as B cells and T follicular helper cells. The miR-17-92 cluster helps regulate T follicular helper cell differentiation as well as B cell maturation while other miRNAs such as miR-10a and miR-181a have also been shown to regulate these processes.
miRNAs and the immune system

- miRNAs play important roles in the development and differentiation of the innate and adaptive immune system.
- The innate immune response to bacterial infection is regulated by an intricate network of miRNA circuits that fine-tune the inflammatory response.
- miRNA expression is highly cell specific and miRNA dysregulation especially in Th17 cells has been implicated in IBD.

MIRNA PROFILING IN IBD

Following numerous studies determining miRNA expression profiles in human health and disease, researchers are now beginning to explore the functional actions of miRNAs. The various experimental techniques are used to investigate miRNAs and have been reviewed recently. Early studies used quantitative PCR (qPCR), following which microarrays have been used to study miRNAs. Microarrays work by hybridisation of the mature miRNA to complementary probe sequences immobilised on a chip or beads, with a detection mechanism usually involving labelling of the 3' end of the miRNA. Most recently next generation sequencing (NGS) has been used to study small...
RNAs. NGS is potentially advantageous over microarray techniques as it provides greater coverage, demonstrates sequence independence and has the potential to identify novel miRNAs. Confirmatory techniques to validate these findings use standard techniques such as qPCR and northern blotting.

Results from early studies exploring the profile of miRNAs expressed in tissues of patients with IBD have been somewhat conflicting and difficult to interpret. Many of the miRNA related IBD studies have been underpowered and the need for large cohorts to perform well-powered studies has been demonstrated by the Cancer Genome Atlas consortia. There has also been a lack of uniformity of the comparator group, with controls consisting of healthy individuals in some studies and ‘symptomatic control’ patients in others and furthermore many of these studies used different methods to normalise miRNA data. There has been difficulty identifying suitable housekeeping genes as a reference for qPCR. Microarray and NGS studies have used different techniques for normalisation; either normalising against total miRNA or using approaches such as scaling and quantile normalisation. Other specific issues include difficulties deciphering whether differentially expressed miRNAs are causal, a consequence of disease or related non-specifically to inflammation, and miRNA levels may vary with disease duration and can be influenced by therapy. Moreover, every cell type possesses its own unique epigenetic signature therefore interpreting the relevance of miRNAs detected in heterogeneous samples (eg, whole blood, intestinal biopsies) is challenging and complicated by the fact that many miRNAs can target the same gene. Recent publications have demonstrated a shift in focus from generating exhaustive tissue and blood miRNA screens (see online supplementary table S1) to carefully designed functional experiments that elaborate actions of individual miRNAs in known pathogenic pathways in IBD as implicated by GWAS. The most consistent evidence to date links miRNAs and autophagy in CD and in NOD2-induced Th17-mediated disease (table 1).

