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## Retinoic acid and microRNA

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### Abstract

Retinoic acid (RA), the biologically active metabolite of vitamin A, regulates a vast spectrum of biological processes, such as cell differentiation, proliferation, apoptosis, and morphogenesis. microRNAs (miRNAs) play a crucial role in regulating gene expression by binding to messenger RNA (mRNA) which leads to mRNA degradation and/or translational repression. Like RA, miRNAs regulate multiple biological processes, including proliferation, differentiation, apoptosis, neurogenesis, tumorigenesis, and immunity. In fact, RA regulates the expression of many miRNAs to exert its biological functions. miRNA and RA regulatory networks have been studied in recent years. In this manuscript, we summarize literature that highlights the impact of miRNAs in RA-regulated molecular networks included in the PubMed.

### 1. Introduction

Retinoic acid (RA) is a metabolite of vitamin A that has a vast spectrum of biological processes, including differentiation, proliferation, apoptosis, and morphogenesis (Hu, Xu, Sun, Teng, & Xiao, 2017; Wang et al., 2012). While all-*trans*-RA is a major form, other isomers such as 13-*cis*-RA and 9-*cis*-RA are also present (Ruhl, Krezel, & de Lera, 2018; Tang & Russell, 1990). In this paper, RA is used to refer to all-*trans*-RA. Pharmacologically, retinoids including RA are used for acne and cancer treatment (Dobrotkova, Chlapek, Mazanek, Sterba, & Veselska, 2018; Leyden, Stein-Gold, & Weiss, 2017). Its effects in treating inflammation, allergy, and autoimmune diseases have also been revealed (Oliveira, Teixeira, & Sato, 2018).

The action of RA is mediated through the nuclear receptors: retinoic acid receptor (RAR $\alpha$ ,  $\beta$ , and  $\gamma$ ) and retinoid x receptors (RXR $\alpha$ ,  $\beta$ , and  $\gamma$ ). Because RXR is an essential partner of many nuclear receptors, RA can regulate the function of other nuclear receptors such as peroxisome proliferator activate receptor and farnesoid x receptor. This allows RA to regulate lipid metabolism (Bushue & Wan, 2010; Chen, Wang, & Wan, 2010; Dai et al., 2003; Goto, 2019; Gyamfi, He, French, Damjanov, & Wan, 2008; Hu et al., 2017; Krezel, Ruhl, & de Lera, 2019; Liu, Wang, & Lin, 2019; Martin, Ma, & Bernard, 2019; Ruhl et al., 2018; Wan et al., 2000, 2000, 2003; Watanabe & Kakuta, 2018). Many RAR and RXR-regulated genes have been identified using genome-wide approaches such as chromatin immunoprecipitation followed by sequencing (Al Tanoury et al., 2014; Fang et al., 2013; He

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et al., 2013; Hu et al., 2013; Hua, Kittler, & White, 2009; Kiss et al., 2017; Liu, Ly, Hu, & Wan, 2014; Penrose, Keenan, Bray, Ramlall, & Siggers, 2019; Tang et al., 2011). In addition to transcriptional regulation, oral administration of RA alters gut microbiota and has an impact on liver regeneration (Liu, Hu, & Wan, 2016). Thus, it is important to understand mechanisms by which RA exerts its effects.

miRNA is small non-coding RNA that silences messenger RNA (mRNA). Its functions via base-pairing with complementary sequences within mRNA. As a result, the targeted mRNA is reduced by either cleavage or destabilization, or has its translational efficiency reduced (Fig. 1). miRNAs regulate the expression of as much as one-third of human gene-encoded proteins (Ganapathy & Ezekiel, 2019). Like RA, miRNAs regulate multiple biological and disease processes (Ganapathy & Ezekiel, 2019; Ivey & Srivastava, 2015). miRNAs have been approved by the FDA as diagnostic tools and for treatment (Dave et al., 2019). This review paper focuses on the miRNAs that mediate or affect the effects of RA. In some cases, RA regulates the expression of miRNA through its receptors such as RAR $\alpha$  and RAR $\beta$ , which bind to the regulatory region of certain miRNAs to alter their expression levels. In other cases, miRNA may target the receptors of RA and affect the effect of RA (Fig. 2). The literature search was limited to the papers included in the PubMed using mammalian cells or animal models.

## 2. miRNAs that are implicated in RA-induced differentiation

### 2.1 Embryonic stem cell differentiation

Dicer is an endoribonuclease that cleaves double stranded RNA critical for miRNA biogenesis. In Dicer-deficient embryonic stem cells, increased dimethylation of histone H3 at lysine 9 (H3K9me2) at over 900 CpG islands has been noted, indicating the significance of miRNAs in epigenome regulation during differentiation. Additionally, the balance between the transcriptionally favorable tri-methylation histone H3 at lysine 4 (H3K4me3) and the unfavorable tri-methylation histone H3 at lysine 27 (H3K27me3) is shifted in the Dicer-deficient epigenome. Homeobox (HOX) transcription factors play pivotal roles in many aspects of cellular physiology, embryonic development, and tissue homeostasis. In response to RA treatment, elevated H3K27me3 is found in the promoters of the caudal type homeobox 2 (*Cdx2*) and homeobox A1 (*Hoxa1*) genes of Dicer-deficient embryonic stem cells. However, forced expression of *let-7g* in Dicer-deficient embryonic cells counteracts the effect of H3K27me3 on the expression of the *Cdx2* and *Hoxa1* genes. *Let-7g* counteracts the effects by reducing the enhancer of zeste homolog 2 (*Ezh2*), a histone-lysine *N*-methyltransferase enzyme, which thereby leads to the differentiated phenotype (Tennakoon, Wang, Coarfa, Cooney, & Gunaratne, 2013).

