Emerging Role of MicroRNAs and Long Noncoding RNAs in Respiratory Disease

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The advent of techniques such as microarrays and high-throughput sequencing has revolutionized our ability to examine messenger RNA (mRNA) expression within the respiratory system. Importantly, these approaches have also uncovered the widespread expression of “noncoding RNAs,” including microRNAs and long noncoding RNAs, which impact biologic responses through the regulation of mRNA transcription and/or translation. To date, most studies of the role of noncoding RNAs have focused on microRNAs, which regulate mRNA translation via the RNA interference pathway. These studies have shown changes in microRNA expression in cells and tissues derived from patients with asthma, pulmonary fibrosis, cystic fibrosis, COPD, and non-small cell lung cancer. Although the evidence is currently limited, we review the work that has been carried out in cell and animal models that has identified the function and mechanism of action of a small number of these microRNAs in disease etiology. In addition to microRNAs, we assess the emerging evidence that long noncoding RNAs regulate respiratory phenotype. Because these investigations into long noncoding RNAs were performed almost exclusively in non-small cell lung cancer, future work will need to extend these into other respiratory diseases and to analyze how microRNAs and long noncoding RNAs interact to regulate mRNA expression. From a clinical perspective, the targeting of noncoding RNAs as a novel therapeutic approach will require a deeper understanding of their function and mechanism of action. However, in the short term, changes in microRNA and long noncoding RNA expression are likely to be of use as biomarkers for disease stratification and/or assessment of drug action.

ABSTRACT

Evidence is accumulating that shows that large sections of the genome are transcribed into noncoding RNAs (ncRNAs) (ie, RNA sequences that are not translated into proteins). The exact proportions are still an area of controversy. Thus, the Encyclopedia of DNA Elements (the “ENCODE” project that aims to catalog all the functional
elements in human DNA) has concluded that approximately 80% of DNA is functional and, importantly, that the majority (approximately 62%) is transcribed into RNA. However, a number of investigators have questioned these conclusions, most notably whether ncRNA is indeed functional.

Despite this controversy, there are many ncRNAs with demonstrated function. At the present time, ncRNAs are divided broadly into three groups: housekeeping RNAs, short ncRNAs (< 200 nucleotides), and long ncRNAs (lncRNAs) (> 200 nucleotides) (Fig 1). The housekeeping RNAs include ribosomal RNA, transfer RNA, small nucleolar RNA, and small nuclear RNA. By far the largest component is the ribosomal RNAs (5S, 18S, and 28S), which represent > 90% of total RNA in mammalian cells and which interact with proteins and transfer RNAs to form the functional ribosome complex that is central to translation. The best characterized family of short ncRNAs is the microRNAs (miRNAs), which regulate the translation of messenger RNA (mRNA) into protein via the RNA interference pathway. Interestingly, recent sequencing studies have identified a tranche of new small RNA families that are commonly located at sites of active transcription; they include transcription initiation RNAs, splice site RNAs, and promoter-associated small RNAs. Finally, the least characterized but largest group by number is the lncRNAs, which are thought to regulate both mRNA transcription and/or translation. Given the paucity of information on the many thousands of lncRNAs, these are commonly subdivided by sequence and position relative to protein coding genes into antisense lncRNAs, pseudogenes lncRNAs, intronic lncRNAs, and intergenic lncRNAs. To date, most studies of the role of ncRNAs in respiratory disease have concerned miRNAs, which will, therefore, form the focus of the current review. However, we also plan to highlight the emerging role of lncRNAs.

miRNAs and the RNA Interference Pathway
As implied by the name, miRNAs are small 21 to 23 nucleotide RNA sequences that are produced from primary miRNA transcripts by the sequential action of two RNase III endonucleases, Drosha and Dicer (Fig 2). The initial primary miRNA transcripts are essentially identical to mRNAs but lack the translational start codon (AUG) and fold to produce a characteristic hairpin structure. These are recognized by Drosha and the DiGeorge syndrome critical region gene 8 and cleaved in the nucleus to produce a precursor miRNA with a stem-loop structure and a length of approximately 70 to 90 nucleotides (Fig 2). The precursor miRNA is exported into the cytoplasm and is cleaved by Dicer to produce an approximately 22-nucleotide double-stranded RNA. This is subsequently unwound, and a single miRNA strand is loaded into the Ago2 protein, an essential component of the RNA-induced silencing complex. Within the RNA-induced silencing complex, miRNAs are able to induce mRNA degradation and/or inhibit the translation of target mRNAs by a mechanism titled RNA interference. This process...
involves noncomplementary binding between the miRNAs, particularly the seed region at residues 2 to 7, and the 3′-untranslated region of the target mRNA. Importantly, the noncomplementary nature of this binding and the short length of the seed region mean that miRNAs can target multiple mRNAs, whereas individual mRNAs contain target sites for multiple miRNAs. Indeed, it is predicted that about 60% of miRNAs can act as targets for miRNAs.8