### Table 1: Functional studies on micro RNAs (miRNAs)

<table>
<thead>
<tr>
<th>First author</th>
<th>Study model</th>
<th>miRNA of interest</th>
<th>mRNA/ pathway target</th>
<th>Findings</th>
</tr>
</thead>
<tbody>
<tr>
<td>Nguyen</td>
<td>AIEC infection in T84 cells and mouse enterocytes. Translational studies in ileal CD biopsies</td>
<td>miR-30C and mir-130A</td>
<td>ATG5, ATG16L1</td>
<td>Adherent <em>Escherichia coli</em> upregulate miRNAs, reduce levels of ATG5 and ATG16L1 and inhibit autophagy</td>
</tr>
<tr>
<td>Zhai</td>
<td>Jurkat T cells, Colonic epithelial cells</td>
<td>miR-142-3p</td>
<td>ATG16L1</td>
<td>Reduced ATG16L1 mRNA and protein levels, regulating autophagy in CD</td>
</tr>
<tr>
<td>Lu</td>
<td>HCT116, SW480, Hela and U2OS cell lines. Colonic biopsies from CD and healthy controls</td>
<td>miR106B, miR93</td>
<td>ATG16L1</td>
<td>Reduced levels of ATG16L1 and autophagy</td>
</tr>
<tr>
<td>Brest</td>
<td>HEK-293 cells, Colonic biopsies</td>
<td>miR-196</td>
<td>IRGM</td>
<td>A risk variant of IRGM alters the binding site for miR-196 and causes deregulation of IRGM-dependent xenophagy in CD</td>
</tr>
<tr>
<td>Brain</td>
<td>Dendritic cell line, miR-29 KO murine models</td>
<td>miR-29</td>
<td>IL-12p40 (direct target), IL-12p19 (indirect target)</td>
<td>NOD2 induces miR-29 release and limits IL-23 release. NOD2 polymorphism alters the expression of miR-29 and contributes to pathogenesis in CD</td>
</tr>
<tr>
<td>Xue</td>
<td>IL-10 KO mice, MyD88 KO mice, RAG KO mice, Murine dendritic cells</td>
<td>miR-10a</td>
<td>IL-12/IL-23p40</td>
<td>miR-10a expression is regulated by the intestinal microbiota and targets the Th17 pathway. This miRNA may play a role in intestinal homeostasis</td>
</tr>
<tr>
<td>Koukos</td>
<td>HCT-116 colonocyte cells, murine models and colonic biopsies from patients with UC</td>
<td>miR-124</td>
<td>STAT3</td>
<td>Downregulation of miR-124 results in proinflammatory response in UC</td>
</tr>
<tr>
<td>Shi</td>
<td>miR-21 KO DSS model and wild type mouse models</td>
<td>mir-21</td>
<td>RhoB</td>
<td>miR-21 is overexpressed in inflammation and tissue injury. miR-21 KO improves survival in DSS colitis mouse model</td>
</tr>
<tr>
<td>Yang</td>
<td>Caco-2 cells, colonic biopsies from UC and healthy controls</td>
<td>miR-126</td>
<td>Targeting RhoB impairs the tight junction integrity and decreases transepithelial resistance and increases inulin permeability</td>
<td></td>
</tr>
<tr>
<td>Nata</td>
<td>IL-10 deficient mice</td>
<td>miR-146b</td>
<td>siah2</td>
<td>miR-146b improves intestinal inflammation and epithelial barrier by activating NF-kB</td>
</tr>
<tr>
<td>Chuang</td>
<td>HCT116 colonic epithelial cells</td>
<td>miR-192, miR-495, miR-512, miR-671</td>
<td>NOD2</td>
<td>Downregulates NOD2 expression, suppresses NF-kB, inhibits IL8 and CXCL3 expression</td>
</tr>
<tr>
<td>Chen</td>
<td>Intestinal epithelial cells, Intestinal biopsies</td>
<td>miR-200b</td>
<td>TGFβ</td>
<td>miR-200b promotes the growth of intestinal epithelial cells by inhibiting epithelial-mesenchymal transition via TGFβ</td>
</tr>
<tr>
<td>Feng</td>
<td>UC intestinal biopsies, HCT116 cells, HT29 cells</td>
<td>miR-126</td>
<td>IL-10</td>
<td>Promotes NF-kB mediated inflammation by targeting IL-10</td>
</tr>
<tr>
<td>Nguyen</td>
<td>Caco2-BBE cells, Mouse epithelial cells, Colonic CD tissues</td>
<td>miR-7</td>
<td>CD8</td>
<td>miR-7 regulates the expression of CD8. CD8 expression upregulated and miR-7 decreased in actively inflamed CD tissues</td>
</tr>
<tr>
<td>Singh</td>
<td>miR-155 KO mice</td>
<td>miR-155</td>
<td></td>
<td>miR-155 KO mice models and demonstrated that these mice are protected from experimental colitis compared with wild type mice</td>
</tr>
<tr>
<td>Wu</td>
<td>miR-21 KO TNBS and T cell transfer model of colitis</td>
<td>miR-21 KO DSS colitis model</td>
<td></td>
<td>miR-21 KO results in reduced DSS induced colitis but exacerbated inflammation in TNBS and T cell transfer model of colitis</td>
</tr>
</tbody>
</table>

*AIEC, adherent invasive *Escherichia coli*; CD, Crohn’s disease; DSS, dextran sulfate sodium; IL, interleukin; IRGM, immunity related GTPase family M protein; KO, knockout; miR, microRNA; NF-kB, nuclear factor-kB; NOD2, nuclear oligomerisation domain-containing protein 2; TGFβ, transforming growth factor β; TNBS, trinitrobenzene sulfonic acid.*
miRNA profiling in IBD

- There is a need to perform large-scale multicentre miRNA profiles in IBD with a well-defined ‘healthy control’ population using NGS techniques.
- miRNA levels can vary with disease duration and therapies.
- Every cell possesses its own epigenetic signature, therefore understanding the relevance of miRNA profiles in whole blood and intestinal biopsies can be challenging.

