



## Review article

# The potential role of miRNA in regulating macrophage polarization

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## ABSTRACT

Macrophage polarization is a dynamic process determining the outcome of various physiological and pathological situations through inducing pro-inflammatory responses or resolving inflammation via exerting anti-inflammatory effects. The miRNAs are epigenetic regulators of different biologic pathways that target transcription factors and signaling molecules to promote macrophage phenotype transition and regulate immune responses. Modulating the macrophage activation, differentiation, and polarization by miRNAs is crucial for immune responses in response to microenvironmental signals and under various physiological and pathological conditions. In terms of clinical significance, regulating macrophage polarization via miRNAs could be utilized for inflammation control. Also, understanding the role of miRNAs in macrophage polarization can provide insights into diagnostic strategies associated with dysregulated miRNAs and for developing macrophage-centered therapeutic methods. In this case, targeting miRNAs to further regulate of macrophage polarization may become an efficient strategy for treating immune-associated disorders. The current review investigated and categorized various miRNAs directly or indirectly involved in macrophage polarization by targeting different transcription factors and signaling pathways. In addition, prospects for regulating macrophage polarization via miRNA as a therapeutic choice that could be implicated in various pathological conditions, including cancer or inflammation-mediated injuries, were discussed.

## 1. Introduction Macrophage

### 1.1. Biogenesis, characteristics, and polarization

Monocytes originate from bone marrow-derived myeloid precursors that include a small proportion of peripheral blood leukocytes (4–10 %) in a healthy human. Due to their short half-life, these cells migrate into tissues and differentiate into long-lived macrophages [1,2]. For years, circulatory monocytes were believed to be the only source of differentiated macrophages. However further studies proved that most tissue-resident macrophages are monocyte-independent cells with self-renewal potential and originate from the yolk

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**Abbreviation**

<b>AAA</b>	abdominal aortic aneurysm
<b>ABCA1</b>	ATP-binding cassette transporter A1
<b>ADAR1</b>	adenosine deaminase acting on double-stranded RNA 1
<b>AIS</b>	acute ischemic stroke
<b>Akt</b>	Ak strain transforming
<b>ALI</b>	acute lung injury
<b>AMD</b>	age-related macular degeneration
<b>AMPK</b>	adenosine monophosphate kinase
<b>ARDS</b>	acute respiratory distress syndrome
<b>Arg1</b>	arginase 1
<b>ATF3</b>	activating transcription factor 3
<b>α-SMA</b>	alpha-smooth muscle active;
<b>BaP</b>	Benzo-a-pyrene; Bcl6, B-cell lymphoma-6 protein
<b>BMDM</b>	bone marrow-derived macrophage
<b>BMP-2</b>	bone morphogenetic protein 2
<b>BPD</b>	bronchopulmonary dysplasia
<b>Btk</b>	Bruton's tyrosine kinase
<b>Cav-1</b>	caveolin-1
<b>CBH</b>	chronic brain hypo perfusion
<b>CDK</b>	cyclin-dependent kinase
<b>CNS</b>	central nervous system
<b>CNV</b>	choroidal neovascularization
<b>COPD</b>	chronic obstructive pulmonary disease
<b>CRC</b>	colorectal cancer cell
<b>CREB-C/EBPβ</b>	cyclic-AMP-response element-binding protein-CCAAT/enhancer-binding protein-beta
<b>CRLM</b>	colorectal cancer liver metastasis
<b>CSE</b>	cigarette smoke extract
<b>CSF-1R</b>	colony-stimulating factor 1 receptor
<b>CVB3</b>	coxsackievirus B3
<b>CYM</b>	Cypermethrin;
<b>DBP</b>	Dibutyl phthalate
<b>DSS</b>	dextran sodium sulfate
<b>EAE</b>	experimental autoimmune encephalomyelitis
<b>EMT</b>	epithelial-mesenchymal transition
<b>EOC</b>	epithelial ovarian cancer
<b>EREG</b>	epiregulin
<b>ERK</b>	extracellular signal-regulated kinase
<b>Ern1</b>	endoplasmic reticulum to nucleus signaling 1
<b>ETV6</b>	E26 transformation-specific variant 6 gene
<b>FOXO1</b>	forkhead box transcription factor 1
<b>GM-CSF</b>	granulocyte monocyte-colony stimulating factor
<b>GMP</b>	granulocyte-monocyte progenitor
<b>GPCR</b>	G-protein coupled receptor
<b>GSK3B</b>	glycogen synthase kinase 3 beta
<b>HIF-1α</b>	hypoxia-induced factor-1 alpha
<b>HNSCC</b>	head and neck squamous cell carcinoma
<b>HMGB1</b>	high mobility group box 1
<b>HPV</b>	human papilloma virus
<b>HSC</b>	hematopoietic stem cell
<b>HUVEC</b>	human umbilical vein epithelial cell
<b>I/R</b>	ischemia/reperfusion
<b>IBD</b>	inflammatory bowel disease
<b>ICAM-1</b>	intercellular adhesion molecule-1
<b>ICH</b>	intracerebral hemorrhagic
<b>IFN-γ,</b>	interferon-gamma
<b>IL,</b>	interleukin
<b>iNOS</b>	induced nitric oxide synthase
<b>IRAK</b>	IL-1 receptor-associated kinase 1

<b>IRF</b>	interferon regulatory factor
<b>JAK</b>	Janus kinase
<b>JMJD1C</b>	Jumonji domain containing 1C
<b>KLF</b>	Kruppel-like factor
<b>KOA SF</b>	knee osteoarthritis synovial fluid
<b>LPS</b>	lipopolysaccharide;
<b>LRP6</b>	low-density lipoprotein receptor-related protein 6
<b>LTBP1</b>	latent transforming growth factor $\beta$ binding protein 1
<b>MATN2</b>	matrilin-2
<b>MAPK</b>	mitogen-activated protein kinase
<b>MCP-1</b>	monocyte chemoattractant protein-1
<b>MDM2</b>	murine double minute 2
<b>MEC</b>	mammary epithelial cell
<b>MEK</b>	mitogen activated protein kinase kinase
<b>MET-1</b>	mammary epithelial tumor cell-1
<b>METTL3</b>	methyltransferase-like 3
<b>MI</b>	myocardial infarction
<b>miR</b>	microRNA
<b>MKP1</b>	mitogen-activated protein kinase phosphatase 1
<b>MMP</b>	matrix metalloproteinase
<b>MRC1</b>	mannose receptor C-type 1
<b>MS</b>	multiple sclerosis
<b>MSC</b>	mesenchymal stem cell
<b>MyD88</b>	myeloid differentiation primary response 88
<b>NF-<math>\kappa</math>B</b>	nuclear factor-kappa B
<b>NGF</b>	neuronal growth factor
<b>NLRP3</b>	NOD-like receptor P3; NO, nitric oxide;
<b>NSCLC</b>	non-small cell lung cancer
<b>OLR1</b>	ox-LDL receptor 1
<b>OSCC</b>	oral squamous cell carcinoma
<b>ox-LDL,</b>	oxidized-low density lipoprotein
<b>PAI-2</b>	plasminogen activator inhibitor 2
<b>PBMC</b>	peripheral blood mononuclear cell
<b>PDAC</b>	pancreatic ductal adenocarcinoma
<b>PDCD4</b>	programmed cell death protein 4
<b>PI3K</b>	phosphoinositide 3-kinase
<b>Pknox1</b>	PBX/Knotted 1 Homebox 1
<b>PLCB3</b>	1-phosphatidylinositol-4, 5-bisphosphate phosphodiesterase beta-3
<b>PM</b>	particular matter; <b>PPAR</b> , peroxisome proliferator-activated receptor
<b>PRKCD</b>	protein kinase C delta type
<b>PTGDS</b>	prostaglandin D2 synthase
<b>PTGS</b>	prostaglandin-endoperoxide synthase 2
<b>PTPRD</b>	protein tyrosine phosphatase receptor type D
<b>PTPRO</b>	protein tyrosine phosphatase receptor type O
<b>PTEN</b>	phosphatase and TENsin homolog deleted on chromosome 10
<b>ROCK2</b>	Rho associated coiled-coil containing protein kinase 2
<b>ROS</b>	reactive oxygen species
<b>RSA</b>	recurrent spontaneous abortion
<b>SCI</b>	spinal cord injury
<b>SCIRI</b>	spinal cord ischemia-reperfusion injury
<b>SFTSV</b>	severe fever with thrombocytopenia syndrome virus
<b>SHIP1</b>	Src homology-2 domain-containing inositol 5-phosphatase 1
<b>SIRP<math>\beta</math>1</b>	signal-regulatory protein beta1
<b>SIRT1</b>	sirtuin1
<b>SOCS</b>	suppressor of cytokine signaling
<b>STAT</b>	signal transducer and activator of transcription
<b>STZ</b>	streptozotocin
<b>T2D</b>	type-2 diabetes
<b>TACE</b>	TNF- $\alpha$ converting enzyme
<b>TAM</b>	tumor-associated macrophage
<b>TBL1X</b>	transducing (beta)-like 1X-linked

