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# miRNAs and rheumatoid arthritis: new update in expression pattern and pathogenicity

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Rheumatoid arthritis (RA) is a polygenic autoimmune disease characterized by systemic inflammation and disability of joints. Early diagnosis and treatment could prevent diseases in RA patients from becoming severe. miRNAs are small, non-coding RNA that regulate the post-transcriptional level of gene expression. miRNAs play important roles in gene expression and pathogenicity of autoimmune diseases as well as RA. Properly using miRNAs regulation potential and detecting different expression patterns and their functions could facilitate and manage effective therapeuticinterventions in RA patients. Herein, we discuss miRNAs as a therapeutic agent in RA patients.

*Keywords:* Rheumatoid arthritis (RA); miRNA; Expression, Regulation

## Introduction

Rheumatoid arthritis (RA) is a chronic autoimmune disease with systemic inflammation and multiple joint destructions. Like most other autoimmune diseases, RA is seen most frequently inwomen and older individuals [1, 2]. The synovial joints are the most important tissue in RA patients. Irreversible joint damage is seen in RA joints characterized by leukocyte infiltration and chronic inflammation [3, 4]. Beside immune cells function in RA joint inflammation, rheumatoid arthritis synovial fibroblasts (RASFs) are important cells in RA pathogenesis and are reported to be major effectors in joint inflammation and destruction [5-7].

Multiple factors are included in the RA pathogenicity, including various genes and environmental factors which trigger the autoimmune condition. Epigenetic variations are other important factors involved in RA pathogenicity [8]. Evidence has revealed the importance of miRNAs in gene expression and the development of autoimmune

diseases like RA [9-14]. The association between miRNAs and RA was reported in 2008 when a significantly different expression pattern was observed in patients [15]. Several studies have reported the dysregulation of miRNAs in inflamed joints and peripheral blood of RA patients. The miRNAs have complete stability in body fluids, because this microenvironment has complexes with proteins that prevent degradation [16]. These molecules could be proper candidates for RA monitoring and treatment factors. Herein, we summarize and update the existing data on miRNA expression patterns, their potential validated targets, and pathologic factors in treatment interventions.

### miRNAs biogenesis and function

miRNAs are characterized as single-strand and small non-coding RNAs. Their mature forms are common negative regulators of gene expression by repressing translation or cleavage of mRNAs,although in some conditions, these molecules can be positive regulators

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of gene expression [17]. miRNA genes comprise only 1-2% of the whole genome, but they regulate around 30% of the protein encoded gene\s expression and 60% of genes have miRNA binding sites[17, 18]. Each miRNA molecule can have different functions in the case of multiple mRNAs or even in different transcripts of a single genes and generates miRNAs are important regulatory machines in various cells [17]. The biogenesis of miRNAsconsists of two different steps in the nucleus and cytoplasm. In the nucleus, the RNA polymerase II transcribes miRNA genes and generates a long primary transcript called primary miRNA (pri-miRNA). Each of these transcripts can be part of various mature miRNAs. The multiprotein complex including DGCR8 (DiGeorge syndrome critical region 8) as an RNA binding protein and Drosha as an endonuclease changes the pri-miRNA to precursor miRNA (pre-miRNA) in the nucleus. Pre-miRNAs are recognized by exportin-5 and transported to the cytoplasm. The other protein complex in the cytoplasm, RNA-induced silencing complex (RISC) which consists of RNase III (Dicer) and rgonaute (Ago), cleaves the pre-miRNA and generates a 19-22 nt asymmetric miRNA duplex. The active strand incorporates RISC and generates aribonucleoprotein complex that could target and degrade specific mRNAs [18]. The mature miRNA in the RISC complex can bind to a complementary sequence in 3'-UTR of mRNA. The degree of thecomplementarity is important in miRNA silencing function. In the case of complete binding, the other member of RISC which is named Ago mediates the regulatory function. The deadenylation or degradation of mRNA by the RISC complex represses gene expression [17, 18].

**Deregulated expression of miRNA in RA**

In Table 1, the different expression patterns of miRNAs in RA patients are classified based on their evaluation media or cells and including whole blood, synovial fluid, plasma, PBMCs, synovial tissue and RASFs in RA patients.

## Role of miRNAs in RA pathogenesis

In Table 2, some of the important roles of miRNAs are summarized based on immune cell function. The miRNAs are classified based on their function in TCR signaling, Th17 and Treg cell differentiation, regulation of B cell and of fibroblast activation.

**Let-7a**

Let-7a targeted Kirsten rat sarcoma virus gene (K-Ras), extracellular signal-regulated kinase 1/2 (ERK1/2), and c-Jun N-terminal kinase (JNK) increase the pro-inflammatory cytokines such as interleukin 1β

(IL-1β) and may play important roles in RA pathogenesis. The downregulation of Let-7a in RA patients may be important in inducing pro-inflammatory cytokine expression [19].