FUNCTIONAL STUDIES IN IBD

miRNAs and autophagy in CD

Autophagy is a cellular process that involves self-digestion of unwanted materials such as damaged mitochondrial products (mitophagy) and pathogenic microbes (xenophagy). A process such as xenophagy requires the coordinated action of a multitude of proteins including, vimentin, NOD2, immunity related GTPase family M protein (IRGM) and a multiprotein complex which includes ATG16L1 and ATG5–ATG12.154 155 In understanding molecular signalling and its effect on autophagy, several groups have investigated the role of miRNAs in these processes (figure 5).

During periods of starvation or hypoxia, mammalian target of rapamycin is inhibited within cells, activating autophagy. Hypoxia-induced autophagy results in upregulation of mir-155 which targets multiple components of mammalian target of rapamycin signalling.156 All genes currently described in the regulation of different stages of autophagy are influenced by miRNAs.157 Several autophagy genes have also been associated with susceptibility to CD, notably IRGM and ATG16L1.158 Interestingly, autophagy regulates miRNA production by targeting miRNA-processing enzymes Dicer and AGO2 through the autophagy receptor nuclear dot protein 4.159 Future challenges include understanding the genetic control of miRNA biogenesis including its own transcriptional activators and repressors.

Immunity related GTPase family M protein

A common exonic synonymous SNP (c.313C>T) in IRGM is associated with CD.160 Although this SNP does not alter the IRGM protein sequence, it is located in the ‘seed’ region where miRNA and miRNA form a RNA induced silencing complex.10 Further analysis revealed that this SNP altered the binding site for miR-196. miR-196 was also shown to be overexpressed in inflamed tissues of patients with CD suggesting that this defective miRNA-miRNA interaction deregulates IRGM-dependent xenophagy in CD.10

ATG16L1

GWAS identified ATG16L1 polymorphism (T300A) as a risk variant in CD. Further studies revealed that this variant results in ineffective xenophagy of pathogens such as Salmonella typhi-
murium.161 Several studies have identified miRNAs that target ATG16L1, although each study associates a different set of miRNAs which may relate to miRNA cell line specificity. In HeLa cell lines, adherent invasive *Escherichia coli* infection results in overexpression of miR-93 and miR106B and downregulation of ATG5 and ATG16L1 thereby disrupting the autophagy pathway and bacterial clearance.146 In adherent invasive *Escherichia coli* infected T84 cells however, miR-30C and miR-130A were upregulated.144 Both studies were able to replicate their findings in endoscopic biopsies from patients with CD. Finally, miR-142-3p has also been shown to target ATG16L1 and autophagy using a different cell line.145

Th17 pathway

Th17 driven inflammation plays an important role in IBD and studies have shown how miRNAs are used by DCs to regulate the inflammatory response. Brain et al demonstrated that NOD2 mediates its effects through miRNAs in DCs, in particular miR-29. The gene most strongly regulated by miR-29 is IL-12B (encoding IL-12/23 p40) while IL23A (encoding IL-23 p19) is indirectly targeted through suppression of its transcription factor ATF2 and mice deficient of this miRNA develop a more severe Th17 driven colitis on DSS exposure.7 Microbiota can also impact on DC miRNA expression. In vivo models have demonstrated the commensal bacteria can negatively regulate miR-10a in DCs.147 Furthermore miR-10 directly targets IL-12/23p40 to limit Th17 driven inflammation and the expression of this miRNA may be regulated in order to maintain intestinal homoeostasis.147

Other inflammatory pathways

The role of the NFκB pathway in IBD has been well described and studies have shown that this pathway is also regulated by miRNAs.162 miR-126 promotes NFκB mediated inflammation by directly targeting IkBα mRNA, an important inhibitor of NFκB signalling pathway. These findings were replicated in colonic biopsies in patients with active UC.152 Conversely, NFκB has also been shown to play an anti-inflammatory role in IBD as demonstrated by the differential expression of miR-146b in IL-10 deficient mice models.150 Administering miR-146b vectors intraperitoneally in DSS colitis mice ameliorated intestinal inflammation via activation of the NFκB mediated pathway.150

Other pathways that have been studied include signal transducer and activator transcription 3 (STAT3) and acetylcholine.