<b>TGF-<math>\beta</math></b> ,	transforming growth factor-beta
<b>Th1</b>	type 1 helper T lymphocyte
<b>TLR</b>	toll-like receptor
<b>TMEM229B</b>	protein transmembrane 229B
<b>TNBC</b>	triple negative breast cancer cell
<b>TNFAIP3</b>	tumor necrosis factor alpha-induced protein 3
<b>TNF-<math>\alpha</math></b> ,	tumor necrosis factor-alpha
<b>Trib1</b>	tribbles homolog 1
<b>TRAF</b>	TNF receptor-associated factor
<b>TRIF</b>	TIR-domain-containing adapter-inducing interferon-beta
<b>TSC2</b>	tuberous sclerosis complex 2
<b>UCB-MSC</b>	umbilical cord blood-derived mesenchymal stem cell
<b>UTR</b>	untranslated region
<b>UVRAG</b>	UV radiation resistance-associated gene protein
<b>VEGF</b>	vascular endothelial growth factor
<b>VSMC</b>	vascular smooth muscle cell

sac during embryonic development. A unique combination of embryonic and monocyte-derived cells forms the unique macrophage composition in each tissue [3,4]. Macrophages are involved in a wide variety of processes. Eliminating pathogens via phagocytosis, modulating adaptive immune responses through processing and presenting antigens, secreting different signaling proteins, and playing as scavengers to clear dead cells and cellular debris [3–5]. Macrophages are highly heterogeneous cell populations with various inflammatory and anti-inflammatory functions [6]. Their flexible phenotype results from a dynamic process known as macrophage polarization and is regulated in response to signals and microenvironmental stimulants. To clear the paradigm about opposite macrophage polarization phenotypes, these cells are classified into M1 and M2 polarization states [7–10].

#### 1.1.1. Classical-activated or M1 phenotype

The classically activated M1 macrophage is primarily induced by type 1 helper T lymphocyte (Th1)-secreted cytokines, including IFN- $\gamma$  and tumor necrosis factor-alpha (TNF- $\alpha$ ). Also, granulocyte monocyte-colony stimulating factor (GM-CSF), lipopolysaccharide (LPS), and other toll-like receptors (TLR) ligands are among the M1-inducers [8,11]. In addition, previous studies showed that oxidized-low density lipoprotein (Ox-LDL), high mobility group box 1 (HMGB1), and caveolin-1 (Cav-1) are involved in the macrophage phenotypic shift to the classical phenotype [12–14]. M1 macrophages, which highly express CD80, CD86, MHC-II, and TLR4 molecules, secrete various pro-inflammatory cytokines and chemokines, including interleukin (IL)-1 $\beta$ , IL-6, IL-12, IL-23, TNF- $\alpha$ , CCL2, CCL5, CXCL1-3, CXCL5, and CXCL8-10, and produce massive amounts of reactive oxygen species (ROS) to support Th1-oriented responses against invading pathogens [15,16]. LPS/TLR4 is considered the main pathway for M1 polarization that activates nuclear factor-kappa B (NF- $\kappa$ B) and interferon regulatory factor 3 (IRF3) and induces pro-inflammatory cytokines including IL-6 and TNF- $\alpha$  [2, 17]. Further studies revealed that LPS/TLR4-dependent classical macrophage activation occurs due to signal transducer and activator of transcription 1 (STAT1) dimerization and activation through a myeloid differentiation primary response 88 (MyD88)-associated pattern [18]. Janus kinase (JAK)-STAT is considered an essential pathway for classical polarization, and IRF5 plays a crucial role in promoting IL-12, IL-23, and TNF- $\alpha$  secretion [19]. Bruton's tyrosine kinase (Btk) was also identified in LPS-induced M1 polarization and Btk absence, which is explicitly associated with M2 polarization [20]. The P2Y(2)R, a G-protein coupled receptor (GPCR) involved in nitric oxide (NO) production [21], the suppressor of cytokine signaling 3 (SOCS3) that activates the NF- $\kappa$ B/phosphoinositide 3-kinase (PI3K) pathway [22], and activating A that downregulates IL-10 expression [23] are among other molecules involved in classical polarization.

#### 1.1.2. Alternative-activated or M2 phenotype

Macrophage activation via Th2-associated factors leads to M2 or alternative-activated polarization involved in injury healing, dead cell clearance, vascularization, and tumor promotion or invasion. Based on the specific inducers, M2 macrophages are categorized into M2a, M2b, M2c, and M2d subsets [24,25]. IL-4 induces the M2a subset, IL-13, fungal, and helminth infections and highly expresses CD206, the decoy IL-1 receptor, and the IL-1 receptor antagonist. IL-1 receptor ligands, immune complexes, TLR agonists, and LPS induce the M2b subset that produces various cytokines such as TNF- $\alpha$ , IL-1 $\beta$ , IL-6, and IL-10. The M2c subset is polarized by IL-10, transforming growth factor-beta (TGF- $\beta$ ), and glucocorticoids and exerts intense anti-inflammatory activities against apoptotic cells by releasing high amounts of IL-10 and TGF- $\beta$ . Also, the M2d subset is induced by TLR agonists via adenosine receptors [26,27]. Collectively, the M2 macrophages are characterized by highly expressed CD163, scavenger, mannose, and galactose receptors, upregulated levels of CXCR1, CXCR2, and CCR2, elevated production of IL-10, vascular endothelial growth factor (VEGF), matrix metalloproteinases (MMPs), ornithine, and polyamines, and low levels of inflammatory factors such as IL-12, CD86, MHC-II, and induced nitric oxide synthase (iNOS) [15,16,28]. The IL-4 and IL-13 cytokines activate macrophages through STAT6 [29,30]. Also, other transcriptional factors, including IRF4, peroxisome proliferator-activated receptor gamma (PPAR $\gamma$ ), and Kruppel-like factor 4 (KLF4), were suggested to promote alternative polarization [31–33].

## 2. microRNA (miRNA)

In 1993, the miRNA was first described in *Caenorhabditis elegans* as non-coding, small, 19–25 nucleotide, endogenous RNA with an evolutionarily conserved sequence [5,34]. Following transcription, miRNAs are processed by Drosha and Dicer enzymes, and their abnormal expression is associated with various disorders [35–37]. The miRNAs control gene silencing in the post-transcription phase and primarily bind to the 3'- or 5'-untranslated region (UTR) of target transcripts to suppress translation and degrade mRNA and influence gene expression, cellular function and various pathophysiological processes, e.g., cell proliferation, metabolism, apoptosis, and organ development [38–40]. Based on bioinformatics predictions, approximately 33 % of protein-coding genes are regulated post-transcriptionally via miRNAs [34].

**Table 1**  
Summary of main miRNAs involved in macrophage polarization.

Type of miRNA	Target	Effects on M1/M2 polarization	Consequences of macrophage polarization	Ref.
miR-21	PDCD4, PTEN/Akt/STAT6, and CSF-1R	M2 ↑	- Chemo resistance in ovarian cancer cells ↑ - Lung cancer progression ↑ - COPD and myocardial ischemia-reperfusion injuries ↓ - Allogenic graft rejection ↓	[52–60]
miR-34a	PI3K, NFκB	M1 ↑	-	[61]
	KLF4	M1 ↑	- Obesity-induced systemic inflammation ↑ - Lung inflammation in ARDS ↑ - NSCLC proliferation ↓	[62–64]
miR-124	Notch1 and NLRP3	M2 ↑	- Hepatic inflammation ↓	[65–67]
	STAT3, TACE, PU.1, and Ern1	M2 ↑	- CNS recovery in the EAE model ↑ - Microglia-associated inflammation in ischemic stroke ↓ - SCIRI-induced neuronal injuries	[68–71]
miR-125a-5p	A20	M1 ↑	-	[48]
	KLF13, IRF5, and ETV6	M2 ↑	- SCI-associated inflammation ↓ - IBD symptoms ↓	[72–75]
miR-125b	A20 and IRF4	M1 ↑	- Antitumor responses ↑ - Inflammation ↑	[76–78]
miR-146a	Notch1, PPARγ, SIRT1, TRAF6, and STAT1	M1 ↑	- Inflammation ↑	[79–81]
	STAT1	M2 ↑	- Renal function in STZ-induced nephropathy diabetes ↑	[82]
miR-146b	IRF5 and TLR4	M2 ↑	- Inflammation and associated pains in endometriosis ↓ - Viral expansion in SFTSV infection ↑	[83–85]
miR-155	SOCS1, SHIP1, Bcl6, C/EBPβ, and TGF-β/Smad	M1 ↑	- Inflammation ↑ - Immune responses against bacterial infections ↑ - CNV ↓	[86–93]
miR-9	ERK1/2, AMPK, SIRT1, and PPARδ	M1 ↑	- Inflammation ↓ - Tumor radio sensitivity ↑	[94–98]
miR-181b	Notch1, KLF4, and PRKCD	M2 ↑	- Atherosclerosis plaques vulnerability ↓ - Osteogenic migration and differentiation ↑	[99,100]
miR-200c	KLF6	M2 ↑	- Tumor proliferation and invasion ↑	[101,102]
	GM-CSF	M1 ↑	- EMT shift toward epithelial signature ↑ - Antitumor responses ↑	[103,104]
miR-223	STAT3, Pknox, HIF-1α, and C/EBPβ	M2 ↑	- Protection against inflammation and CVB3-associated injuries ↑ - Anti-inflammatory responses ↑	[105–110]
miR-511	PTGDS, CCL2, LTBP1, ROCK2, TLR4, and C/EBPα	M2 ↑	-	[111–113]
Let-7c	C/EBPδ	M2 ↑	- Bactericidal activity ↓	[114]
Le-7f	A20	M1 ↑	-	[115]
miR-98	Trib1	M1 ↑	- Tumor invasion ↓	[116]