**miR-10a**

One important miRNA in RA pathogenesis could be miR-10a, which was reported to increase the expression of inflammatory mediators such as IL-6, IL-8, TNF, IL-1, MCP1, matrix metalloproteinase1 (MMP1), and MMP13, which are important in RA development [20]. miR-10a also regulates the differentiation of TH17 cells that are important in RA development [21, 22].

**miR-15a, miR-16**

miR-16 is positively correlated with disease activity and determined by erythrocyte sedimentation rate (ESR), tender joint count (TJC), C-reactive protein (CRP), and the disease-activity-score-of-28-joints (DAS28) index [23, 24]. One of the important pro-inflammatory factors is tumor necrosis factor-α (TNF-α), which is targeted by miR-16 and can be a regulatory mechanism of inflammation in RA [23]. It was recently reported that low expression levels of miR-15a and miR-16 resulted in the upregulation of their target, SRY-Box Transcription Factor 5 (SOX5), which induced cell migration, invasion, and IL-1β and TNFα expression in RASFs [25].

**miR-17~92 cluster**

This cluster encoded 6 distinct members: miR17, 18a, 19a, 19b, 20a, and 92a. miR-17 upregulation in serum exosome was correlated with a decreased Treg proportion in RA patients [26]. The disturbed expression level of miR17~92 cluster altered the analogy of different subsets of T γδ cells in RA patients [27]. Other evidence revealed that miR-17 acts as a negative regulator of TNF-α by targeting TNF receptor-associated factor 2 (TRAF2) in RASFs, repressing the production of IL-6, IL-8, MMP-1, and MMP-13 in these cells. The downregulation of miR-17 in RASFs resulted in the promotion of inflammation in RA joints [28].

The other member of the cluster, upregulated miR-18a, increased inflammation by targeting tumor necrosis factor-alpha-induced protein 3 (TNFAIP-3), a negative regulator of NF-κβ signaling and protein inhibitor of activated STAT-3 (PIAS-3) that suppressed the STAT-3 signaling pathway. miR-18a induced the expression of inflammatory mediators such as IL-6, IL8, MCP, and MMP1 and regulated the activation of normal T cells[29].

It has been reported that miR-19a/b regulates the expression of TLR2 in RASFs, which reduces inflammation by decreasing IL-6 and MMP-3 [30].

The suppression of cytokine signaling 3 (SOCS3) was reported to be another important target of miR-19a-3p, which was upregulated in response to the low expression levels of miR-19a-3p which inhibited proliferation and induced apoptosis in RASFs [31]. miR-20, another member of the miR-17~92 cluster, also exhibits anti-inflammatory properties. It has been reported to control pro-inflammatory cytokine production by RASFs. miR-20-dependent apoptosis signal-regulating kinase 1 (ASK1) repression decreases the production of IL-6 and MMP-3 [30, 32]. The important roles of ASK1 in RA development and pro–inflammatory cytokine production have been reported in different animal models [33, 34]. A disintegrin and metalloproteinase domain‑ containing protein 10 (ADAM10) is another target of miR-20a, and the downregulation of miR-20a results in cell viability, migration and invasion, and the expression of inflammatory cytokines in RASFs [35].

**miR-21**

Lower levels of miR-21expression were correlated with increased ratios of T-helper 17 (Th17) to regulatory T cells (Treg). miR-21 may also be correlated with increased expression of signal transducer and activator of transcription 3 (STAT3), an important transcription for Th17 differentiation. miR-21 has a high expression level in Tregs compared to conventional T cells and is important for Th17 differentiation [36]. In another study, the upregulation of miR-21 was reported to be associated with a significant increase in NF-κβ levels and cell proliferation in RASFs [37].

**miR-22, miR-23b and miR-30a**

Lower expression levels of miR-22 were correlated with increased expression of cysteine-rich angiogenic inducer 61 (CYR61) as a direct target gene. CYR61 is an extracellular matrix protein produced by RASFs and stimulates these cell expansions and IL-6 production, which is an important factor in inflammation and Th17 differentiation [38]. miR-22 also targets Sirtuin 1 (SIRT1) in RASFs, and a decrease in miR-22 results in cell proliferation and the release of inflammatory cytokines, including TNF-α, IL-1β, and IL-6 [39]. IL-6R is also a target of miR-22 and plays important roles in the Nuclear factor kappa B (NF-κB) signaling pathway [40].

   miR-23b regulates the expression of TNF-α, IL-17, and IL-1β by targeting TGF-β-activated kinase 1/ MAP3K7 binding protein 2 (TAB2), TAB3, and inhibiting nuclear factor κ-B kinase subunit α (IKK-α) in RASFs. Downregulated miR-23b, which increases the expression of these cytokines,may be important in the pathogenesis of RA [41].