miRNAs inhibit mouse embryonic stem cell self-renewal and stabilize their differentiated states. In mouse embryonic stem cells, RA upregulates *miRNA-134*, *miR-296*, and *miR-470*, which induces differentiation by targeting the pluripotency genes *Nanog*, octamer-binding transcription factor 4 (*Oct4*), and sex determining region Y-box 2 (*Sox2*) (Tay et al., 2008; Tay, Zhang, Thomson, Lim, & Rigoutsos, 2008). *miRNA-134* inhibits *Nanog* and the liver receptor homolog 1 (*LRHI*), both of which positively regulate *Oct4* (Tay, Tam, et al., 2008). In addition, *miR-134*, *miR-296*, and *miR-470* are all involved in the lineage specific

repression of mouse embryonic stem cell renewal (Zhang et al., 2015). Elevated forkhead box protein M1 (FOXO1) contributes to the maintenance of human stem cell pluripotency by directly regulating the *Oct4* promoter. *miR-134* over-expression reduces FOXO1 and promotes the differentiation effect of RA (Chen et al., 2015). Additionally, by reducing either *miR-200b* or *miR-200c*, RA inhibits the expression of pluripotency genes and increases the ectodermal marker *Nestin*, a type VI intermediate filament protein (Zhang, Gao, et al., 2015).

## 2.2 Neuronal differentiation

The significance of *miR-10* in neuronal differentiation has been revealed. The *hsa-miR-10* family is substantially increased (~95-fold) during the RA-induced neuronal differentiation of human embryonic stem cells (Parsons, 2012). In addition, during RA-induced neural lineage specific progression, *hsa-miR-302* family is reduced and the expression of the *Hox* gene, *hsa-miR-10*, and *let-7* are induced (Parsons, Parsons, & Moore, 2012). Similarly, the expression of *Hoxd4* and *miR-10b* is coordinated in the RA-induced neural differentiation of P19 cells. This suggests the importance of *miR-10b* (Phua et al., 2011). Through the *let-7*-dependent mechanism, phosphorylation of a highly conserved RNA-binding protein called LIN28A fosters neural differentiation of P19 cells (Liu et al., 2017). Moreover, the differentiation of embryonic stem cells is also accompanied with increased *miR-10a-5p*, *miR-219-5p*, and *miR-219-2-3p*. The increase of *miR-219* and its mimics also promote mouse embryonic stem cell differentiation into neural cells (Wu et al., 2017). In contrast, *miR-125b-2* over-expression suppresses this differentiation (Deng, Zhang, Xu, & Ma, 2015).

Sirtuin 1 (SIRT1) plays a negative role in inducing the differentiation of induced pluripotent stem cells (iPSCs) into neural stem cells. When SIRT1 is inhibited, the differentiation continues and is marked by increased *miR-34a*, which silences *SIRT1* (Hu et al., 2014). In mouse neuroblastoma N2a cells, P19 embryonal carcinoma cells, and the mouse brain, increased *miR-124* reduces RAR $\gamma$ , thereby inhibiting neurite outgrowth (Wang, Yao, Lu, Li, & Ma, 2010) (Su, Gu, Zhang, Li, & Wang, 2020). There are many other miRNAs that may be implicated in neural cell differentiation (Hu et al., 2017). RA treatment of adipose-derived mesenchymal stem cells leads to changes in 76 miRNAs that have a greater than twofold difference (Hu et al., 2017).

## 2.3 Spermatogonia differentiation

Tyrosine-protein kinase Kit, a receptor tyrosine kinase protein, plays an essential role in cell proliferation, hematopoiesis, etc. The tyrosine-kinase receptor Kit is also essential for the maintenance of primordial germ cells in both sexes, and RA-induced differentiation of spermatogonia is accompanied by Kit induction. Recent data reveals that RA-induced *miR-26b* promotes the transition from Kit-negative to Kit-positive spermatogonia (Tu et al., 2018). *miR-26b* can silence a transcriptional factor named promyelocytic leukemia zinc finger protein (*Plzf*) in undifferentiated spermatogonia. It also downregulates the methylcytosine dioxygenase (*Tet3*) gene, thus reducing 5-hydroxymethylcytosine in spermatogonia. Together, through various mechanisms including epigenetic regulation, RA regulates spermatogonia differentiation (Tu et al., 2018).