**Abbreviation** Akt; Ak strain transforming, **ARDS**; acute respiratory distress syndrome, **C/EBPα**; cyclic-AMP-response element-binding protein-CCAAT/enhancer-binding protein-alpha, **CNS**; central nervous system, **COPD**; chronic obstructive pulmonary disease, **CSF-1R**; colony-stimulating factor 1 receptor, **CVB3**; coxsackievirus B3, **EAE**; experimental autoimmune encephalomyelitis, **EMT**; epithelial-mesenchymal transition, **Ern1**; endoplasmic reticulum to nucleus signaling 1, **ETV6**; E26 transformation-specific variant 6, **GM-CSF**; granulocyte monocyte-colony stimulating factor, **HIF-1α**; hypoxia-induced factor-1 alpha, **IBD**; inflammatory bowel disease, **KLF**; Kruppel-like factor, **LTBP1**; latent transforming growth factor β binding protein 1, **NLRP3**; NOD-like receptor P3, **NSCLC**; non-small cell lung cancer, **PDCD4**; programmed cell death protein 4, **Pknox**; PBX/Knotted 1 Homeobox 1, **PPARγ**; peroxisome proliferator-activated receptor, **PRKCD**; protein kinase C delta type, **PTGDS**; prostaglandin D2 synthase, **PTEN**; phosphatase and TENsin homolog deleted on chromosome 10, **ROCK2**; Rho associated coiled-coil containing protein kinase 2, **SCI**; spinal cord injury, **SCIRI**; spinal cord ischemia-reperfusion injury, **SFTSV**; severe fever with thrombocytopenia syndrome virus, **SIRT1**; sirtuin1, **STAT1**; signal transducer and activator of transcription 1, **STZ**; streptozotocin, **TACE**; TNF-α converting enzyme, **TRAF6**; TNF receptor-associated factor 6, **Trib1**; tribbles homolog 1.

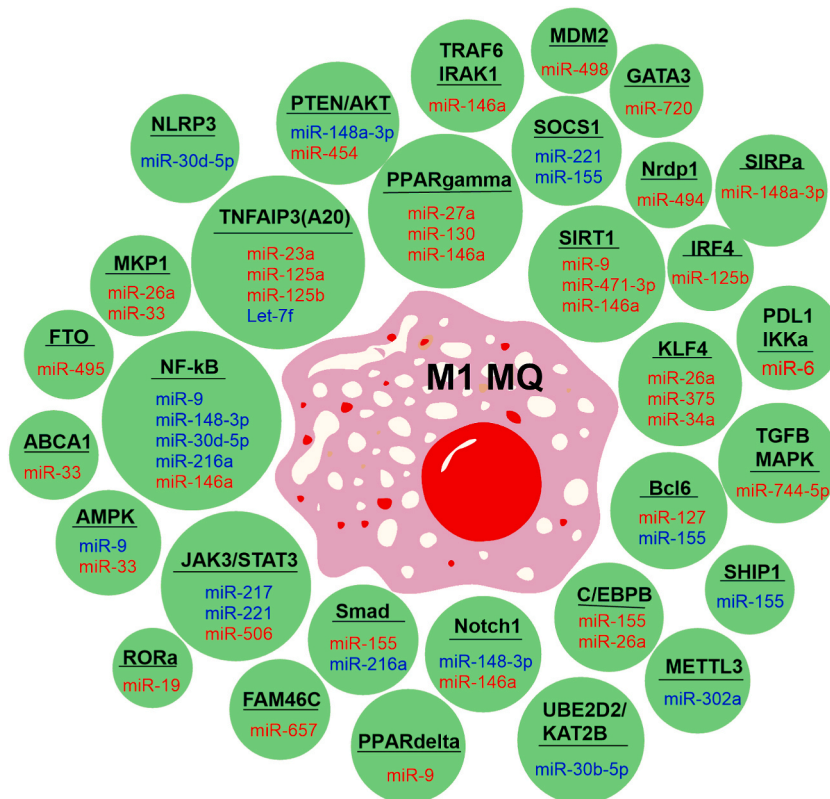
## 2. miRNA and macrophage polarization

Macrophages are dynamic cells with phenotypic transition abilities and a microenvironment *milieu*-based activation potential [41]. Multiple lines of evidence support associations between miRNAs deregulation and inadequate or overloaded inflammatory responses [42]. Monocyte-derived macrophages originate from hematopoietic stem cells (HSC), and miRNAs are critical regulators of HSC's renewal and fate [43]. As increased activation of PU.1 is in favor of granulocyte-monocyte progenitor (GMP) differentiation to monocyte lineage, this transcription factor induces the expression of multiple miRNAs, including miR-146a, miR-342, miR-338, and miR-15, which are involved in various steps of myeloid cell differentiation and control monocyte and macrophage maturation. For instance, miR-146 overexpression negatively regulates innate immune responses and is enough to induce stem cell maturation into monocyte during hematopoiesis [44–46].

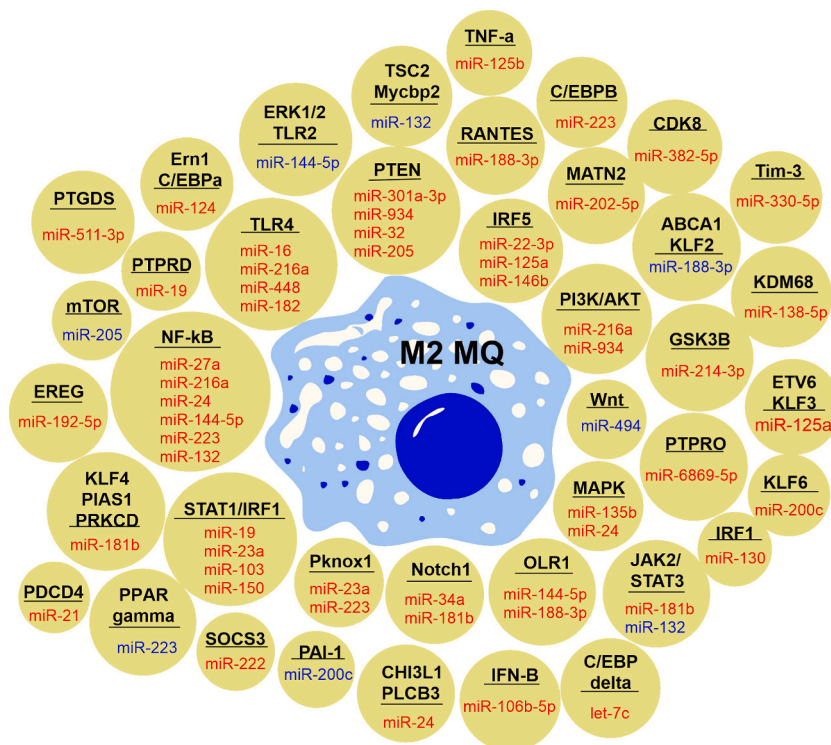
Zhang et al. evaluated the miRNA expression profile during macrophage polarization in murine bone marrow-derived macrophages (BMDM). The results of microarray analysis showed that miR-109 expression was altered between M1 and M2 phenotypes. Also, the expression of miR-181a, miR-155-5p, miR-204-5p, and miR-451 was upregulated in classically activated macrophages compared to the alternative form, while a downregulation was reported in the miR-125-5p, miR-146a-3p, miR-143-3p, and miR-145-5p expressions [47]. Also, Graff et al. conducted a comprehensive study using TaqMan low-density array human miRNA assays to evaluate different miRNA expressions in various M1, M2a, M2b, and M2c subsets. They reported specifically expressed miR-125a-3p and miR-26a in the M1 and miR-222, miR-132, miR-29b, miR-27a, and miR-193b in the M2b subset [48].

In another study, Cobos Jimenez and colleagues analyzed the miRNA profile in peripheral blood mononuclear cell (PBMC)-derived polarized monocytes and reported upregulation or downregulation in the expression of 303 different miRNAs. In this case, miR-125a-5p, miR-125b-5p, miR-181a-5p, and miR-193b-3p were significantly upregulated in M1-polarized macrophages and dysregulated in M2 macrophages. In addition, upregulation in miR-146a-5p, miR-145-5p, miR-29b-3p, and miR-193a-5p and downregulation in miR-629-5p were observed only in classic phenotype. Also, elevated miR-502-3p and miR-500a-5p and reduced miR-181-5p expressions were observed in the M2a-polarized macrophage, while increased expressions in miR-22-3p, miR-21-5p, and miR-146b-5p and decreased levels in miR-200a-3p and miR-339-3p were reported in the M2c phenotype [49].

The miRNA-mediated macrophage polarization is a fully-conserved process controlled by specific transcription factors that promote different polarization patterns and maintain their balance [48,50,51]. Here, we categorized and summarized the prominent miRNAs involved in macrophage polarization in Table .1. Also, miRNA and identified targets were illustrated in Fig. 1 and Fig. 2 as



**Fig. 1.** Schematic representations of miRNAs and identified targets that promote M1 macrophage polarization. The miRNAs highlighted in red suppress their targets to promote M1 phenotype, while miRNAs in blue positively influence targets to induce the M1 subset. (For interpretation of the references to color in this figure legend, the reader is referred to the Web version of this article.)