   Lower expression levels of miR-30a were associated with increased expression of Beclin-1 (BECN-1) and reduced apoptosis in RA synovium[42].

**miR-24**

miR-24 is positively correlated with CRP, DAS28, the visual analog scale of general health (VAS), and disease activity. It can increase the inflammatory response by targeting the expression of the furin enzyme, which is important in transforming growth factor-beta 1(TGF-β1) processing and peripheral tolerance maintenance [43].

**miR-26a**

miR-26a may be correlated with Th-17 differentiation, which is important in RA pathogenesis [44]. It has recently been reported that the overexpression of miR-26a-5p activates phosphoinositide 3-kinase (PI3K)/ protein kinase B, PKB (AKT) by targeting phosphatase and tensin homolog (PTEN) in RASFs. Overexpression of miR- 26a-5p induces proliferation, G1/S transition, invasion, and apoptosis resistance in RASFs [45].

**miR-27a**

The downregulation of miR-27a in RASFs results in the overexpression of follistatin-like protein 1 (FSTL1) which has been suggested to play a key role in RA development. This miRNA can repress important mediators such as MMP2, MMP9, and MMP13, and Rho family proteins (Rac1, CDC42, and RhoA). The expression of TLR4 and NF-κB is also inhibited by miR-27a in RASFs,as it inhibits the cell migration and invasion of RASFs which are important in RA pathogenicity [46].

**miR-29a**

Low expression levels of miR-29a in RASFs, which target STAT3, results in greater proliferation and apoptosis resistance [47].

**miR-30a-3p**

miR-30a-3p targets B cell-activating factor (BAFF) in RASFs, which results in decreased synthesis and release from these cells. Low expression levels of miR-30a-3p result in more BAFF release as well as B cell survival and autoimmune response in RA patients [48].

**miR-34a, miR-34b**

The hypermethylation of miR-34a promoter leads to the downregulation of miR-34a in RASFs in RA patients. The X-linked inhibitor of apoptosis protein (XIAP),which has been known to be an important direct target of miR-34a, is upregulated in RASFs. Decreased expression of this miRNA is associated with prolonged cellular lifespan and more inflammation and destruction in the joints of RA  patients [49]. It has recently been reported that miR- 34a can also target cyclin I to activate the ATM/ataxia telangiectasia and Rad3-related (ATR)/p53 signaling  pathway and inhibit

RASF proliferation and inflammation in RA joints [50]. Another recent study has revealed that miR-34a-5p targets X-box binding protein 1 (XBP1). Increased expression of XBP1 results in proliferation and overproduction of TNF-α and IL-6 in RASFs [51]. Murine double minute 4 (MDM4) is another target of miR‑34a‑3p in RASFs. Low expression levels of miR‑34a‑3p are correlated with the upregulation of cyclin-dependent kinase 2 (CDK2), cell division cycle 25A (CDC25A), and cyclin D1 which induce proliferation and are correlated with the induced production of MMP-1, MMP-9, and pro-inflammatory cytokines such as TNF-α and IL-6 in RASFs [52]. The decreased expression of the cAMP response element-binding proteins (CREBs) is correlated with dysfunction in RASFs and RA pathogenesis [53]. CREBsare a direct target of miR-34b and may be associated with RA disease activity [54].

### miR-101

Inducible T-cell co-stimulator (ICOS)-deficient mice are resistant to collagen-induced arthritis. The ICOS is one of the best targets of miR-101 and might be a therapeutic candidate for RA [55]. Downregulation of miR101-3p in RASFs results in the overexpression of prostaglandin-endoperoxide synthase 2 (PTGS2), which induces cell proliferation, migration, and invasion and attenuates apoptosis [56, 57].

### miR-103a

A previous study has shown that miR-103a upregulation is correlated with the downregulation of DICER1, argonaute RISC component 1(AGO1), cAMP responsive element-binding protein 1(CREB1), death-associated protein kinase 1 (DAPK1), and P53; the exact role of this miRNA, however, remains to be clarified [58].