What Is the Physiologic Function of miRNAs in the Respiratory System?

Before examining the role of miRNAs in respiratory disease, it is important to understand their function under physiologic conditions. In general, analysis of multiple organs and cells indicates that miRNAs have a dual role as both regulators of development (in nondifferentiated cells) and in the maintenance of homeostasis in differentiated cells.9,10 In the respiratory system, their importance in the former is underlined by the widespread changes in miRNA expression observed during lung development11 and in studies in Dicer knockout mice, in which miRNA processing is disrupted, that demonstrate a lethal phenotype resulting from impaired lung growth.12 Our understanding of the role of individual miRNAs during lung development is limited, although profiling studies have shown downregulation of the miR-154 family and the miR-17 to about 92 cluster (miR-17, -18a, -19a, -20a, 19b-1, and -92-1) and increases in the miR-29 family and miR-127.11,13 Blocking the reduction in expression of the miR-17 to about 92 cluster using transgenic mice resulted in abnormal (and lethal) lung development that was characterized by continued proliferation and impaired differentiation of epithelial cells.14

The centrality of miRNAs in the maintenance of homeostasis in the adult (differentiated) lung is supported by expression studies that demonstrate no change in miRNA expression during the process of lung aging.12 Examination of the profile of expression in the adult lung shows that this is dominated by a small number of miRNAs, with miR-21 being the most highly expressed at about 30% of the total (Table 1). Indeed, when added together, it was found that the 10 and 50 most expressed miRNAs represent approximately 68% and approximately 97% of the total, respectively (Table 1). Interestingly, although some miRNAs are expressed in a cell-specific manner, many of these highly expressed...
miRNAs, including let-7 and miR-21, are common among all differentiated cells/tissues (miRNA expression in specific cells and tissues can be found at http://www.mirbase.org). This has led to speculation that they regulate common phenotypes such as proliferation and apoptosis and that changes in their expression are associated with cancer (see the miRNAs and Non-small Cell Lung Cancer section).

Attempts to elucidate the role of miRNAs have primarily involved the measurement of their differential expression in cells/tissues obtained from patients with the relevant respiratory disease, whereas subsequent functional and mechanistic studies have involved overexpression and inhibition of these miRNAs in cell and animal models. We have, therefore, adopted this systematic approach to reviewing the role of miRNAs in various respiratory diseases.

### miRNAs and Asthma

Asthma is characterized by chronic airway inflammation and reversible airflow obstruction, the latter commonly occurring in response to environmental challenges such as allergens and infections. Initial studies using airway biopsy specimens obtained from mild asthmatics were unable to show changes in miRNA expression, although it was speculated that this may have resulted from the mixed cell populations in the biopsy specimens and/or the phenotype of those with mild asthma. These problems were addressed subsequently by two studies using isolated bronchial epithelial cells, in which Jardim et al showed differential expression of 66 miRNAs in patients with mild asthma, and Solberg et al demonstrated changes in 217 miRNAs and 200 miRNAs in steroid-naive and steroid-using patients with asthma respectively. Of relevance, the variations in miRNAs observed by Solberg et al could be recapitulated by...
exposing epithelial cells to IL-13, a cytokine implicated in the development of asthma.\textsuperscript{19}