**Fig. 2.** Schematic representations of miRNAs and identified targets that promote M2 macrophage polarization. The miRNAs highlighted in red suppress their targets to promote M2 phenotype, while miRNAs in blue positively influence targets to induce the M2 subset. (For interpretation of the references to color in this figure legend, the reader is referred to the Web version of this article.)

regulators of M1 and M2 phenotypes, respectively.

**2.1. miR-21**

Due to its involvement in pathophysiological conditions, including solid tumors, cardiac injuries, and inflammation, miR-21 is considered one of the most critical mammalian miRNAs [117]. Recent studies showed that miR-21 promotes M2 macrophage polarization, significantly inhibits apoptosis, and induces chemoresistance in ovarian cancer cells, while miR-21 inhibitors reverse the mentioned effects [52]. In addition, mesenchymal stem cells (MSC) and KEL endometrial cancer cells under hypoxic conditions secrete miR-21-enriched exosomes that induce M2 polarization and promote lung cancer [53,54]. The programmed cell death protein 4 (PDCD4) is a tumor suppressor that activates NF-κB and inhibits IL-10 expression as a pro-inflammatory protein. Recent studies reported that miR-21 negatively regulated PDCD4 and was upregulated in different cancers as an oncomir [55,56]. Sheedy and colleagues reported that miR-21 suppressed PDCD4 expression in a MyD88-or TIR-domain-containing adapter-inducing interferon-beta (TRIF)-dependent manner. Also, in pre-miR-21-transfected RAW264.7 cells, suppressed NFκB signaling and elevated IL-10 production were observed following LPS stimulation [57]. In addition, miR-21 was upregulated in IL-1β-treated MSCs, and miR-21-enriched exosomes derived from treated MSCs effectively promoted M2 polarization both *in vivo* and *in vitro*. PDCD4 was the target gene for miR-21, and significant amelioration in symptoms and an increased survival rate were observed in the murine model of sepsis following miR-21-oriented M2 polarization [118].

Another interesting interaction between miR-21 and the tumor microenvironment is the positive feedback between miR-21-induced M2 polarization and the epithelial-mesenchymal transition (EMT) process. The EMT transcription factor Snail activates miR-21 transcription, and miR-21-enriched exosomes secreted by HNSCC effectively inhibit the expression of M1 factors and promote M2 polarization, which can lead to angiogenesis and tumor progression [119]. In addition, Song et al. discovered another side of this feedback. They observed that exosomal miR-21-5p derived from EC109 and EC9706 tumor cells induce M2 macrophage transformation via the phosphatase and TENsin homolog deleted on chromosome 10 (PTEN)/Akt strain transforming (Akt)/STAT6 signaling pathway. Subsequently, TGF-β secretion by M2-polarized macrophages promotes esophageal cancer cell EMT through the TGF-β/Smad2 axis [59]. Along with these results, another study revealed that miR-21 integrates colony-stimulating factor 1 receptor (CSF-1R)/pTyr-721/PI3K axis signals, suppresses pro-inflammatory polarization, and induces the M2 phenotype. They observed that approximately 80 % of CSF-1R/miR-21 axis molecular targets are pro-inflammatory agents. Also, signal-regulatory protein beta1 (SIRPβ1) induces M2-associated responses as activators of the mitogen-activated protein kinase (MEK)/ERK1/2 pathway. Knockout of miR-21 reduced the expression of arginase 1 (Arg1), mannose receptor 1, IL-4Ra, and Fizz as alternative associated markers. Also, the

administration of miR-21 inhibitors in mice increased the recruitment of inflammatory monocytes and the LPS responsiveness of peritoneal macrophages [60]. Furthermore, miR-21-mediated macrophage polarization was investigated in other inflammatory conditions, including chronic obstructive pulmonary disease (COPD), myocardial ischemia-reperfusion injury, and allogeneic graft rejection [95,120,121]. Lu et al. proved that elevated miR-21 expression in cigarette smoke extract (CSE)-exposed RAW264.7 cells is correlated with M2 polarization and miR-21 inhibitors effectively reduce lung tissue degeneration in the murine model of COPD [95]. Also, Shen et al. proved that MSC-derived exosomal miR-21 polarized M1 macrophages to the M2 phenotype following IL-10 induction and IL-6 suppression and reduced inflammation in the murine model of myocardial ischemia-reperfusion injury [120]. In addition, Li et al. reported that adenosine deaminase acting on double-stranded RNA 1 (ADAR1) treatment in a murine model of allogeneic skin graft, efficiently suppresses mir-21 expression, downregulates Foxo1, induces IL-10 production that leads to M2 polarization, and impedes allogeneic graft rejection [121].

However, a recent study demonstrated miR-21 involvement in pro-inflammatory M1 phenotype induction in macrophages. They reported that miR-21-transfected macrophages significantly upregulated macrophage inflammatory status and exosomes from these cells are rich in miR-21 and polarize naïve macrophages toward a pro-inflammatory phenotype partially in a PI3K- and NFκB-dependent manner [61].

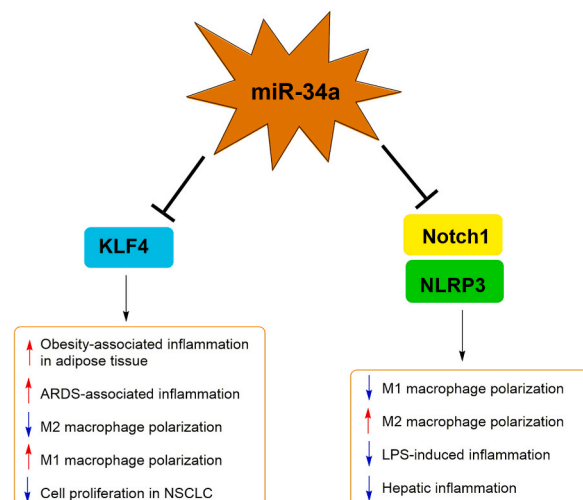
The interaction between miR-21 and macrophage polarization seems to be an attractive therapeutic target for cancer and inflammatory disorders. Inhibiting miR-21 using antagomirs or pharmacologic agents could effectively induce antitumor immune responses and inflammatory M1 macrophages while administering strategies that upregulate miR-21 expression is crucial to suppress inflammation and induce M2 polarization to resolve inflammation-related injuries.

## 2.2. miR-34a

Both M1 polarization and M2 induction were observed to be mediated by miR-34a (Fig. 3). KLF4 was identified as the main target of miR-34a to promote M1 polarization. Overexpressed miR-34a in the adipose tissue aggravates obesity-induced systemic inflammation via suppressing KLF4, accumulating M1 pro-inflammatory macrophages [63]. In addition, adipocyte-derived exosomal miR-34a suppressed M2 polarization and enhanced metabolic dysregulation following uncontrolled obesity-associated inflammation [64]. The miR-34a suppression improved lung inflammation and histological symptoms in the murine acute respiratory distress syndrome (ARDS) model following KLF4 overexpression, which led to M2 phenotype polarization [62]. In addition, miR-34a overexpression in macrophages co-cultured with non-small cell lung cancer (NSCLC) cells leads to M2-to-M1 polarization following KLF4 suppression and decreases cell proliferation and clonogenic potential [122].

The other side of miR-34a-macrophage polarization interactions promotes M2 macrophages. Recent studies showed that miR-34a blocks pro-inflammatory responses in LPS-stimulated macrophages by targeting Notch1, critical for producing LPS-mediated inflammatory cytokines, e.g., TNF- $\alpha$  and IL-6 [67]. In addition, adipocyte-derived exosomal miR-34a potentially targets NOD-like receptor P3 (NLRP3) and suppresses M1 polarization in the murine model of titanium-induced osteolysis [66]. Also, a recent study demonstrated that prolonged exposure to Benzo-a-pyrene (BaP) and Dibutyl phthalate (DBP) environmental pollutants in the rat model of hepatic injuries leads to aggravated hepatic inflammation as result of a deregulated M1/M2 balance. Further investigations revealed that downregulating miR-34a-5p, followed by upregulation in Notch signaling; induce M1 polarization and results in uncontrolled inflammatory responses [65].

Totally, it seems that miR-34a is an important regulator of macrophage polarization and controversial findings in promoting M1 or M2 phenotype may be due to variations in study models and conditions. Hence, further in-depth and mechanistic investigations are



**Fig. 3.** Schematic representations of potential targets and clinical outcomes of miR-34a involvement in macrophage polarization toward both pro-inflammatory and anti-inflammatory subsets.



required to clarify the exact role of miR-34a in macrophage polarization and administer it in human clinical trials as a therapeutic strategy.