Epithelial barrier integrity

Dysfunctional epithelial barrier has been implicated in the pathogenesis of UC.163 164 GWAS data demonstrated IBD associated genes that play a role in maintaining intestinal epithelial barrier integrity and examples include LAMB-1 that regulates basement membrane stability and CDH-1 that regulates stability of adherens junctions via E-cadherin.165 Recent studies have investigated miRNAs in epithelial barrier function, in particular miR-21 and miR-200B.5 149 151 Murine miR-21 KO models with experimental DSS colitis survive longer and have less tissue inflammation than wild type mice and this miRNA targets RhoB, a target gene involved in regulating intestinal permeability.149 Similarly miR-200b has been shown to help maintain epithelial barrier integrity by targeting transforming growth factor β1 and inhibiting epithelial-mesenchymal transition, a process that promotes loss of intestinal epithelial cells and contributes to the pathogenesis in IBD.151

miRNA studies in IBD

- miRNAs have been shown to regulate several pathways involving susceptibility loci found in IBD by GWAS.
- Recent data implicate miRNAs in the dysregulation of autophagy and Th17 signalling in CD.
- Increased expression of miR-21 is the most consistently replicated finding and represents a novel therapeutic target.
- miRNAs have also been shown to regulate intestinal barrier integrity in UC.

TRANSLATION TO CLINICAL PRACTICE: LESSONS LEARNED FROM OTHER DISEASES

miRNAs as disease biomarkers

Insights from contemporary cancer research highlight the exciting potential of miRNAs as biomarkers. Research in this area was stimulated by the initial finding that miRNA profiles can accurately differentiate between different cancer lineages and successfully classify poorly differentiated cancers based on tissue profiling. In 2008, miRNAs were also discovered to be present in serum in a cell-free state, sparking excitement about their potential use as non-invasive biomarkers. Extracellular miRNAs have now been found in most biological fluids including serum, urine, tears, saliva and breast milk. Packaged in vesicles consisting of microparticles, lipoproteins or RNA binding proteins, these miRNAs are very stable and protected from degradation. Their profiles have been studied in various diseases including cardiovascular diseases, cancer and neurological diseases.

Despite the optimism that miRNAs may represent robust biomarkers, the results should be treated with some circumspection; recent reviews showed that up to 58% (n=47) of the reported tumour related miRNAs are not disease specific. Only 33% of the reported miRNAs in non-neoplastic diseases (n=139) were deemed biologically plausible and represented non-ubiquitous miRNA expression in disease-appropriate cell types.

The therapeutic application of miRNA modulation

miRNA related therapeutic intervention may involve either miRNA antagonists or miRNA mimics. Antagomirs, an example of miRNA antagonists, can be applied to allow gain of function within diseased states by introducing a chemically modified RNA that binds to the active miRNA of interest to inhibit its activity and rescue the repression of its target. Conversely miRNA mimics are used to restore a loss of function by the introduction of miRNAs into diseased cells to mimic a healthy cell state.

Within the GI literature, there are several studies highlighting the potential therapeutic application of specific miRNAs including miR-155 and miR-210. Recently, miR-141 has been shown to play a critical role in colonic leucocyte trafficking by targeting CXCL12β. Treatment with pre-miR141 protects mice against the development of trinitrobenzenesulfonic acid and IL-10KO colitis. In contrast, anti-miR141 aggravates trinitrobenzenesulfonic acid-induced colitis through CXCL12β suppression. Several miRNA-based therapies are either in the preclinical phase or the clinical trial phase, with ‘miravirsen’ miR-122 targeting in HCV being the most developed therapy.
Challenges to therapeutic translation

There are several issues associated with miRNA therapeutics. First, there appears to be functional redundancy exhibited by miRNAs. Studies have shown that genetic deletion of miRNAs does not alter phenotypes or disease processes nor does it result in lethality in the vast majority of miRNAs. For some miRNAs that exist within ‘families’, this may be explained by intrafamilial redundancy however for others this may represent target sharing by several distinct miRNAs. Temporary inhibition of miRNAs however seems to have an effect, as shown by the inhibition of miR-21. The discrepancy in effect between permanent deletion and temporary inhibition of miRNAs may be a result of ‘off-target’ influences or could be explained by adaptive compensation by cells to chronic loss of functional miRNAs over time. Interestingly miRNAs may be particularly important under conditions of stress, such that miRNA deficient developmental phenotypes in controlled laboratory environments may not always be expected.

Uptake of miRNAs beyond the target organ poses a potential challenge when developing miRNA therapies aimed at over-expressing miRNA. For example miR-26a suppresses hepatocellular carcinoma but has also been shown to have pro-oncogenic properties in glioma formation by repressing its target, phosphatase and tensin homolog. Second, miRNA-based drug delivery to the relevant cells must take into account the high rates of degradation by RNases in blood. Finally, owing to a wide repertoire of several target genes, each miRNA-based therapy has the potential to cause varied side effects. Examples include germ line deletion of the oncogenic miR-17-92 cluster resulting in skeletal and growth defects in humans. As such the long-term inhibition of target miRNAs must be rigorously tested. Studies have shown that although short-term inhibition of miR-122 has beneficial effects on circulating cholesterol synthesis and repressing HCV replication in the liver, long-term inhibition of miR-122, as seen in KO mice models, results in an age-dependent increase in hepatocellular carcinoma and steatohepatitis.