T cells are believed to be important orchestrators of the chronic inflammatory response in asthma. Circulating CD4\textsuperscript{+} T cells from mild and moderate asthmatics showed differential expression of miR-132, miR-223, miR-374a, and miR-1290, whereas CD3\textsuperscript{+} T cells from bronchial biopsy specimens of patients with mild asthma exhibited downregulation of miR-125b, miR-19a, miR-19b, and miR-106b.\textsuperscript{20} Our own studies using circulating CD4\textsuperscript{+} and CD8\textsuperscript{+} T cells showed downregulation of miR-146a and miR-146b in patients with severe asthma, but not in those with nonsevere asthma.\textsuperscript{21} Given that miR-146a and miR-146b negatively regulate the immune response,\textsuperscript{22} we speculated that a reduction in their expression might contribute toward T-cell activation. In addition to studies of T cells, a number of reports have examined peripheral blood mononuclear cells and have shown miR-192 downregulation in mild asthmatics\textsuperscript{23} and miR-211 and miR-485-3p upregulation in pediatric patients with asthma.\textsuperscript{24,25}

In addition to their role in airway constriction, human airway smooth muscle cells (HASMs) are thought to contribute to the airway thickening (hypertrophy) and the chronic inflammatory response that is characteristic of asthma. Indeed, isolated HASMs exhibit increased proliferation and release of inflammatory mediators in response to exogenous stimulation.\textsuperscript{26} At the present time, no studies have examined miRNA expression in asthmatic samples, although there are reports on the function of individual miRNAs in isolated HASMs. As detailed in Table 2, this includes a role for miR-140-3p\textsuperscript{27} and miR-133a\textsuperscript{14} in contractility, miR-26a\textsuperscript{31} and miR-221\textsuperscript{28} in proliferation, and miR-25\textsuperscript{30} and miR-221\textsuperscript{28} in the inflammatory response.

The functional relevance of individual miRNAs has also been assessed using a number of mouse models of allergic asthma, including those induced using ovalbumin, house dust mite, and IL-13 transgenics. Using intratracheal or intranasal delivery of antisense oligonucleotides targeted at individual miRNAs, these studies have identified potential roles for miR-21,\textsuperscript{36} miR-126,\textsuperscript{33,35} miR-145,\textsuperscript{54} miR-106a,\textsuperscript{32} miR-1,\textsuperscript{29} let-7,\textsuperscript{14} and miR-221\textsuperscript{25} in the development of allergic asthma through the targeting of various cytokines and transcription factors (Table 2).

miRNAs and Idiopathic Pulmonary Fibrosis

Idiopathic pulmonary fibrosis (IPF) is localized to the lung interstitium, is characterized by fibrosis, and is thought to result from the excessive production of extracellular matrix components by fibroblasts and myofibroblasts. It is speculated that this results from an aberrant wound-healing response linked to excessive transforming growth factor (TGF)-\(\beta\) production. Most studies of the role of miRNAs in IPF have used a combination of human lung samples, isolated lung fibroblasts, and the bleomycin-induced mouse model of lung fibrosis. A range of miRNAs, including let-7d,\textsuperscript{36} miR-21,\textsuperscript{36} miR-29,\textsuperscript{59} miR-200,\textsuperscript{60} miR-154,\textsuperscript{25} the miR-17 to about 92 cluster,\textsuperscript{27} miR-145,\textsuperscript{60} and miR-199-5p, have been shown to be differentially expressed in human IPF lung tissue, TGF-\(\beta\)-stimulated fibroblasts, or both.\textsuperscript{41} With the exception of miR-154,\textsuperscript{61} these changes in miRNA expression were confirmed in bleomycin-induced lung fibrosis. Crucially, inhibition of let-7d,\textsuperscript{36} miR-21,\textsuperscript{39} miR-29,\textsuperscript{39} miR-200,\textsuperscript{60} the miR-17 to about 92 cluster,\textsuperscript{37} miR-145,\textsuperscript{60} and miR-199-5p\textsuperscript{41} was also shown to impact bleomycin-induced lung fibrosis in mice, suggesting that these miRNAs may represent novel therapeutic targets.