### 2.3. miR-124

The anti-inflammatory potential of miR-124 in polarizing macrophages toward the M2 phenotype was proved following miR-124 mimic transfection into RAW264.7 cells that suppressed LPS-induced IL-6 and TNF- $\alpha$  production and directly targeted STAT3 and TNF- $\alpha$  converting enzyme (TACE) [71]. In addition, miR-124 upregulation in both IL-4- and IL-13-treated macrophages was reported, while miR-124 knockdown suppressed M2 markers (Ym1 and CD206) and induced M1 hallmarks (TNF, iNOS, and CD86) [123]. Under normal physiological conditions, most tissue-resident macrophages appear to have an alternative-like phenotype. In the central nervous system (CNS), microglia, as CNS-resident macrophages, express alternative-associated genes, including Ym1, Fizz 1, IL-10, and IL-10 [124]. In brain microglia, elevated expression of miR-124 leads to direct targeting of C/EBP $\alpha$  and PU.1 in downstream that control M2 alternative polarization and is suggested to be a key regulator in the CNS microenvironment [70]. Further analysis in experimental autoimmune encephalomyelitis (EAE) as a murine model of multiple sclerosis (MS) revealed the therapeutic potential of miR-124 for reducing total numbers of macrophages, activating CD45<sup>high</sup> microglia, ameliorating inflammation and clinical symptoms, and also increasing CNS recovery [70]. In addition, administering the liposomal miR-124 in a murine model of ischemic stroke showed the therapeutic efficacy of miR-124 in a time-dependent manner. Application of a therapeutic regimen in the sub-acute phase and 48 h after stroke significantly reduced inflammatory microglia, while no significant effects were observed when miR-124 was administered ten days after stroke [68]. A similar therapeutic potential of miR-124-3p was observed in the spinal cord ischemia-reperfusion injury (SCIRI) murine model. In this case, BM-MSC-derived exosomal miR-124-3p targets endoplasmic reticulum to nucleus signaling 1 (Ern1) and induces M2 polarization, which results in amelioration of SCIRI-induced neuronal injuries [69].

In addition to the CNS, miR-124-polarized alternative macrophages are essential in regulating allergic immune responses. The miR-124 overexpression was observed in IL-4- and IL-13-exposed RAW264.7 and BMDM cells. Further investigations showed that the miR-124 inhibitor suppresses Ym1 and CD206 expression while upregulating CD86, NOS2, and TNF- $\alpha$  levels. In addition, increased numbers of CD14<sup>+</sup> CD16<sup>+</sup> intermediate monocytes with high levels of miR-124 were observed in allergic bronchial asthma patients [123]. The application of miR-124 mimics suppressed LPS-associated myeloperoxidase activity and relieved acute lung injuries in animal models. Functionally, the adhesion molecule-1 (ICAM-1) suppresses monocyte chemoattractant protein-1 (MCP-1) expression through miR-124 upregulation and induces M2 polarization [125].

Collectively, it seems miR-124-induced M2 polarization could potentially be administered for various inflammatory conditions by promoting alternative macrophages and suppressing the M1 inflammatory phenotype.

### 2.4. miR-125

The miR-125 family includes miR-125a and miR-125b, which are widely involved in regulating macrophage polarization. Recent studies showed that miR-125a-5p is upregulated in LPS-stimulated macrophages, and the mimic transfection increased the expression of classic phenotype-associated transcriptions via targeting A20 [48]. The ubiquitin-editing enzyme A20, also known as tumor necrosis factor alpha-induced protein 3 (TNFAIP3), is a negative regulator of the NF $\kappa$ B signaling pathway in different immune cells [126]. On the other hand, various studies have reported miR-125a-mediated M2 polarization. Banerjee et al. observed higher miR-125a expression in alternative macrophages compared to a classic phenotype that suppresses M1 activation and bactericidal activities while promoting alternative polarization and phagocytic potential for apoptotic cell ingestion through targeting KLF13 [72]. E26 transformation-specific variant six genes (ETV6) was another identified miR-125a-5p target for inducing M2 polarization and facilitating bone regeneration [74]. Also, administering BM-MSC-derived exosomal miR-125a in a murine model of spinal cord injury (SCI) showed neuroprotective effects by inducing M2 polarization and suppressing the M1 phenotype via targeting IRF5 [73]. In addition, Shi et al. administered Dioscin in the murine model of dextran sodium sulfate (DSS)-induced colitis. They reported suppressed M1 and facilitated M2 polarization followed by increased levels of miR-125a-5p that improved intestinal epithelial barrier function and ameliorated inflammatory bowel disease (IBD) symptoms [75].

Overexpressed miR-125b, which plays an essential role in improving antigen presentation, T cell activation, and antitumor responses, was observed in M1 macrophages [127]. The miR-125b activates pro-inflammatory macrophages by targeting IRF4 and TNFAIP3 [76,77]. In this case, recent studies showed that tumor cell-derived exosomal miR-125b reprogrammed macrophages to a classically activated phenotype with elevated levels of co-stimulatory factors and increased responses to the IFN- $\gamma$  [78]. Also, the active form of vitamin D, 1, 25 (OH)<sub>2</sub> D3, alleviates colitis through downregulating miR-125b, promoting M1-to-M2 macrophage polarization, and regulating macrophage subsets [128,129]. On the other hand, multiple studies have observed miR-125b suppression following LPS stimulation [130,131]. Also, it seems that miR-125b targets 3'UTR of TNF- $\alpha$  transcript, reduces stability, and negatively regulates inflammatory responses [132–134].

### 2.5. miR-146

The miR-146 family consists of two evolutionally conserved members. The miR-146a is highly expressed in M2 macrophages and is crucial in modulating macrophage polarization by targeting Notch1 and PPAR $\gamma$  and promoting the M1 subset [80]. Also, a recent study showed that particular matter 2.5 (PM2.5) upregulates miR-146a-5p to induce M1 macrophage polarization by targeting SIRT1 [81]. Primarily, miR-146a was introduced as a negative feedback regulator of macrophage activation by targeting TLR signaling

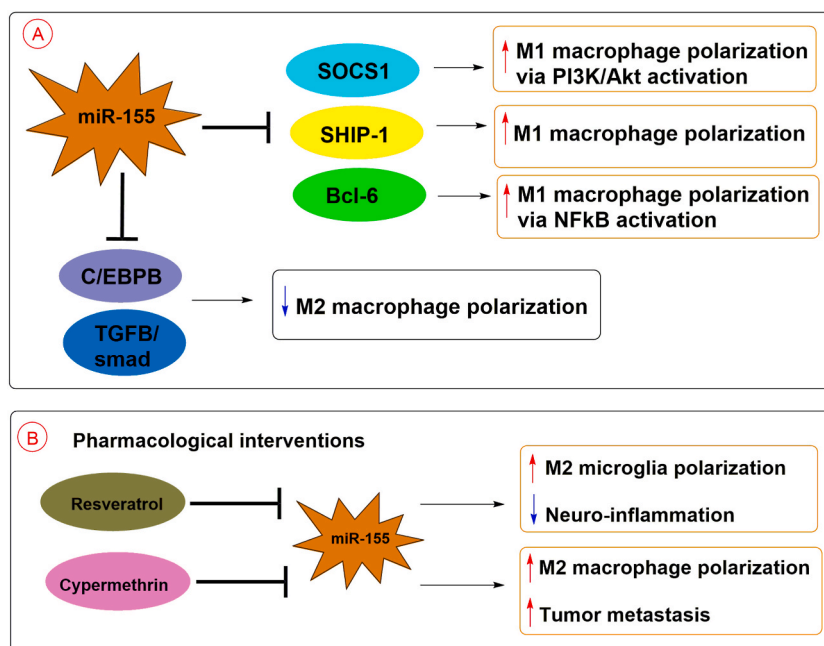
downstream molecules such as IL-1 receptor-associated kinase 1 (IRAK1), TNF receptor-associated factor 6 (TRAF6), and NF $\kappa$ B [135–137]. Chen et al. reported that neonatal murine cardiomyocyte-derived exosomal miR-146a-5p significantly increased VEGFA expression and promoted M2-to-M1 macrophage polarization via targeting TRAF6. Interestingly, unlike the miRNA mimic, exosomal miR-146a-5p reduced iNOS and TNF- $\alpha$ . Hence, it seems that cardiomyocyte-derived exosomal miRNA promotes M1 polarization and induces inflammatory responses by targeting TRAF6 [79]. In contrast to above-mentioned results, different results were observed in other studies. Human umbilical cord blood (UCB)-derived MSC administration leads to significant upregulation in miR-146a-5p that shifts the M1-to-M2 macrophage phenotype by suppressing the STAT1/TRAF6 signaling pathway and reviving renal function in the murine model of the streptozotocin (STZ)-induced model of nephropathy diabetes [82].

The miR-146b is on the opposite side; it is highly expressed in M1 macrophages and regulates macrophage polarization by targeting IRF5 and suppressing the M1 phenotype [84]. The miR-146b is an IL-10-dependent miRNA in human and murine systems that targets multiple factors, including TLR4, MyD88, IRAK-1, and TRAF6, promoting anti-inflammatory status. Multiple lines of evidence emphasize that miR-146b overexpression in THP-1 cells dramatically reduces the LPS-dependent secretion of pro-inflammatory cytokines and chemokines, including TNF- $\alpha$ , IL-6, IL-8, CCL2, CCL3, CCL7, and CXCL10 [83]. In addition, Zhang et al. demonstrate that miR-146b ameliorates inflammation by suppressing IRF5, and miRNA variants are related to endometriosis and associated pains [85]. Similar results were observed in severe fever with thrombocytopenia syndrome virus (SFTSV) infection where increased expression of miR0146b targets STAT1 and promotes M2 macrophage polarization to facilitate virus shedding and expansion [138].