While glial cell-derived neurotrophic factor (GDNF) is essential for the self-renewal of spermatogonia stem cells, RA is critical for the differentiation of spermatogonia. *miR-202-3p*, which is abundantly found in the testis, can be induced by GDNF but is reduced by RA. *miR-202-3p* prevents stem cells from premature differentiation by suppressing RNA binding fox-1 homolog 2 (*Rbfox2*). In addition, the inhibition of *miR-202-3p*, but not of *miR-202-5p*, induces the differentiation of spermatogonia stem cells (Chen et al., 2017).

RA-induced differentiation of spermatogonia has reduced *miR-146*, which targets the mediator complex subunit 1 (*Med1*), a co-activator of RARs and RXRs. *miR-146* can also inhibit the expression of stimulated by retinoic acid 8 (*Stra8*) and the spermatogenesis- and oogenesis-specific basic helix-loop-helix 2 (*Sohlh2*) (Huszar & Payne, 2013). Thus, RA-reduced *miR-146* is critically important for RA-induced differentiation of spermatogonia. In addition, RA also reduces *miR-17-92* (*Mirc1*) and *miR-106b-25* (*Mirc3*), both of which function cooperatively to promote mouse spermatogonia differentiation (Tong, Mitchell, McGowan, Evanoff, & Griswold, 2012).

#### 2.4 Pre-adipocytes and myoblast differentiation

RA inhibits the differentiation of 3T3-L1 pre-adipocytes by reducing lipid metabolism (Stoecker, Sass, Theis, Hauner, & Pfaffl, 2017). Such an action is through *miR-27a* and *miR-96* induction that leads to the rearrangement of the actin cytoskeleton as well as inhibition of the citric acid cycle (Stoecker et al., 2017).

Excess RA also inhibits myoblast differentiation and proliferation. In an embryonic tongue-derived myoblast C2C12 cell line, RA induce *miR-27b-3p*, which silences the  $\alpha$ -dystrobrevin (*DTNA*) gene to inhibit proliferation and differentiation (Li et al., 2017). In addition, RA-induced *miR-31-5p* targets the  $Ca^{2+}$ /calmodulin-dependent protein kinase II  $\delta$  gene (*CankII $\delta$* ) and is implicated in the RA-induced myogenic abnormalities of tongue (Liu et al., 2017). *miR-133a*, *210*, and *34a* are also involved in the RA-induced myoblasts differentiation and proliferation (Vecellio et al., 2012).

*miR-10a* targets the histone deacetylase 4 (*Hdac4*) gene and has a critical role in the RA-induced differentiation of mouse embryonic stem cells into smooth muscle cells (Huang et al., 2010). In addition, nuclear factor kappa B (NF $\kappa$ B), through binding to the *miR-10a* promoter, has a significant role in the differentiation process. Inhibiting the nuclear translocation of NF $\kappa$ B reduces *miR-10a* and prevents the RA-induced differentiation smooth muscle cells (Huang et al., 2010).

#### 2.5 Hematopoietic progenitor cell differentiation

RA induces *miR-223*, which acts as a translational inhibitor to regulate lineage specification and differentiation of mouse hematopoietic stem cells (Chen, Li, Lodish, & Bartel, 2004). Transcription factors nuclear factor I-A (NFI-A) and CCAAT/enhancer-binding protein-alpha (C/EBP $\alpha$ ) compete for binding to the *miR-223* promoter. In response to RA treatment, the induction of *miR-223* requires the release of NFI-A and the binding of C/EBP $\alpha$ . Taken together, the RA regulated differentiation of granulocytes is mediated by *miR-223* expression controlled by two transcriptional factors (Fazi et al., 2005).

### 3. miRNAs that are implicated in RA-regulated inflammatory signaling and immunity

Signal-regulatory protein  $\alpha$  (SIRP $\alpha$ ) is essential for modulating leukocyte inflammatory responses. The *SIRP $\alpha$*  gene is commonly targeted by *miR-17*, *miR-20a*, and *miR-106a*. RA reduces these miRNAs and increases *SIRP $\alpha$*  expression in SIRP $\alpha$ -negative promyelocytic cells. However, bacterial lipopolysaccharides (LPS) increases *miR-17*, *miR-20a*, and *miR-106a* in macrophages, which leads to SIRP $\alpha$  reduction and macrophage activation. Thus, *miR-17*, *miR-20a*, and *miR-106a* regulate macrophage inflammatory responses by repressing SIRP $\alpha$ . (Zhu et al., 2013).

RA-induced *miR-10a* is abundantly found in naturally occurring regulatory T cells (Treg). *miR-10a* inhibits the development of inducible T regulatory cells (iTregs) into follicular helper T cells by suppressing both the transcriptional repressor B-cell lymphoma 6 (*Bcl6*) and the co-repressor nuclear receptor co-repressor 2 (*Ncor2*). In addition, *miR-10a* attenuates the differentiation process into the T(H)17 subset of helper T cells (Takahashi et al., 2012). In contrast to RA, transforming growth factor- $\beta$  (TGF- $\beta$ )-induced iTregs in vitro are unstable and do not have *miR-10a*. Thus, RA-induced *miR-10a* is selectively expressed and plays a role in stabilizing iTregs (Jeker et al., 2012).