As with other respiratory diseases, the mechanism of action of only a small proportion of these miRNAs is understood (Table 2). Interestingly, miR-29 is known to target a host of extracellular matrix proteins and has been implicated as a key regulator in a range of fibrotic diseases.\textsuperscript{62} However, in the case of IPF, miR-29 also appears to target expression of TGF-\(\beta\), connective tissue growth factor, and Smad3.\textsuperscript{39} Also of potential mechanistic relevance is the upregulation of the maternally imprinted miR-154 region.\textsuperscript{61} Having shown previously that this region is downregulated during lung development,\textsuperscript{11} this has led to speculation that IPF represents a reversion to a fetal lung phenotype.\textsuperscript{41} Finally, the expression of many of these miRNAs has been linked to the activation of Smad3, a key transcription factor in the TGF-\(\beta\) signaling pathway.\textsuperscript{36,39}
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whereas miR-34a and miR-199a-5p were increased in smokers with COPD. Only two studies have examined the role of miRNAs in isolated cells from patients with COPD. Using human lung fibroblasts, Sato et al observed reduced miR-146a expression in patients with COPD and showed that this increased expression of PGE₂ through the targeting of COX-2 (Table 2). The second publication by Lewis et al showed that miR-1 was downregulated in quadriceps muscles and speculated that this is linked to the muscle weakness observed in COPD.

miRNAs and Non-small Cell Lung Cancer

As with COPD, non-small cell lung cancer (NSCLC) is thought to result from long-term exposure to cigarette smoke and can be divided roughly equally between adenocarcinoma and squamous cell carcinoma, which together account for approximately 80% of total lung cancers. There are nearly 1,000 publications relating to miRNAs and lung cancer, and this short report will distill some of the major conclusions; readers are referred to more in-depth reviews.

Expression studies have identified a number of miRNAs linked to NSCLC. Early studies demonstrated that reduced expression of the members of the let-7 family was associated with a poor prognosis. Interestingly, let-7 acts as a tumor suppressor by targeting the downregulation of the tumor promoting proteins, ras, and HMGA2. Other miRNAs that have been identified as having a similar tumor-suppressing action include miR-15a, miR-16, miR-31, miR-487b, and miR-4423 by targeting myc and ras, the cell cycle regulators Rb and G₁ cyclins, the large tumor suppressor 2, and the epigenetic regulators, SUZ12, BMI1, and WNT5A (Table 2). In contrast, the expression of miR-155, the miR-17 to about 92 cluster, miR-221/222, miR-21, and miR-135b is reduced in NSCLC. In this case, these miRNAs are thought to promote tumor formation because their reduced levels result in increased expression of their proteins targets. These targets include many known tumor promoters including PTEN, programmed cell death 4, the sprouty and hippo pathway, and hypoxia-inducible factor-1α pathway (Table 2).

miRNA and Cystic Fibrosis

As may be expected, the analysis of miRNA function in cystic fibrosis (CF) has focused exclusively on lung airway epithelial cells and has examined their role in regulating the expression of the cystic fibrosis transmembrane conductance regulator (CFTR) or in the innate immune response.
A number of miRNAs, including miR-101, miR-145, miR-223, miR-384, miR-494, miR-509-3p, and miR-1246, have been demonstrated to target CFTR expression. However, only the expression of miR-145, miR-223, miR-494, and miR-509-3p were upregulated in patients with CF and shown to be further increased in response to inflammatory mediators such as tumor necrosis factor-α, IL-1β, and Pseudomonas aeruginosa. A report by Amato et al. identified a single nucleotide polymorphism within the 3'-untranslated region of a number of patients with CF and CFTR-related disorders that do not contain mutations within the coding sequencing. Because this single nucleotide polymorphism was located within the predicted binding site for miR-433 and miR-509-3p, they speculated that it may act as a mild CFTR mutation by enhancing the repression of multiple genes involved in CFTR biosynthesis and regulation.

In addition to their actions on CFTR, changes in miRNA expression in patients with CF are thought to impact the immune response to infection. Oglesby et al. found that decreased expression of miR-126 in CF epithelial cells resulted in the elevation of target of Myb1 (TOM1), a protein involved in regulating toll-like receptor- and tumor necrosis factor-α-induced signaling pathways. Similarly, Bhattacharyya et al. showed upregulation of miR-155 and speculated that targeting SHIP1 expression would in turn lead to activation of the PI3K/Akt pathway and the production of IL-8. In a subsequent report, Tsuchiya et al. showed that exposure of lung epithelial cells to P. aeruginosa resulted in suppression of miR-155 and increased production of a range of miRNAs including miR-215, which may impact the survival and immune response in the epithelial cells.