## 2.6. miR-155

The miR-155 is a multifunctional miRNA that plays multiple roles in inflammation and immune responses [139]. Various stimulants including IFN- $\beta$ , TNF- $\alpha$ , IL-1, TLR2, TLR3, TLR4, and TLR9 signals, and specific antigens, upregulating miR-155 expression [132,140]. The crucial role of miR-155 in macrophage polarization was proved following the effects of miRNA knockdown on the M1-to-M2 transition [141]. Yi-Hong et al. showed that *Toxoplasma gondii* infection induces M1 macrophage polarization through miR-155 upregulation [86]. In addition, Zhang et al. reported that obese mice adipocyte-derived exosomal miR-155 promotes M1 macrophage and regulates insulin signaling and glucose uptake by adipocytes [90]. In this regard, pharmacologic regulation of miR-155 seems to be an interesting approach. For example, using resveratrol suppressed miR-155 expression and promoted M2 microglia polarization to ameliorate neuro-inflammation induced following cerebral ischemia [142]. In addition, the critical role of Cypermethrin (CYM), a type II pyrethroid, in facilitating tumor metastasis is exerted by suppressing miR-155 expression and M2 macrophage promotion [143].

Various studies investigated potential targets for miR-155 as a pro-inflammatory miRNA that promotes M1 macrophage polarization. They identified multiple vital genes such as SOCS1, Src homology-2 domain-containing inositol 5-phosphatase 1 (SHIP1), and B-cell lymphoma-6 protein (Bcl6), which are negative regulators of inflammatory responses [87–89,91,92]. Xu et al. revealed the potential role of the SOCS1/miR-155 axis in PI3K/Akt1-mediated classic macrophage polarization in mouse models of *Staphylococcus*



**Fig. 4.** (A) Schematic representations of miR-155 potential targets to induce M1 or M2 macrophage polarization under different circumstances; (B) Targeting miR-155 by pharmacological agents to interfere macrophage polarization as therapeutic approaches

*aureus*-induced respiratory infection [144]. In addition, another study reported significantly increased expression of miR-155 in GM-CSF/IFN- $\gamma$ /LPS-polarized primary human BMDMs and microglia, while miR-155 downregulates SOCS1 and influences the expression of pro-inflammatory cytokines and co-stimulatory surface markers [145]. Shi et al. observed miR-155-5p overexpression following the co-culture of PBMC-derived macrophages with knee osteoarthritis synovial fluid (KOA SF) that induces M1 macrophage polarization through targeting SOCS1 and suppresses macrophage apoptosis via targeting caspase 3 [146]. Hu et al. implicated miR-155 inhibition in reducing M1-induced sympathetic neuronal remodeling and ventricular arrhythmia. Mechanistically, miR-155 suppression reduces M1 polarization and SOCS1/NF $\kappa$ B-dependent inflammatory responses that result in neuronal growth factor (NGF) upregulation [147]. These results highlighted the importance of miR-155-mediated macrophage polarization through targeting SOCS1 in immune responses against bacterial pathogens and CNS adaptive immunity. O'Connell and colleagues revealed that SHIP1, a negative regulator of TLR pathways, was targeted and suppressed by miR-155 in LPS-stimulated wild-type primary macrophages [148]. In addition, in pro-inflammatory macrophages, miR-155 directly targeted Bcl6 as an essential negative regulator of the NF $\kappa$ B pathway [88]. Recent studies have implied that the role of miR-155 in macrophage polarization is not limited to M1 promotion but influences M2 markers and suppresses alternative hallmarks [149]. The C/EBP $\beta$ , considered an alternative feature that regulates Arg-1 expression, is suppressed by miR-155 through the interacting 3'UTR region [150]. Arranz and colleagues observed that Akt protein kinases primarily influence the polarization of mouse peritoneal macrophages. In this case, Akt1 deletion induces the M1 phenotype, and Akt2 deletion promotes the alternative phenotype, and all these processes are mediated by the miR-155-C/EBP $\beta$  interaction [130, 151]. Also, Zhang et al. showed that miR-155 inhibited C/EBP $\beta$  activation and subsequent M2 macrophage polarization, leading to choroidal neovascularization (CNV) suppression [93]. Another identified target of miR-155 was the TGF- $\beta$ /Smad signaling pathway. Smad2 targets IL-13R $\alpha$ 1 and suppresses STAT6 activation in human primary macrophages [51, 152].

Although miR-155 was introduced as a pro-inflammatory macrophage inducer, multiple lines of evidence implied that miR-155 negatively regulates inflammatory processes via targeting crucial elements involved in pro-inflammatory signal transduction. Tili et al. reported that by inducing TNF- $\alpha$  production, miR-155 directly targets transcripts of various anti-inflammatory and pro-apoptotic proteins involved in the LPS signaling pathway, such as Fas-associated death domain protein, IKK $\epsilon$ , and receptor-interacting serine-threonine kinase 1. Hence, it is suggested that miR-155 acts as both a negative and positive regulator of LPS signaling [132]. In this line, Tange et al. identified MyD88, which is involved in the negative regulation of *Helicobacter pylori*-induced inflammation, as a target gene for miR-155 [153].

It seems that miR-155 exerts pleiotropic roles under different physiological and pathological conditions and promotes macrophage polarization toward both pro-inflammatory and anti-inflammatory phenotypes under different conditions (Fig. 4a). Hence, targeting and manipulating miR-155 could be a therapeutic approach to modulating immune hemostasis (Fig. 4b).

## 2.7. miR-9

It was reported that miR-9 overexpression, followed by downregulation of the extracellular signal-regulated kinase 1/2 (ERK1/2) phosphatase Dusp6 by CCL2, could increase macrophage-mediated inflammatory responses [94]. Also, miR-9-5p targets NF- $\kappa$ B, adenosine monophosphate kinase (AMPK), and sirtuin 1 (SIRT1) to regulate macrophage polarization in both *in vitro* and *in vivo* models. Activated NF- $\kappa$ B and AMPK and suppressed SIRT1 expression led to miR-9-mediated M1 induction and M2 suppression that promoted osteoarthritis progression in the mouse model [154]. In this case, miR-9-associated strategies such as miR-9 antagomir could be considered a potential therapeutic method for osteoarthritis. The PPAR $\delta$ , a well-known lipid and glucose hemostasis regulator, is another identified target for miR-9 to promote the M1 phenotype. The LPS-exposed human primary monocytes showed elevated levels of miR-9 and suppressed PPAR $\delta$  expression. This situation was reversed following anti-miR-9 transfection [96]. In this case, Tong et al. reported that miR-9-enriched exosomes derived from human papillomavirus (HPV)-infected head and neck squamous cell carcinoma (HNSCC) downregulate PPAR $\delta$  expression and induce M1 polarization, which finally increases tumor radiosensitivity [97].

## 2.8. miR-181

The potential role of miR-181b in promoting M2 macrophage polarization through various targets was proven in different studies. Although Notch1 was introduced as the direct target of miR-181b to induce the M2 phenotype and reduce atherosclerotic plaque vulnerability [99], another mechanism was identified for miR-181b to promote M2 and suppress M1 polarization in atherosclerosis. The miR-181b activates KLF4 and PIAS1 SUMOylation in macrophages, leading to M1-to-M2 polarization [155]. In addition, exosomal miRNA in different *in vitro* and *in vivo* models implied M2 promotion by miR-181b. It was observed that exosomal miR-181b significantly induces the M2 phenotype, inhibits inflammation, and increases osteointegration through suppressing protein kinase C delta type (PRKCD) and activating *p*-Akt. Also, they showed that miR-181b-mediated M2 polarization indirectly promotes osteogenic migration and differentiation via secreting VEGF and bone morphogenetic protein 2 (BMP-2) [100]. In another study, Ma et al. showed miR-181b in exosomes isolated from the serum of NSCLC patients and NSCLC cells. Co-culture of macrophages with exosomal miR-181b promotes M2 polarization through the JAK2/STAT3 signaling pathway [156].