T-cell receptor (TCR) signaling and TGF- $\beta$  regulate the production of peripheral regulatory T (pTreg) cell. The expression of *miR-31* is triggered by TCR signaling but inhibited by TGF- $\beta$ . *miR-31* directly targets the retinoic acid-inducible protein 3 (*Gprc5a*), a member of the type 3G protein-coupled receptor family. The deficiency of this protein leads to the impairment of pTreg-cell induction as well as an increased severity of experimental autoimmune encephalomyelitis (Zhang et al., 2015). Therefore, by targeting *Gprc5a*, *miR-31* reduces the production of pTreg (Zhang, Ke, et al., 2015).

RA induces the secretion of exosomes in gut-tropic T cells that causes an upregulation of integrin  $\alpha 4\beta 7$  that binds to mucosal vascular addressin cell adhesion molecule 1 (MAdCAM-1). Addressins are the ligands to the homing receptors of lymphocytes, which determine which tissue the lymphocyte will enter. miRNA profiling suggests that exosomes that originate from the gut tropic T cells contain a large quantity of miRNAs, such as *miR-132* and *miR212*, which target NKX2.3, a transcription factor important for the expression of MAdCAM-1 (Park et al., 2019).

Metabolism controls immune cell fate and function. *miR-33* not only represses genes involved in cholesterol efflux and fatty acid oxidation, but also polarization of immune cells. Macrophage-specific *miR-33* deletion promotes M2 macrophage polarization. Interestingly, inhibiting *miR-33* enhances the expression of RA-producing enzyme aldehyde dehydrogenase family 1, subfamily A2 (ALDH1A2), as well as the activity of retinal dehydrogenase in macrophages. Such findings are in consistent with the ability of RA to foster iTregs. Furthermore, treating hypercholesterolemic mice with *miR-33* inhibitors leads to accumulation of inflammation-suppressing M2 macrophages and forkhead box P3<sup>+</sup> (foxp3<sup>+</sup>) Tregs in plaques. This treatment thereby inhibits the progression of atherosclerosis. Together, inhibiting *miR-33* benefits metabolism and inflammation (Ouimet et al., 2015).

## 4. miRNAs that are implicated in RA-induced differentiation of cancer cells

### 4.1 Embryonic carcinoma

RA has a profound effect in inducing the differentiation of embryonic carcinoma F9 cells into endodermal cells (Wan, Orrison, Lieberman, Lazarovici, & Ozato, 1987; Wan, Wang, & Wu, 1994; Wu, Wang, & Wan, 1992). In the F9 cell line, RA induces *miR-485*, which silences the  $\alpha/\beta$ -hydrolase domain-containing protein 2 (*Abhd2*). The reduction of *Abhd2* leads to ERK1/2 phosphorylation and differentiation of embryonic carcinoma cells (Yu, Zhang, Liu, Liu, & Guo, 2019).

### 4.2 Brain tumors

RA treatment enhances gap junctions which leads to an increased *miR-124-3p*-mediated antiproliferation in glioblastoma cells (Suzhi et al., 2015). RA also induces glioma cell death by elevating *miR-302b*, and silences E2F3, a transcriptional glioma growth regulator (Chen et al., 2014). In addition, reduced *miR-452* found in gliomas promotes their stem-like features and tumorigenesis because *miR-452* inhibits many stemness regulators like polycomb complex protein BMI-1, lymphoid enhancer binding factor 1 (LEF1), and transcription factor 4 (TCF4), (Liu et al., 2013).

### 4.3 Neuroblastoma

Several miRNAs have changes in their expression levels when the human neuroblastoma cell line SH-SY5Y is treated with RA and a dopamine cocktail (Das & Bhattacharyya, 2014). Among them, *miR-432* plays a key role in differentiation of human neuroblastoma cells by suppressing *NESTIN* and the repressor element-1-silencing transcription factor (REST) corepressor 1 (*RCOR1*) (Das & Bhattacharyya, 2014). RA induces neuronal differentiation via *miR-29b* and *miR-664a-5p* (Jauhari, Singh, & Yadav, 2018; Watanabe, Yamaji, & Ohtsuki, 2018). *miR-29b* reduces the P53 inhibitor P85 $\alpha$ , which in turns increases *miR-145* to silence OCT4, SOX2, and kruppel-like factor 4 (KLF4) during SH-SY5Y differentiation (Jauhari et al., 2018). Further studies are required to understand the function of *miR-664a-5p* (Watanabe et al., 2018).