### miR-124a

Increased expansion of RASFs may be associated with the lower expression of miR-124a. Overexpression of miR-124a leads to the inhibition of monocyte chemoattractant protein-1 (MCP-1), CDK-2, and vascular endothelial growth factor (VEGF) expression, resulting in decreased angiogenesis and inflammation and more apoptosis in RASFs [59]. Thus, a low level of miR-124a results in the overexpression of MCP-1, also known as chemokine (C-C motif) receptor 2 (CCR2), and the recruitment of monocytes into inflamed joints. Moreover, it has been reported that phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit alpha (PIK3CA) is one of the direct target genes for miR-124a. It is not surprising that lower miR-124a expression contributes to the activation of the PIK3/Akt/NF-κβ signaling pathway and induces the

production of pro-inflammatory factors like TNF-α and IL-6 in RASFs [60].

### miR-99a/miR-100/miR-125b, miR125a

miR-125b is co-expressed with miR-99 and miR-100. miR-125b and miR125a have been reported to activate the NF-κB signaling pathway which is involved in the production of pro-inflammatory cytokines, and they may initiate the inflammation response in RA joints [61].

### miR-126-3p

In 2012, Wang et al. reported the decreased expression of miR-126-3p in RA plasma; however, a 2013 study reported markedly elevated miR-126-3p levels in RA plasma [43, 62]. Recently, the downregulation of miR-126 in RASFs has been reported, which results in the upregulation of IL-23R, TNF-α, and IFN-γ in these cells [63]. However, another study has revealed that miR-126 overexpression in RASFs targets phosphoinositide-3-kinase regulatory subunit 2 (PIK3R2) expression and promotes proliferation while inhibiting apoptosis [64,65].

### miR-128-3p

miR-128-3p targets histone deacetylase 4 (HDAC4) in RASFs. miR-128-3p/HDAC4 axis regulates RA development through AKT/mTOR pathway. miR-128-3p upregulation results in more proliferation, migration, invasion, inflammation, and apoptosis resistance in RASFs [66].

### miR-132

The expression of miR-132 is increased in PBMCs; however, the monocyte fraction of RA expresses more than threefold expression of miR-132 compared to the lymphocyte fraction [23]. The plasma level is decreased and correlates inversely with TJC and is possibly a consequence of inflammation in RA [24].

### miR-137

miR-137 targets the C-X-C motif chemokine ligand 12/ stromal cell-derived factor 1 (CXCL12/ SDF1) in RASFs, resulting in reductionsinthe proliferation, invasion, migration, and expression of inflammatory cytokines from RASFs [67].

### miR-140-3p, miR-140-5p

Lower expression levels of miR140-3p and miR-140-5p in RASFs increase proliferation responses, migration, and cytokine production abilities, while they decrease apoptosis. miR-140-3p and miR-140-5p target SIRT1 and stromal cell-derived factor 1 (SCDF1) in RASFs [68]. Recently, STAT3 was reported to be the target of miR140-5p in RASFs [69].

### miR-133a, miR-142-3p, miR-142-5p

The miR-142 expression level was ten times more than that of miR-133 in RASFs. The runt-related transcription factor 2 (Runx2), which is essential for

osteoblast differentiation, is a target of miR-133 [70]. This gene is also a suppressor of cell division control protein 42 (CDC42) and is involved in cellular differentiation and cell cycle progression [71]. Downregulation of miR-142-3p inhibits the aggressive phenotypes of RASFs by inhibiting the NF-κB signaling pathway. miR-142-3p targets interleukin-1 receptor-associated kinase 1 (IRAK1) in RASFs and is correlated to the upregulation of IL-6, MMP-3, and B cell lymphoma 2 (Bcl-2) as well as the downregulation of BCL2 associated x, apoptosis regulator (Bax), and BCL2 associated agonist of cell death (Bad), which reduce apoptosis and promote proliferation and inflammation in RASFs [72].

**miR-143**

miR-143 targets insulin-like growth factor binding protein 5 (IGFBP5) in RASFs. Upregulated miR-143 results in IGFBP5 deficiency that increases the sensitivity of RASFs to TNFα stimulation and promotes IL-6 and NF-κβ activity in these cells [73]. miR-143-3p can also target insulin-like growth factor 1 receptor (IGF1R) in RASFs. Moreover, it increases cell proliferation and reduces apoptosis by targeting these genes and promotes Ras/p38 mitogen-activated protein kinase (MAPK) signaling pathways [74]. TNF alpha-induced protein 3 (TNFAIP3) is the target of miR-143-3p and is downregulated in RASFs, which leads to induced proliferation, inflammation, and attenuated apoptosis [75].

**miR-145**

miR-145 targets semaphorin 3A (SEMA3A) in RASFs. miR-145 overexpression results in more susceptibility to vascular endothelial growth factor (VEGF) that increases the survival, migration, and invasion of RASFs [73]. miR-145-5p aggravates RA development by promoting the NF-κB pathway, which enhances secretion of MMP-3, MMP-9, and MMP-13 in RASFs [76].