## 2.9. miR-200c

The miR-200c belongs to the miR-200 family, and this miR's aberrant expression is associated with tumor progression, metastasis, and drug resistance in various types of tumors, including lung, ovarian, and colorectal cancer [103]. Following miR-200c restoration in triple-negative breast cancer cells (TNBC), the levels of IL-10 and plasminogen activator inhibitor 2 (PAI-2) were increased, which

**Table 2**  
Summary of other miRNAs involved in macrophage polarization.

Type of miRNA	Target	Effects on M1/M2 polarization	Consequences of macrophage polarization	Ref.
miR-10a-5p	pro-inflammatory genes	M2 ↑	- Adipose tissue inflammation ↓	[168]
miR-16	IKKα/NFκB and PD-L1	M1 ↑	- Antitumor responses ↑	[169,170]
miR-16-5p	TLR4	M2 ↑	- Septic lung injuries ↓	[171]
miR-19	RORα	M1 ↑	- Lung inflammation ↑	[172]
miR-19a-3p	STAT1/IRF1	M1 ↓	- Lung inflammatory responses ↓	[165]
			-	
miR-19b-3p	PTPRD	M2 ↑	- Tumor invasion, migration, and metastasis ↑	[173]
miR-22-3p	IRF5	M2 ↑	- Tissue inflammation ↓	[174]
			- Progression of I/R injuries ↓	
miR-23	IRF1 and Pknox1	M1 ↓	- Formation and deposition of calcium oxalate crystals in the kidney ↓	[175]
miR-23a	A2	M1 ↑	- Neuropathic pains ↑	[176]
miR-24	PLCB, NFκB, CHI3L1, and MAPK	M2 ↑	- MI-associated myocardial regeneration ↑	[177,178]
miR-26	KLF4 CREB-C/EBPβ MKP1	M1 ↑	- Anti- Mycobacterium tuberculosis immunity ↑	[179,180]
miR-27a	TLR2/4 and NFκB	M2 ↑	- ALI ↓	[181,182]
			-	[58]
	PPARγ	M1 ↑	- Obesity-associated low-grade chronic inflammation and insulin resistance ↑	[58]
miR-29a-3p	SOCS1/STAT6	M2 ↑	- Carcinoma progression ↑	[183]
miR-30b-5p	UBE2D2/KAT2B	M1 ↑	-	[184]
			-	[185]
mir-30d-5p	NF-κB, COSC1, SIRT1, and NLRP3	M1 ↑	- Sepsis-related ALI-dependent inflammation ↑	
miR-32	PTEN	M2 ↑	- Glioma progression ↑	[186]
miR-101	ABCA1 MKP1/p38/JNK	M1 ↑	-	[166,187]
miR-103	STAT1/IRF1	M2 ↑	- RSA ↓	[188]
miR-106b-5p	IRF1/IFN-β	M2 ↑	- Glioblastoma progression ↑	[189]
miR-127	BCL-6 and Dusp1 phosphatase	M1 ↑	-	[190]
miR-130	PPARγ	M1 ↑	- Adipose tissue inflammation and insulin resistance ↑	[191,192]
			- 4T1 cancer cells migration and invasion ↓	
miR-132	STAT3 and NFκB Mycbp2 E3 ubiquitin ligase	M1 ↓ M2 ↑-	- Anti-inflammatory potential of alveolar macrophages ↑	[193,194]
miR-135	MAPK6	M2 ↑	- Cartilage degeneration in osteoarthritis ↓	[98]
miR-138-5p	KDM68	M2 ↑	- Lung metastasis ↓	[195]
miR-144-5p	TLR2 and OLR1	M2 ↑	- AAA ↓	[196]
miR-145-5p	IL-16	M2 ↑	- The proliferation of LPS-treated HUVEC ↓	[197,198]
miR-148-3p	PTEN/Akt SIRPα	M1 ↑	- TAM recruitment ↓	[199–201]
miR-150	STAT1	M2 ↑	- Colorectal cancer cell viability ↓	
			- VSMC proliferation and migration ↓	[202]
			- Intimal hyperplasia ↓	
miR-182-5p	TLR4 FOXO1	M2 ↑	- Myocardial injuries ↓	[203,204]
miR-188-3p	KLF2 ABCA1 RANTES OLR1	M1 ↓	- Liver regeneration ↑	
			- Intravascular lipid oxidation and accumulation ↓	[205]
miR-192-5p	EREG	M2 ↑	- Ankle joint swelling ↓	[206]
			- Synovial inflammatory cell infiltration ↓	
miR-195	CX3CL1 and CX3CR1	M2 ↑	- CBH ↓	[207]
miR-202-5p	MATN2	M2 ↑	- Allergic airway inflammation ↓	[208]
miR-205	PI3K/Akt/mTOR	M2 ↑	- Invasion, migration, and EMT of tumor cells ↑	[209]
miR-214-3p	GSK3B	M2 ↑	- Allergic nasal mucosa inflammation ↓	[210]
miR-216a	Smad3/NFκB TLR4/NFκB/PI3K/Akt	M1 ↑ M2 ↑	- Atherosclerosis progression ↑	[211,212]
			- Functional recovery in SCI ↑	
miR-217	JAK3/STAT3	M2 ↓	- Ovarian cancer progression ↓	[213]
miR-221	SOCS1, STAT3, and STAT1	M1 ↑	- Inflammation ↑	[214]
miR-222-3p	STAT3/SOCS3	M2 ↑	- Increased the tumor size, micro vessels, and lymphatic veins	[215]
miR-301a-3p	PTEN/PI3K	M2 ↑	- Pancreatic cancer metastasis ↑	[216–218]
miR-302a	METTL3/SOCS2	M1 ↑	- Development of glioma ↓	[219]
miR-330-5p	Tim-3	M2 ↑	- Insulin resistance ↓	[220]
miR-375	KLF4	M1 ↑	- Atherosclerosis progression ↑	[221,222]
miR-382-5p	CDK8 and STAT1	M2 ↑	- BPD ↓	[223]

(continued on next page)

Table 2 (continued)

Type of miRNA	Target	Effects on M1/M2 polarization	Consequences of macrophage polarization	Ref.
miR-448	TLR4	M1 ↓	- T2D development ↑	[224]
miR-471-3p	SIRT1	M1 ↑	-	[225]
miR-494	Nrdp1	M1 ↑	- Brain edema and neurologic dysfunction in ICH ↑	[226,227]
miR-494-3p	TBL1X and LRP6		- Atherosclerotic plaque formation ↑	[228]
miR-495	FTO	M1 ↑	- Insulin resistance ↑	[229]
			- Adipose tissue inflammation ↑	
miR-498	MDM2/ATF3	M1 ↑	- Esophageal cancer progression ↓	[230]
miR-505-5p	TMEM229B	M2 ↑	- AMD progression ↓	[231]
miR-506	STAT3	M1 ↑	- PDAC progression ↓	[232]
miR-520a-3p	UVRAG	M1 ↑	- Atherosclerosis progression ↑	[233]
miR-657	FAM46C	M1 ↑	- Gestation Mellitus diabetes progression	[234]
miR-720	GATA3	M1 ↑	-	[235]
miR-744-5p	TGF-β1 and MAPK	M2 ↓	- Glioma progression ↓	[236]
miR-934	PTEN/PI3K/Akt	M2 ↑	- CRLM ↑	[237]
miR-6869-5p	PTPRO	M2 ↑	- Gestation mellitus diabetes ↓	[238]

**Abbreviation** AAA, abdominal aortic aneurysm; **ABCA1**, ATP-binding cassette transporter A1; **Akt**, Ak strain transforming; **ALI**, acute lung injury; **AMD**, age-related macular degeneration; **ATF3**, activating transcription factor 3; **BPD**, bronchopulmonary dysplasia; **CBH**, chronic brain hypo perfusion; **CDK**, cyclin-dependent kinase; **CREB-C/EBPβ**, cyclic-AMP-response element-binding protein-CCAAT/enhancer-binding protein-beta; **CRLM**, colorectal cancer liver metastasis; **EMT**, epithelial-mesenchymal transition; **EREG**, ephregulin; **FTO**, Fat mass and obesity associated; **FOXO1**, forkhead box transcription factor 1; **GSK3B**, glycogen synthase kinase 3 beta; **HUVEC**, human umbilical vein epithelial cell; **I/R**, ischemia/reperfusion; **ICH**, intracerebral hemorrhagic; **IFN**, interferon; **IL**, interleukin; **IRF**, interferon regulatory factor; **JAK**, Janus kinase; **KLF**, Kruppel-like factor; **LPS**, lipopolysaccharide; **LRP6**, low-density lipoprotein receptor-related protein 6; **MATN2**, matrilin-2; **MAPK**, mitogen-activated protein kinase; **MDM2**, murine double minute 2; **METTL3**, methyltransferase-like 3; **MI**, myocardial infarction; **miR**, microRNA; **MKP1**, mitogen-activated protein kinase phosphatase 1; **NF-κB**, nuclear factor-kappa B; **NLRP3**, NOD-like receptor P3; **OLR1**, ox-LDL receptor 1; **PDAC**, pancreatic ductal adenocarcinoma; **PI3K**, phosphoinositide 3-kinase; **Pknox1**, PBX/Knotted 1 Homeobox 1; **PLCB3**, 1-phosphatidylinositol-4, 5-bisphosphate phosphodiesterase beta-3; **PPAR**, peroxisome proliferator-activated receptor; **PTPRD**, protein tyrosine phosphatase receptor type D; **PTPRO**, protein tyrosine phosphatase receptor type O; **PTEN**, phosphatase and TENsin homolog deleted on chromosome 10; **RANTES**, Regulated on Activation, Normal T Expressed and Secreted; **RSA**, recurrent spontaneous abortion; **SCI**, spinal cord injury; **SIRPα**, signal-regulatory protein alpha; **SIRT1**, sirtuin1; **SOCS**, suppressor of cytokine signaling; **STAT**, signal transducer and activator of transcription; **T2D**, type-2 diabetes; **TAM**, tumor-associated macrophage; **TBL1X**, transducing (beta)-like 1X-linked; **TGF-β**, transforming growth factor-beta; **TLR**, toll-like receptor; **TMEM229B**, protein transmembrane 229B; **UVRAG**, UV radiation resistance-associated gene protein; **VSMC**, vascular smooth muscle cell.

promoted tumor-associated macrophages (TAM) to an M2-like phenotype that led to the malignant progression of the tumor [101]. Also, Xiong et al. reported that miR-200c was overexpressed in exosomes isolated from the serum of ovarian cancer patients. In this case, miR-200c induces M2 macrophage polarization by targeting KLF6 and promotes tumor cell proliferation and invasion [102].