RA has anti-metastatic and anti-migratory activities via *miR-10a* and *miR-10b*, both of which target the SR-family splicing factor SFRS1 (*SF2/ASF*) (Meseguer, Mudduluru, Escamilla, Allgayer, & Baretino, 2011). They also induce neuronal differentiation by silencing *NCOR2* which inhibits neurite growth (Foley et al., 2011). Moreover, other RA-induced miRNAs, including *miR-9* and *miR-103*, control neuroblastoma differentiation by reducing a differentiation inhibitor molecule called Inhibitor of DNA-binding 2 (Id2) (Annibali et al., 2012). RA can also decrease *miR-17* in SH-SY5Y cells. *miR-17* is involved in the regulation of the mitogen-activated protein kinase (MAPK) signaling pathway, synaptic plasticity, and other markers of neuronal differentiation (Beveridge, Tooney, Carroll, Tran, & Cairns, 2009). RA- and brain-derived neurotrophic factor (BDNF)-induced *miR-125b* and *miR-124a* also positively regulate the differentiation of SH-SY5Y cells and

neurite outgrowth of human neural progenitor ReNcell VM cells by targeting multiple genes (Le et al., 2009).

The mutant amyloid precursor protein (APP)<sub>L17C</sub> [the leucine (L) residue 17 is replaced by a cysteine (C) residue in amyloid  $\beta$  peptide (A $\beta$ )] increases amyloid precursor protein dimerization which leads to reduced neurite outgrowth. The overexpression of a mutant amyloid precursor protein (APP)<sub>L17C</sub> in human neuroblastoma SH-SY5Y cells inhibits neurite outgrowth (Luu et al., 2019). *miR-34a* expression is greatly decreased in APP<sub>L17C</sub> compared to APP<sub>WT</sub> cells, and overexpression of *miR-34a* restores neurite outgrowth in the mutant cells (Luu et al., 2019). Thus, *miR-34a* expression has a pivotal role in APP-mediated neurite outgrowth (Luu et al., 2019).

DNA demethylation mediated by miRNAs promotes RA-induced differentiation of neuroblastoma cells. The ectopic overexpression of *miR-152* that targets the DNA methyltransferase 1 (*DNMT1*), contributes to the differentiated phenotypes, including reduced invasiveness and anchorage-independent growth in a human neuroblastoma cell line SK-N-BE (Das et al., 2010).

Other miRNAs are implicated in the differentiation of neuroblastoma cells. During the differentiation of NT2 cells, the stemness phenotype-associated *miR-302* is reduced, but *let-7*, *miR-125b*, and *miR-132* are increased (Pallocca et al., 2013). *miR-128* is also increased that in turn reduces Reelin and Doublecortin, where both are involved in the migratory potential of neural cells (Evangelisti et al., 2009). Moreover, during the RA-induced differentiation of neuroblastoma BE (2)-C cells, tumor suppressor *miR-449a* is increased. *miR-449a* targets the microfibril associated protein 4 (*MFAP4*), plakophilin 4 (*PKP4*), and TRNA splicing endonuclease subunit 15 (*TSEN15*), which are associated with poor survival of neuroblastoma patients (Zhao et al., 2015). Moreover, *miR-449a* induces cell cycle arrest by inhibiting the cyclin dependent kinase 6 (*CDK6*) and lymphoid enhancer binding factor 1 (*LEF1*) (Zhao et al., 2015).

RA-induced differentiation of the human neuroblastoma SK-N-BE cells have overexpressed *miR-34a* that directly targets the *E2F3* and lowers its protein. E2F3 is a potent transcriptional inducer for cell-cycle progression. In addition, overexpression of *miR-34a* in neuroblastoma cell lines prevents cell proliferation by inducing the caspase-dependent apoptotic pathway. Furthermore, *miR-34a* is reduced in primary neuroblastoma tumors and cell lines when compared to normal adrenal tissue (Welch, Chen, & Stallings, 2007). *miR-184* is also implicated in the apoptosis pathway as RA-induced *miR-184* promotes the apoptosis of human neuroblastoma cell lines including KELLY or SK-N-AS (Chen & Stallings, 2007).

#### 4.4 Hematopoietic malignancies

Acute promyelocytic leukemia (APL) is caused by translocation of the promyelocytic leukemia (*PML*) gene located on chromosome 15 and the *RAR $\alpha$*  gene on chromosome 17, which generates a fusion oncogene *PML/RAR $\alpha$*  and differentiation arrest.

In hematopoietic malignancies, high c-Myc expression is correlated with a poor prognosis (Delgado & Leon, 2010). It has been shown that reduced PML/RAR $\alpha$  due to loss of c-Myc is miRNA-dependent. In addition, tumor suppressor *let-7* has been identified to target both the *c-Myc* and the PML/RAR $\alpha$  (Ding et al., 2016). Moreover, PML/RAR $\alpha$  binds to the RA responsive element of the host genes such as the *let-7c* (Careccia et al., 2009; Pelosi et al., 2014). However, RA treatment induces a conformational change in the host promoter thus regulating *let-7c* (Pelosi et al., 2014). Taken together, RA by inducing *let-7c*, which silences PML/RAR $\alpha$ , can lead to the differentiation of APL (Ding et al., 2016).