**miR-146a, miR-146b**

miR-146a is one of the most studied miRNAs in RA patients. Increased expression of miR-146a was detected in various cells such as T cells, B cells, monocytes, and IL-17-producing CD4+ cells [15, 23, 44, 77-79]. However, decreased expression in plasma of RA patients was reported in some studies [62, 80]. miR-146a inhibits the TH1 mediated response and requires Treg (regulatory) activity, which is importantin RA inflammation [81, 82]. Overexpression of miR- 146a suppresses T cell apoptosis by regulating Fas-associated factor 1, which is important in cellular apoptosis [77]. Different studies have reported conflicting evidence regarding the role of miR-146a in RA pathogenesis. Some have reported a positive correlation between miR-146a and

disease indices like CRP, ESR, DAS28, and plasma ; however, others have reported no correlation or inverse correlation with TJC [23, 24, 77, 79]. miR-146b is positively correlated with IL-17 producing lymphocytes and enabling the infiltration of these pathogenic cells to the synovium[44]. Both of these miRNAs regulate various essential genes in apoptosis and inflammation and could be linked to RA pathogenesis [23, 77, 78]. miR-146a levels were upregulated in RASFs after IL-1β and lipo-polysaccharide (LPS) stimulation [15]. Promotor analysis revealed that NF-κB, an essential transcription factor in response to pro-inflammatory cytokines, induced the expression of miR-146a under conditions of inflammation [83]. The TNF receptor-associated factor 6 (TRAF6) and IRAK1 were two target genes of miR-146a; however, the upregulated miR-146a did not change the expression pattern of these genes in RA patients. Under normal conditions, upregulated miR-146a can inhibit the expression of TRAF6 and IRAK1, which in turn results in the downregulation of TNF-α.In RA conditions, however, it seems that upregulated miR-146a is not sufficient to control TNF-α expression [23, 83]. Some other putative targets, including interferon regulatory factor-5 (IRF5) and signal transducer and activator of transcription-1 (STAT1) which are involved in type I IFN signaling pathway and Fas-associated factor-1 (FAF1), Fas-associated death domain proteins (FADD) which are involved in activation-induced cell death (AICD), and FAS-mediated apoptosis in T cells, should be investigated to clarify better the miR-146a pathogenicity in RA inflammation [77, 83-85]. miR-146a could affect osteoclast differentiation by targeting the master genes of osteoclastogenesis, such as c-Jun, nuclear factor of activated T-cells, cytoplasmic 1 (NF-ATc1), PU.1, and tartrate-resistant acid phosphatase (TRAP) [83, 86, 87]. In CIA mice treated with miR-146a, a significant decrease in cartilage and bone destruction has been reported; however, inflammation has not been inhibited [88].

**miR-150**

High expression levels of miR-150 are correlated with IL-17 producing cells, disease activity, and joint destruction. miR-150 is also important in the differentiation of IL-17-producing cells, an important pathogenic factor in RA [44, 89, 90]. Another recent study has shown that miR-150 overexpression results in the downregulation of its target, SOCS1, which induces pro-inflammatory cytokine production and proliferation of RASFs [91].

**miR-152**

miR-152 targets ADAM10 in RASFs. Downregulation of miR-152 significantly increases cell proliferation,

TNF-α, IL-1β, IL-6, and IL-8 production and inhibits cell apoptosis in RASFs [92]. miR-152 also targets DNA methyltransferase (DNMT1), resulting in the inhibition of canonical Wnt signaling. Low expression levels of this miRNA in RASFs induce DNMT1 and Wnt signaling; however, upregulated DNMT1 induces miR-152 expression in these cells [93, 94].