On the other hand, the antitumor potential of miR-200c via suppressing the M1-to-M2 shift was observed in different studies [157]. William et al. showed that miR-200c significantly suppressed the proliferation of mouse mammary epithelial tumor cell-1 (MET-1) *in vivo*. In this case, overexpressed miR-200c enhanced GM-CSF expression and induced antitumor M1 macrophage polarization, regulating EMT toward epithelial signatures and prognosis for better survival in breast cancer patients [104]. In addition, Raue et al. reported that miR-200c overexpression reduced the expression of migration-associated miRNAs and inhibited the tumor infiltration potential of macrophages [103].

The miR-223 expression is associated with the M2 phenotype, and miRNA downregulation promotes LPS-induced IL-1β and IL-6 release [105]. The miR-223 overexpression in RAW264.7 macrophages suppresses LPS-induced IL-6 and IL-1β secretion through targeting STAT3 [106]. PPARγ is a crucial regulator of macrophage activation that induces miR-223 expression following IL-4 and IL-13 stimulation of murine macrophages. Consistent with these results, miR-223 ablation in the murine model inactivated PPARγ-regulated anti-inflammatory responses in macrophages [158]. In addition to alternative phenotype promotion, miR-223 suppresses pro-inflammatory polarization by suppressing the NFκB/JNK axis by inhibiting PBX/Knotted 1 Homeobox 1 (Pknox1) [109]. The miR-223 suppresses M1 macrophage polarization by targeting Pknox1 and protects against inflammation and coxsackievirus B3 (CVB3)-induced injuries [110]. The miR-223 is widely expressed in bone marrow and adipose-isolated macrophages and is crucial in regulating adipose tissue inflammation. Dramatic miR-223 overexpression was observed in IL-4-treated BMDMs, while LPS stimulation poorly decreased miRNA expression. In addition, miR-223<sup>-/-</sup> macrophages showed an increased response to LPS, and PPARγ and Arg-1 expression was significantly reduced. MiR-223 deficiency promotes inflammatory responses and downregulates insulin signaling in the adipose tissue of fat-diet mice. It leads to deregulated adipokine expression [109]. The hypoxia-induced factor-1 alpha (HIF-1α) and C/EBPβ are other identified targets for miR-223. Dang et al. reported that miR-223 interferes with glycolysis pathways by targeting HIF-1α and induces anti-inflammatory responses due to suppressed M1 macrophage polarization [107]. Also, it was shown that miR-223-mediated C/EBPβ suppression inhibits inflammatory macrophage differentiation from human circulatory monocytes and THP-1 cells [108].

## 2.10. miR-511

In humans and mice, miR-511-3p expressed by the fifth intron of the mannose receptor C-type 1 (MRC1) gene encoding CD206 and transcriptionally co-regulated by MRC1 is involved in macrophage activation [159,160]. Recent studies have implied that miR-511-3p controls macrophage-mediated antimicrobial responses and increases intestinal inflammation [161]. Also, miR-511-3p overexpression using miRNA mimics inhibits M1 macrophage polarization and promotes the M2 phenotype through interacting prostaglandin D2 synthase (PTGDS) [113]. Although, CCL2, latent transforming growth factor  $\beta$  binding protein 1 (LTBP1), and Rho-associated coiled-coil containing protein kinase 2 (ROCK2) are direct targets, TLR4 and C/EBP $\alpha$  are indirect targets of miR-511-3p [112]. Squadrito et al. reported robust and bioactive expression of miR-511-3p in alternative macrophages. In addition, miRNA overexpression widely and precisely tunes down the expression of alternative-associated genes [159]. The miR-511-3p directly and selectively targets ROCK2 serine-threonine kinase [111] and phosphorylates IRF4 as an M2 macrophage inducer [162,163]. Unexpectedly, enforced miR-511-3p activity in TAMs ameliorates pro-tumor genetic programs in MRC1+ TAMs and inhibits blood vessel formation and tumor progression [159]. These results suggest that, although promoting alternative macrophages, miR-511-3p could reprogram the pro-tumor phenotype to the anti-tumor subset. Also, Karo-Atar and colleagues demonstrated that miR-511 expression was increased following IL-4 and IL-13 stimulation in both *in vitro* and *in vivo* mouse models of respiratory allergic disease. In addition, global transcriptome analysis following miR-511 overexpression suggested that this miRNA modulates various activities of alternative macrophages, such as cellular proliferation, metabolism, and immune responses [164].

## 2.11. Let-7 family

The Let-7 family was among the first identified tumor-suppressive miRNAs, including 12 highly-conserved genes that encode nine different miRNAs, including Let-7a-i and miR-98 [165]. Banerjee et al. observed higher levels of Let-7c in alternative BMDMs and alveolar macrophages than in classic phenotypes. In addition, Let-7c mimics transfection into BMDMs, significantly reduces classic hallmarks, and decreases bactericidal activities while promoting alternative polarization and potential apoptotic cell engulfment. Also, Let-7c siRNA induces M1 polarization in BMDMs. The mechanistic analysis identified C/EBP $\delta$  as the direct target of Let-7c [114]. Further investigations highlighted the critical role of Let-7c in regulating macrophage polarization. Zhang et al. showed that epigenetic loss of Let-7c upregulates EZH2-induced PAK1 expression and promotes pro-inflammatory polarization [166]. Another study showed that Let-7e upregulates in LPS-stimulated macrophages and overexpresses Let-7e in Akt1 $-/-$  macrophages, which influences sensitivity and tolerance to LPS through targeting TLR4 [130]. Kumar et al. observed that Let-7f downregulation suppressed inflammatory responses by directly targeting A20 in macrophages involved in Mycobacterium tuberculosis infection, while overexpression of Let-7f significantly increased TNF- $\alpha$  and IL-1 $\beta$  production by inflammatory polarized macrophages [115]. The miR-98 downregulation following LPS treatment intensifies TLR4-triggered IL-10 production, while miR-98 overexpression reverses these effects. Hence, it seems that miR 98 controls pro-inflammatory immune responses [116]. Li et al. reported that miR-98 induces M2-to-M1 polarization and inhibits tumor invasion and TAM-induced EMT in hepatocellular carcinoma [116]. Also, Peng et al. reported that miR-98-5p knockout increases tribbles homolog 1 (Trib1) expression and induces M2 polarization, which relieves symptoms in the murine model of IBD [167].

## 2.12. Other miRNAs

Multiple lines of evidence indicated the role of other miRNAs in regulating macrophage polarization through limited studies that are summarized in Table 2.

## 3. Concluding remarks and future prospective

The miRNAs epigenetically regulate hundreds of genes involved in various physiological and pathological processes. The role of miRNAs in macrophage polarization has attracted much attention. Recent studies proved that over 60 miRNAs influence multiple adaptor proteins and transcription factors to regulate macrophage polarization. Hence, alterations in miRNA expression could affect M1 and M2 phenotype switching. Applying specific miRNA mimics or antagomirs could control the immune response and inflammation by regulating macrophage polarization under different physiological and pathological conditions. For example, antagomirs inhibiting pro-inflammatory miRNA promote M2 macrophage polarization, limiting inflammation and related injuries. On the other hand, M1-associated miRNA overexpression could effectively enhance antitumor immune responses and limit tumor proliferation, invasion, and metastasis. In this case, various studies implicated miRNAs in human clinical trials. A liposomal miR-34a mimic called MRX34 was administered on advanced solid tumor patients in phase I clinical trial [239]; an anti-miR-17 oligonucleotide called RGLS4326 was applied for polycystic kidney disease [240]; an anti-miR-12 called Miravirsen was used for hepatitis C virus (HCV) infection [241]; and for cardiovascular disease and wound healing, MRG-110, an anti-miR92a, was administered [242]. Unlike single-gene therapy, miRNAs are considered more effective and suitable therapeutic approaches. In this case, each miRNA could target multiple genes involved in macrophage polarization. Also, each gene could be targeted by multiple miRNAs. Hence, implicating miRNA mimics or targeting miRNAs using antagomirs holds promise for therapeutic approaches through regulating macrophage polarization. The other importance of miRNA-macrophage interactions is their biomarker potential. For example, monitoring the macrophage polarization status in *in vivo* disease conditions or even *in vitro* models could be served by miRNA potential. In addition, the development of technologies associated with miRNA modification and delivery systems is potential approach that could provide

insights into the dynamic changes in macrophage polarization through miRNA regulation in deregulated conditions and also helps translate the primary findings into clinical applications.

Finally, identifying the exact mechanism of miRNA-macrophage polarization interaction seems necessary. Much more research should be conducted to overcome limitations in miRNA-based therapeutic approaches.

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No data was used for the research described in the article.

## CRediT authorship contribution statement

**Shaho Khayati:** Conceptualization, Writing – original draft. **Sajad Dehnavi:** Conceptualization, Writing – original draft, Writing – review & editing. **Mahvash Sadeghi:** Writing – original draft, Writing – review & editing. **Jalil Tavakol Afshari:** Writing – review & editing. **Seyed-Alireza Esmaeili:** Writing – original draft. **Mojgan Mohammadi:** Conceptualization, Writing – original draft, Writing – review & editing.

## Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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