The synergism between c-Myc and *miR-17-19b*, a truncated version of the *miR-17-92* cluster, is well-established for tumor initiation (He et al., 2005; Mu et al., 2009). RA not only reduces *c-Myc* mRNA but also *miR-17-92* to induce APL cell differentiation (Yu et al., 2019). In the APL NB4 cell line, RA induces *miR-10b*, *miR-194*, *miR-195*, *miR-196a*, and others. Many of them are transcriptionally silenced by PML/RAR $\alpha$  which leads to oncogenesis (Saumet et al., 2009). To add on, a long non-coding RNA named *HOTAIRM1* increases the RA-induced degradation of PML/RAR $\alpha$  via the autophagy pathway. In fact, *HOTAIRM1* can function as a miRNA sponge to regulate the expression of autophagy-related genes by competing for miRNA bindings sites (Chen et al., 2017).

Other mechanisms are involved in RA-mediated differentiation of APL. Knockdown adenylate cyclase 9 (*ADCY9*), which converts ATP into cAMP, inhibits RA-induced differentiation of APL. Similarly, *miR-181a*, which directly targets *ADCY9* and reduces cAMP, has a negative role in RA-induced APL differentiation (Zhuang et al., 2014). *miR-17-5p* also inhibits RA-induced APL cell differentiation (Yu, Hu, et al., 2019). In contrast, RA induces granulocytic differentiation through *miR-382-5p* that silences the suppressor gene phosphatase and tensin homolog (*PTEN*) (Liu et al., 2019).

By regulating miRNA, RA treats APL (van Gils, Verhagen, & Smit, 2017). RA treatment causes a loss of imprinting on chromosome 14q32 that regulates the overexpression of many miRNAs (Manodoro et al., 2014). RA treatment of APL cells increases many tumor suppressor miRNAs, such as the *let-7* family (Garzon et al., 2007; van Gils et al., 2017). RA treatment of APL cells also increases *miR-107*, which silences the *NFI-A* (Fazi et al., 2005) (Garzon et al., 2007). RA also reduces many miRNAs such as *miR-17* and *miR-25* in APL cells (Garzon et al., 2007; Rossi et al., 2010). Moreover, by reducing *miR-301a-3p* to increase ubiquitin-specific protease 48 (USP48), RA is effective in APL differentiation (Li et al., 2018).

RA increases *miR-145* in myeloid leukemia cells which thereby reduces RAS-responsive element-binding protein 1 (RREB1), which prevents granulocytic differentiation of myeloid leukemia cells (Yao et al., 2019). In addition, *miR-29a*, which targets the *CDK6*, and *miR-142-3p*, which silences the TGF- $\beta$ -activated kinase 1/MAP3K7 binding protein 2 (*TAB2*), contributes to RA-induced granulocytic differentiation of HL-60, THP-1, or NB4 cells. Forced expression of either *miR-29a* or *miR-142-3p* in hematopoietic stem cells induces myeloid differentiation (Wang et al., 2012). Ectopic *miR-638* overexpression, which targets the cyclin-dependent kinase 2 (*CDK2*), also increases RA-induced differentiation of leukemic cell lines and primary acute myeloid leukemia blasts (Lin et al., 2015). Moreover,



RA increases the expression of tumor suppressor *miR-663* and inhibits HL-60 cell proliferation. Exotic overexpression of *miR-663* also induces HL-60 cell differentiation (Jian et al., 2011).

Autophagy regulated by miRNA has a role in the regulation of myeloid differentiation. Autophagy genes (*ATG*) are frequently repressed in primary acute myeloid leukemia patients. These reduced levels are likely due to increased *miR-106a*, which targets a transcriptional factor for several ATG genes (Jin et al., 2018). By mediating other mechanisms such as regulation of transcriptional machinery, miRNA is important for differentiation. In malignant myeloid cells, transcription factor CDX2 induces *miR-125b* expression. Increased *miR-125b* prevents the differentiation of myeloid cells and promotes leukemogenesis by inhibiting the core binding factor $\beta$  (*CBFB*) translation. RA treatment decreases CDX2 activity, reduces *miR-125b*, and increases the *CBFB* during myeloid cell differentiation and in patients. Thus, *miR-125b* is important for RA-induced differentiation (Lin et al., 2011).

HOXB4, which has a function in stem cell expansion, along with *miR10a*, is highly expressed in atypical myeloproliferative neoplasms. However, overexpression of *miR-10a* has no effect on proliferation, differentiation or self-renewal of normal hematopoietic progenitors. (Dumas et al., 2018). RA reduces HOXA9 in acute leukemia cells leading to the inhibition of proliferation and promotion of differentiation of leukemia cells. The downregulation also interferes with tumor growth by modulating certain miRNAs. For example, during the leukemia cell differentiation induced by HOXA9 downregulation, *miR-663* and *miR-494* are increased and *miR-10a* and *miR-181* are decreased (Chen, Yu, Lv, & Zhang, 2017).