**miR-155**

Based on previous studies, two opposite functions of miR-155 should be noticed in RA pathogenicity: detrimental involvement and protective involvement. Most studies have revealed the increased expression level of miR-155 in different cells such as RASFs, synovial fluid CD14+ cells, and synovium macrophages, which is correlated with the lower expression of important target genes such as Src homology 2-containing inositolphosphatase-1(SHIP-1), a potent inhibitor of inflammation that increases the risk of autoimmunity in patients [15, 95, 96]. Overexpression of miR-155 in CD14+ cells stimulates the production of pro-inflammatory cytokines including IL-1β, IL-6, IL-8 and TNF-α [95]. IL-10 is downregulated by miR-155 and can modulate miR-155 itself [95, 97]. Like miR-146a, miR-155 might regulate various signaling pathways, and it plays roles in RA pathogenicity [15, 95, 98]. miR-155 is required for Treg, TH1 and TH17 differentiation and function [44, 83, 95, 99]. miR-155 is involved in TH17 differentiation, antigen-driven B cell maturation, and differentiation of Ig class-switched cells [100, 101]. The level of miR-155 in RASFs is upregulated after pro-inflammatory cytokine stimulation such as IL-1β, TNF-α, or TLR ligands [15]. A recent study reported that miR-155 targets Janus Kinase (JAK2/STAT3) and inhibits IL6-mediated activation in RASFs [102]. It has also been recently reported that by targeting forkhead box protein O3a (FOXO3a), miR-155 promotes the secretion of inflammatory cytokines such as IL-1β, IL-6, and TNF-α and induces the proliferation of RASFs [103]. Some other target genes which might be important in RA inflammation include PU.1 and musculoaponeuroticfibrosarcoma(c-Maf), which are important in dendritic cell maturation and hematopoietic development FADD;IkB kinase (IKK) that is a positive regulator of NF-κB;and the receptor-interacting serine-threonine kinase 1 (RIPK1).These genes need to be investigated to clarify the roles of miR-155 in RA pathogenesis. By reducing cytotoxic T-lymphocyte-associated protein 4 (CTLA-4) expression in CD4+ human T cells and promoting T cell-dependent tissue inflammation, miR-155 could enhance inflammation in RA joints [104, 105]. In miR-155 deficient mice, decreased systemic levels of IL-6

and IL-17 are seen after the induction of CIA; however,these mice do not develop either clinical or histologic signs of CIA [95, 106-108].

Some studies also have reported the protective function of miR-155 in RA patients. The overexpression of miR-155 reduces the expression of MMP-3 and impairs MMP-1 and MMP-3 induction by cytokine and TLR ligands in RASFs [15]. Downregulation of MMPs could alleviate tissue damage in inflamed joints. It is proposed that the microenvironment in RA synoviumupregulates miR-155 expression and controls feedback on the inflammatory response [95]. miR-155 is involved in Treg differentiation and maintaining its proliferative activity [100, 109].

**miR-181a**

miR-181a could potentially be important in RA pathogenicity. Any decreased or increased expression level affects the T cell maturation and selection process which increases the risk of autoimmunity. Downregulated miR-181a increases TCR sensitivity, while upregulated miR-181a increases the stimulation threshold of TCR. miR-181a also targets an important gene in T cell function called the protein tyrosine phosphatase non-receptor type 22 (PTPN22), which is important in RA pathogenicity [110-112].

**miR-188-5p**

miR-188-5p may target cell migration-inducing and hyaluronan-binding protein (CEMIP also named KIAA1199) and indirectly regulate collagen type I alpha (COL1A1 and COL12A1) expression in RASFs. Decreased miR-188-5p results in greater activation and migration of RASFs [113].

**miR-192**

Caveolin 1 (CAV1) is identified as a direct target of miR-192. Upregulated CAV1 results in increased cell proliferation and inhibition of apoptosis in RASFs. miR-192 is downregulated in RA synovial tissues, which elicits growth effects on RASFs by targeting CAV1 [114].

**miR-199a-3p**

miR-199a-3p targets retinoblastoma 1 (RB1) mRNA and suppresses its expression in RASFs. Reduced MiR-199a-3p in RASFs results in RB1upregulation which increases cellular proliferation and decreases apoptosis in these cells [115].

**miR-203**

Elevated expression of miR-203 stimulates the production of MMP-1 and the NF-κB-related production of IL-6, which is associated with activated RASFs and inflammation in RA joints [116]. A recent study revealed that HMG-box transcription factor 1 (HBP1) is a target of miR-203. HBP1 suppresses cell

proliferation and the production of inflammatory cytokines including IL-6, IL-1β, IL-8, and TNF-α, while it inhibits apoptosis in RASFs [117].

**miR-204, miR-211**

miR-204 and miR-211 target activating transcription factor 2 (ATF2) in RASFs. Downregulated miR-204 and miR-211 result in increased inflammation in RA joints [118]. It has recently been reported that miR-204-5p targets nuclear paraspeckle assembly transcript 1 (NEAT1) in RASFs. Upregulated NEAT1 in these cells induces the NF-κβ pathway and increases cellproliferationandinflammatory cytokine production while inhibiting cell apoptosis [119]. **miR-212-3p** The SOX5 gene is a target of miR-212-3p in RASFs. Decreased expression of miR-212-3p promotes cell growth and reduces cell apoptotic rates, which are important in RA pathogenesis [120].

**miR-218-5p**

RASFs have multilineage differentiation potential, including osteoblasts. miR-218-5p is overexpressed in the early phase of osteogenic differentiation and then decreased. miR-218-5p targets roundabout 1 (ROBO1) and indirectly decreases dickkopf-related protein 1 (DKK1) secretion, which promotes osteogenic differentiation [121].