**IncRNA in Respiratory Disease**

Emerging evidence suggests that changes in IncRNA expression are associated with the development of various types of cancer. It is, therefore, unsurprising that, as with miRNAs, most studies of the role of IncRNAs in respiratory disease have been performed in NSCLC. Indeed, one of the first IncRNAs was discovered in a screen of genes associated with lung adenocarcinoma and was named metastasis associated in lung adenocarcinoma transcript 1 (MALAT1). Interestingly, this large noncoding transcript (>8 kb) is expressed at high levels in most cells, and initial mechanistic studies indicated that the nuclear-localized MALAT1 regulated alternative splicing through an interaction with serine/arginine splicing factors. However, more recent examination of knockdown in cell and animals models has shown that MALAT1 regulates gene expression and not splicing, and specifically those genes involved in cell migration, colony formation, and metastasis.

Two well-characterized and highly expressed IncRNAs whose levels are also increased in NSCLC are HOTAIR and H19. HOTAIR, which is known to regulate chromatin structure through an interaction with the polycomb response complex 2, has been shown to upregulate cell migration and anchorage-independent cell growth. Interestingly, a possible interaction between lncRNA and miRNAs has been uncovered from studies showing that the increased expression of the paternally imprinted H19 IncRNA may act as a sponge for let-7, thereby explaining the downregulation of this miRNA in NSCLC.

Expression changes in four additional IncRNAs have also been linked to NSCLC and/or COPD, including smoke and cancer-associated IncRNA-1 (SCAL1), GAS6-antisense 1, maternally expressed gene 3 (MEG3), and IncRNA low expression in tumor (LRET). SCAL1, whose expression is driven by nuclear factor erythroid 2-related factor, is increased in NSCLC and following exposure to cigarette smoke in vivo and vitro. A protective role for this IncRNA was indicated in studies that demonstrated increased cigarette smoke-induced toxicity following SCAL1 knockdown.

In contrast, MEG3 expression was reduced in NSCLC, and overexpression of MEG3 increased MDM2 and p53 expression, resulting in increased proliferation and reduced apoptosis. Interestingly, we have also shown reduced expression of MEG3 in the circulating CD8+ T cells of patients with severe asthma, as well as the differential expression of an additional 18 IncRNAs.

**miRNAs as Biomarkers of Respiratory Disease**

In addition to their role in disease, there is now a growing literature to suggest that miRNAs obtained from either blood, tissue, or exhaled breath may provide reliable biomarkers for the diagnosis and prognosis of respiratory disease. A recent comparison of exhaled condensates showed consistent reduction in miRNA expression in asthmatic patients (miR-1248, let-7a, miR-155, miR-21, miR-328, and miR-133a) and patients with COPD (miR-21 and miR-328) compared with control subjects. Examination of circulating exosomes,
which are vesicular structures released into the blood stream by cells, has also demonstrated differential expression of miRNAs, including let-7a and miR-21, in mild asthma\(^9\) and increased expression of muscle-specific miRNA species (miR-1, miR-133, miR-206, and miR-499) in patients with COPD that was suggestive of muscle breakdown.\(^8\) As may be expected, there is a considerable body of biomarker work in NSCLC,\(^99,100\) including reports showing that tissue and plasma miRNA signatures can be correlated with prognosis and disease classification.\(^101\) As a specific example, laser capture from bronchial brushings was able to identify two miRNAs that could discriminate between small cell lung cancer and NSCLC (miR-29a and miR-375) and adenocarcinoma and squamous cell carcinoma (miR-205 and miR-34a).\(^102\)

**Conclusions**

There is now increasing evidence that the expression of miRNAs is altered in the airways and lungs of patients with a broad range of respiratory diseases. Whether these are simply a reflection of the disease or an important mediator of the underlying pathology has yet to be determined. However, knockdown studies in animal models of asthma and IPF suggest that miRNAs are indeed important in the cause of disease and may offer potential therapeutic targets using approaches such as antisense oligonucleotides and short interfering RNAs. Although not related to respiratory disease, the targeting of the liver-specific miR-122 using an antisense-based approach is currently undergoing human trials for the treatment of the hepatitis C virus.\(^103\) Given the accessibility of the lung to topical administration, this approach may also be of use in tackling respiratory disease.\(^104\) In contrast to miRNAs, much less is known regarding the role of the many thousands of lncRNAs, and this is likely to provide an exciting and fertile new area of scientific discovery. However, given that therapeutic modulation of ncRNAs is a medium to long prospect (5-10 years), it is likely that their short-term application will be as biomarkers in disease classification and/or the assessment of novel drugs.

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