Delivery of miRNA therapies to their target organ has also been difficult. While antagonirs can be delivered systemically, the delivery of miRNA mimics has been challenging, similar to the difficulties encountered with small interfering RNA therapeutics. As single RNA strands are >10 times less effective in vitro and in vivo, miRNA mimics are delivered as synthetic duplexes. There are however several issues that should be highlighted with this conformation. As mentioned earlier, cellular uptake can occur even in tissues that do not express the relevant miRNA, potentiating undesired effects. In addition, these RNA duplexes can also stimulate the innate immune system through TLRs. Finally, the passenger strands of these duplexes can incorporate themselves into miRNA induced silencing complexes and act as antagonirs with undesired side effects. Improvements in delivery strategies and RNA chemistries may combat some of these issues and miRNA replacement therapies for cancer using miRNA mimics have advanced to Phase 1 clinical trials.

There has also been much interest in studying innovative methods to deliver synthetic miRNAs. Studies have used lentiviral, adeno or adeno associated virus vectors to restore activity, however delivery using viral vectors certainly poses safety concerns. The mechanisms of extracellular miRNAs packaged in vesicles are also being studied. Examples include exosomal delivery of small interfering RNAs to the mouse brain by systemic injection and exosomal delivery of let-7a to target epidermal growth factor receptor in RAG (−/−) mice.

CONCLUDING REMARKS: THE IMMEDIATE RESEARCH AGENDA

The field of miRNA research has advanced dramatically with strong data associating miRNAs in IBD, notably in functional studies of autophagy and Th17 regulation. However in order to understand the role of miRNAs in disease pathogenesis, translational studies that take into account their plasticity and cellular specificity is critical. Novel miRNA biomarker discoveries are on the horizon, with studies using the dynamic properties of miRNAs to generate expression profiles in different stages of IBD and disease phenotype, or in response to immunomodulatory therapy.

Studies are now exploring miRNA regulatory and extracellular transport biology with a view to devising novel therapeutic targets that are cell specific and alter gene expression in target cells. The in vivo application of miRNA-based therapies packaged in genetically engineered extracellular vesicles provides a glimpse of the future translational potential of miRNA-based research in chronic inflammatory diseases.

Contributors RK wrote the initial draft of the manuscript and subsequently all authors have been involved with the amendments and final report. The authors thank B H Ramsahoye for reviewing the manuscript.

Competing interests None.

Provenance and peer review Not commissioned; externally peer reviewed.

Open Access This is an Open Access article distributed in accordance with the Creative Commons Attribution Non Commercial (CC BY-NC 4.0) license, which permits others to distribute, remix, adapt, build upon this work non-commercially, and license their derivative works on different terms, provided the original work is properly cited and the use is non-commercial. See: http://creativecommons.org/licenses/by-nc/4.0/
REFERENCES


Iliopoulos D, Hirsch HA, Struhl K. An epigenetic switch involving NF-kappaB.


Recent advances in basic science


MicroRNAs: new players in IBD

R Kalla, N T Ventham, N A Kennedy, J F Quintana, E R Nimmo, A H Buck and J Satsangi

Gut 2015 64: 504-513 originally published online December 4, 2014
doi: 10.1136/gutjnl-2014-307891

Updated information and services can be found at:
http://gut.bmj.com/content/64/3/504

These include:

Supplementary Material
Supplementary material can be found at:
http://gut.bmj.com/content/suppl/2014/12/04/gutjnl-2014-307891.DC1.html

References
This article cites 207 articles, 59 of which you can access for free at:
http://gut.bmj.com/content/64/3/504#BIBL

Open Access
This is an Open Access article distributed in accordance with the Creative Commons Attribution Non Commercial (CC BY-NC 4.0) license, which permits others to distribute, remix, adapt, build upon this work non-commercially, and license their derivative works on different terms, provided the original work is properly cited and the use is non-commercial. See: http://creativecommons.org/licenses/by-nc/4.0/

Email alerting service
Receive free email alerts when new articles cite this article. Sign up in the box at the top right corner of the online article.

Topic Collections
Articles on similar topics can be found in the following collections

GUT Recent advances in basic science (74)
Open access (184)

Notes

To request permissions go to:
http://group.bmj.com/group/rights-licensing/permissions

To order reprints go to:
http://journals.bmj.com/cgi/reprintform

To subscribe to BMJ go to:
http://group.bmj.com/subscribe/