#### 4.5 Breast cancer

Retinoids are promising for breast cancer prevention and treatment. In estrogen receptor (ER)-positive breast carcinoma cells (MCF-7), RA induces *miR-21* to counteract the anti-proliferative action of RA but may have a benefit in reducing cell motility. The pro-inflammatory cytokine IL1B, the adhesion molecule ICAM-1, and the tissue-type plasminogen activator (*PLAT*) are the identified *miR-21* target genes (Terao et al., 2011). In addition, *miR-21* targets the tumor suppressor gene tropomyosin 1 (*TPMI*) that is implicated in cell migration, as well as the programmed cell death 4 (*PDCD4*), and the mammary serine protease inhibitor (*Maspin*) (Terao et al., 2011). Thus, *miR-21* inhibitors may be used for breast cancer treatment.

Other miRNAs are implicated in RA-mediated anti-breast cancer effects. Nearly 70% of human breast carcinomas have reduced HOXA5. In addition, loss of HOXA5 in human breast cancer correlates with the progression to higher-grade lesions, suggesting its tumor suppressor effect (Jeannotte, Gotti, & Landry-Truchon, 2016). However, via *miR-130a* reduction, RA induces HOXA5 in breast cancer tissue (Yang, Miao, Mei, & Wu, 2013). RA also acts as a inducer for *miR-10a*, which counteracts the reduced *miR-10a* and RAR $\beta$  in breast cancer cells (Khan et al., 2015). To add on, RA increases *miR-210* and *miR-23a/24-2* but decreases *miR-17/92* and *miR-424/450b* in breast cancer cells. However, estrogen can counteract the effect of RA on expression of those four miRNAs (Saumet et al., 2012).

In a specific subgroup of HER2-positive breast cancer cells, SKBR3, RA and Lapatinib treatment regulates the expression of 174 miRNAs (Fisher et al., 2015). Together, RA-regulated miRNAs have a significant impact on growth or mobility of SKBR3 cells (Fisher et al., 2015).

#### 4.6 Digestive system cancers

RAR $\beta$  is an upstream regulator and downstream effector of *miR-22*. In other words, RAR $\beta$  can transcriptionally induce *miR-22*, which in turn epigenetically regulates the expression and function of RAR $\beta$  and another orphan receptor named NUR77. As a result, nuclear NUR77 exports to cytosol converting its oncogenic effect into apoptotic effect thereby killing colon cancer cells (Hu et al., 2019). RA by itself or in combination with synthetic and natural HDAC inhibitors including short-chain fatty acids can induce *miR-22*. Thus, in addition to RAR $\beta$ -mediated transcription, epigenetic mechanism also regulates *miR-22* expression. Additionally, it is interesting that *miR-22* targets multiple protein deacetylases including HDAC1, HDAC4, as well as SIRT1 and has HDAC inhibitory effect used to fight for cancer. Thus, RA-induced *miR-22* is a tumor suppressor for colon cancer (Hu et al., 2019). Furthermore, reduced *miR-22* is found in many other types of cancers including liver, colon, etc., and is considered as a tumor suppressor (Yang, Hu, Liu, & Wan, 2015). In consistency with the role of *miR-22* being a tumor suppressor, *miR-22* has been characterized as a metabolic silencer (Hu et al., 2020).

In metastatic pancreatic adenocarcinoma cells, *miR-10a* is overexpressed and regulates the metastatic behavior by suppressing HOXB1 and HOXB3. As mentioned above, *miR-10a* is important for RA-mediated differentiation of neuronal cells. However, in pancreatic adenocarcinoma, RAR antagonists reduce *miR-10a* and has an anti-cancer effect (Weiss et al., 2009).

Reduced *miR-452* promotes stem-like features and tumorigenesis in glioma as mentioned above (Liu et al., 2013). However, increased *miR-452* significantly promotes hepatocellular carcinoma (HCC) cell proliferation in vitro and in vivo (Zheng et al., 2016). *miR-452* is overexpressed in the chemo-resistant hepatospheres and human HCCs (Zheng et al., 2016). Thus, *miR-452* over-expression predicts poor survival for liver cancer patients (Zheng et al., 2016). Moreover, RA combined with doxorubicin reduces *miR-452* and inhibits HCC metastasis (Zheng et al., 2016). Furthermore, *miR-452* silences the *Sox7*, which suppresses the Wnt/ $\beta$ -catenin signaling pathway (Chan, Mak, Leung, Chan, & Ngan, 2012; Zheng et al., 2016).

#### 4.7 Other cancers

As a tumor suppressor, reduced RAR $\beta$  can be an indicator for prognosis. In papillary thyroid carcinoma, reduced RAR $\beta$  is associated with increased *miR-146b-5p* (Czajka et al., 2016). Overexpression of *miR-146a-5p* and *miR-146b-5p* results in reduced RAR $\beta$  mRNA (Czajka et al., 2016). In contrast, toll-like receptor 3 (TLR3) activation induces RAR $\beta$  re-expression and tumor inhibition, which is due to increased *miR-29b*, *-29c*, *-148b*, and *-152* as well as re-expression of epigenetically silenced genes (Galli et al., 2013).

Another miRNA that targets RAR $\beta$  is *miR-29b*. Tuberous sclerosis complex (TSC) is an incurable multisystem disease featured by mTORC1-hyperactive tumors. It has been found that by targeting RAR $\beta$ , *miR-29b* has an oncogenic effect in TSC2-deficient cells. In addition, inhibition of *miR-29b* suppresses oncogenic property of TSC2-deficient tumors in vivo (Liu et al., 2019).