**miR-221/miR-222**

miR-221 and miR-222 are co-expressed and target the same genes. Overexpression of these miRNAs could enhance the production of pro-inflammatory cytokines, promote the activation and migration of RASFs, and prolong the cellular lifetime through apoptosis resistance [122]. miR-221 targets DKK2 and bone morphogenetic proteins (BMPs), resulting in decreased mineralization, apoptosis, and osteoblastogenesis and pro-inflammatory cytokines production in RASFs [96, 122, 123].

**miR-223**

miR-223 regulates the differentiation of osteoclasts and has important roles in the state of RA joints[124]. Overexpression of miR-223 could suppress the production of cathepsin K as well as osteoclast-related genes, and it has a function in the renewal of bone and osteoclastogenesis [124]. One of its important target genes is neurofibromatosis type 1 (NF-1A), which is repressed and results in osteoclast differentiation [125]. The main sources of high concentrations of miR-223 in inflammation sites seem to be macrophages, monocytes, CD4+ T cells, RASFs, and peripheral T cells [24, 59, 124, 126]. However, the expression level of miR-223 might have no correlation with DAS28, CRP, anti-citrullinated peptide antibody (ACPAs), or disease duration; have a strong correlation with rheumatoid factor (RF); and have a negative correlation with TJC index [24, 54, 126, 127].

CIA mice treated with miR-223 showed decreased arthritis scores and no pannus formation [128]. miR-223 also targets IL-17RD in RASFs and contributes to the pathogenesis of RA by downregulating the expression of IL-17RD and increasing the production of IL-6 in these cells [129]. It also targets the NLR family pyrin domain containing 3 (NLRP3). Upregulated NLRP3 induces proliferation and inflammatory cytokine secretion and attenuates apoptosis in RASFs [130].

**miR-301a-3p**

The expression of RAR-related orphan receptor gamma (RORγt) and STAT3 is increased in the PBMCs of RA patients, which is correlated with increased TH17 frequency and pro-inflammatory cytokines. miR-301a-3p targets the protein inhibitor of activated STAT3 (PIAS3), the main cellular inhibitor of STAT3, and downregulated miR-301a-3p, resulting in more expression of STAT3 in RA patients [131].

**miR-320a**

Low expression levels of miR-320a correlate with decreased Bax/Bcl-2 ratios, which inhibits apoptosis in RASFs. miR-320a expression levels also correlate with MAPK ERK1/2 signaling pathways[132].

**miR-323-3p**

The higher expression level of miR-323-3p in RASFs inhibits its target genes, including BTRC (β-transducin repeat containing E3 ubiquitin-protein ligase) and β-catenin inhibitor, and enhances theWnt/cadherin signaling pathway. The increase in Wnt/cadherin signaling and upregulation of β-catenin have been described as important factors in the activation and function of RASFs[96, 133].

**miR-338-5p**

The nuclear factor of activated T-cells 5 (NFAT5) is a target of miR-338-5p in RASFs. Overexpressed miR-338-5p increases the proliferation, migration, and invasion of these cells which are important in RA pathogenesis [134].

**miR-340-5p**

miR-340-5p targets STAT3 in RASFs. Downregulated miR-340-5p results in increased proliferation and decreased apoptosis in these cells [135].

**miR-346**

miR-346 is upregulated after LPS treatment in RASFs. Suppression of miR-346 results in IL-18 release and might have a regulatory function in inflamed joints [136]. miR-346 targets Bruton's tyrosine kinase (BTK) and tristetraprolin (TTP), resulting in TNF-α expression and more inflammation by RASFs [137].

**miR-363, miR-498**

miR-363 and miR-498 are decreased in the CD4+ T cells of RA patients [77]. These miRNAs are elevated in RA peripheral blood or synovial fluid, but their role

in RA pathogenesis remains unclear [77].

## miR-375

miR-375 plays a critical role in the promotion of the canonical Wnt signaling pathway by targeting the Frizzled 8 (FZD8). The decreased expression level of miR-375 results in inflammation and plays a pathogenic role in RA development [138]. It has recently been reported that miR-375 targets TAK1-binding 2 (TAB2) in RASFs. TAB2 enhances cell cycle, proliferation and inflammatory response while inhibiting apoptosis in RASFs [139].

## miR-410-3p

Downregulated miR-410-3p correlates with the production of pro-inflammatory cytokines including TNF-α, IL-1β, IL-6, and MMP-9 by regulating the NF-κB signaling pathway in RASFs [140]. It has been verified that miR-410-3p regulates inflammation by targeting Yin Yang 1 (YY1) in these cells [141].

## miR-451

Increased expression of miR-451 has been reported in RA peripheral blood T cells, but its downregulation has also been reported in RA neutrophils [62, 99, 142]. Suppression of miR-451 in neutrophils could enhance chemotaxis by p38 MAPK [142]. The level of miR-451 has been decreased in T cells after treatment compared to active RA patients [99]. miR-451 is also positively correlated with DAS28, ESR, and IL-6 concentrations in serum [99].

## miR-483-3p

miR-483-3p targets IGF1 which is important in RA pathogenesis. Upregulated miR-483-3p results induced proliferation, the G0/G1-to-S phase transition, and attenuated apoptosis in RASFs [143].

## miR-495

Decreased expression of miR-495 in RASFs results in the upregulation of β-catenin, MMP-2, MMP-9, IL-6,IL-11, and TNF-α and induces proliferation in these cells [144].

## miR-506

The downregulation of miR-506 results in attenuated apoptosis along with a decrease in the activities of cysteine-aspartic proteases, cysteine aspartases, and cysteine-dependent aspartate-directed proteases (caspase-3 and -8). Toll-like receptor 4 (TLR4) is an important target of miR-506 in RASFs. Enhanced expression of TLR4 inhibits apoptosis and induces proliferation in these cells [145].

## miR-522

The over expression of miR-522 increases the expre-ession levels of TNF-α, IL-1β and MMP-1, MMP-3, and MMP-13 by targeting SOCS3 in RASFs [146].

## miR-539

miR-539 targets osteopontin (OPN) in RASFs. Decreased levels of miR-539 result in an increased level of OPN in the blood and synovial fluid of RA patients that promotes cellular proliferation in RA joints [147].

## miR-548a-3p

Serum exosomal miR-548a-3p is downregulated and associated with high levels of CRP, RF, and ESR in the serum of RA patients. miR-548a-3p targets the TLR4/NF-κB signaling pathway. Low expression levels of miR-548a-3p increase NF-κβ-mediated inflammation and might promote proliferation and activation of inflamed cells in RA patients [148].

## miR-573

miR-573 has been introduced as an anti-inflammatory miRNA which represses the expression of thioredoxin domain-containing 5 (TXNDC5) in the synovial tissue of RA patients, which in turn regulates MMP-3 expression. It also decreases the expression of IL-6 and COX2 in RA patients. miR-573 can target TLR2 and EGFR, which reduce the inflammation and angiogenesis in synovial tissue. Moreover, it attenuates different signaling pathways, including PI3K/Akt, ERK1/2, MAPK, and STAT3, in response to lipopolysaccharides (LPS) [149, 150].

## miR-613

DKK1 is a target of miR-613 in RASFs. Enhanced DKK1 in RASFs induces cellular proliferation, and invasion and decreases apoptosis in these cells [151].

## miR-650

miR-650 targets RAC-beta serine/threonine-protein kinase (AKT2) in RASFs. Downregulation of miR-650 results in the upregulation of AKT2 which increases the proliferation, migration, and invasion of RASFs and decreases apoptosis in these cells [152]. It has recently been shown that miR-650 targets 2',3'-cyclic nucleotide 3'-phosphodiesterase (CNP). Upregulated CNP promotes cell proliferation, inflammatory response, invasion, migration, and suppressed apoptosis in RASFs [153].

## miR-663

miR-663 targets the adenomatous polyposis coli (APC) which triggers the canonical Wnt signaling through the accumulation of β-catenin in RASFs. Increased miR-663 enhances cellular proliferation and the production of MMP3 and fibronectin in RASFs [154].

## Conclusion

Unraveling the etiology of autoimmune diseases remains a big challenge in the field of immunology and genetics. In recent years, miRNAs have been important research objects in various laboratories.

miRNAs play a multi-faceted role in the development of RA and are part of an extensive complex network Unraveling the etiology of autoimmune diseases remains a big challenge in the field of immunology and genetics. In recent years, miRNAs have been important research objects in various laboratories. miRNAs play a multi-faceted role in the development of RA and are part of an extensive complex network in autoimmunity. A plethora of miRNA alterations in different cells affect pathophysiology and the disease process. Furthermore, the exact expression pattern of various miRNAs in only a single cell and, more importantly, their interaction and different target genes by only one miRNA are still not entirely understood. However, different miRNAs target genes could be a completely complex network in the development and pathology of RA. Each miRNA and its expression pattern could be a potential target of therapeutic agents, but this could also be a double-edged sword and induce more inflammation in already-inflamed joints.

The identification of miRNAs as therapeutic agents involves other issues, including multiple regulators for a single mRNA, the synergistic or antagonistic activity of other miRNAs, and the participation of various regulators of gene expression such as genetic or epigenetic agents.

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