In addition to RAR $\beta$ , miRNAs also affect the expression of other RA receptors. *miR-27a* overexpression, which silences RAR $\alpha$  and RXR $\alpha$ , is found in aggressive rhabdomyosarcomas cells (Tombolan et al., 2015). Additionally, RA can enhance the binding of RAR $\alpha$  to the *miR-27a* promoter, leading to the inactivation of *miR-27a* transcription, which increases glycogen synthase kinase-3 $\beta$  (GSK-3 $\beta$ ) in laryngeal cancer cells. However, the mechanism by which RAR $\alpha$  reduces *miR-27a* remains to be understood (Chen et al., 2017).

The effects of other retinoids in regulating miRNA have been studied. For example, the treatment effect of 9-*cis* RA, a ligand for RXR, is revealed in an adrenocortical xenograft mouse model. 9-*cis* RA together with mitotane reduce circulating *hsa-miR-483-5p* in the adrenocortical xenograft mouse model and can potentially be a predictor of treatment efficacy (Nagy et al., 2015). Additionally, tomato-derived bioactive antioxidants such as carotenoids and lycopene also inhibit tumor growth. In PC3 prostate cancer cells, lycopene increases *let-7f-1* to silence the *AKT2* and induce apoptosis (Li, Chen, Zhao, Hao, & An, 2016).

## 5. miRNAs that are implicated in other RA-regulated health issues

### 5.1 Liver diseases

Overexpression of *miR-34a* in human hepatoblastoma HepG2 cells reduces RXR $\alpha$  mRNA and protein. An inversely correlated expression pattern exists between *miR-34a* and RXR $\alpha$  protein in 14 liver specimens, with fibrotic livers having increased *miR-34a* but reduced RXR $\alpha$ . p53 can up-regulate *miR-34a* and promote liver fibrosis. Thus, by reducing RXR $\alpha$ , *miR-34a* has a role in liver fibrosis (Oda et al., 2014).

### 5.2 Atherosclerosis

*miR-10a* is a potential diagnostic molecule because reduced *miR-10a* in aortic endothelium and serum is linked with atherosclerosis (Lee et al., 2018). Moreover, RAR $\alpha$ /RXR $\alpha$ -specific agonists induce *miR-10a* in vascular endothelial cells and inhibit atherosclerotic lesion formation. Thus, the RA-induced *miR-10a* can be a potential target for treating atherosclerosis (Lee et al., 2018).

### 5.3 Congenital diseases

Through hypermethylation, *miR-124a* is reduced and p38 is deactivated in RA-induced spina bifida fetuses compared with healthy rats. In addition, p38 deactivation is accompanied by increased apoptosis suggesting the role of *miR-124a* in RA-induced congenital defect (Qin et al., 2017). RA also reduces *miR-9/9\**, *miR-124a*, and *miR-125b*, all of which are implicated in the development of spina bifida in rat models (Zhao et al., 2008). The up-

regulation of *miR-9*, *miR-124a*, and *miR-138* as well as down-regulation of *miR-134* are found in the amniotic fluid of RA-induced spinal bifida fetuses compared with that of control fetuses (Qin et al., 2016).

#### 5.4 Aging

miRNAs that are implicated in stress-induced premature senescence have been identified in primary cultures of human diploid fibroblasts and human trabecular meshwork cells. Senescence is associated with reduced *miR-15* and *miR-106b* as well as increased *miR-182* and *-183*. In addition, *miR-106b* and *miR-182* target the *p21<sup>CDKN1A</sup>* and the *RARG*, respectively, and are thereby implicated in senescence (Li, Luna, Qiu, Epstein, & Gonzalez, 2009).

#### 5.5 Myopia

Mutation of the paired box gene 6 (*PAX6*) gene, which controls oculogenesis, is implicated in the development of myopia. RA induces *miR-328*, which targets the *PAX6*, in retinal pigment epithelial cells leading to increased retinal pigment epithelial cell proliferation and reduced scleral cell proliferation. Thus, the reduction of *miR-328* contributes to the prevention or treatment of myopia (Chen et al., 2012).

#### 5.6 Alzheimer's disease

Overexpression of *miR-138* is found in the N2a/APP cells expressing human amyloid precursor proteins (APP) 695 protein (APP695, APPwt) and HEK293/tau cells (human embryonic kidney 293 cells expressing human tau protein). In HEK293/tau cells, increased *miR-138*, which directly targets the *RAR $\alpha$* , activates GSK-3 $\beta$ , and enhances tau phosphorylation. In contrast, elevated *RAR $\alpha$*  inhibits GSK-3 $\beta$  and reduces tau phosphorylation (Wang et al., 2015).

### 6. Conclusion

miRNA has a significant role in mediating the functions of RA. Among the above-mentioned miRNAs, there are a few such as *let-7*, *miR-10*, and *miR-17* are implicated in multiple biological processes and disease models.

The *let-7* family has a wide variety of implications. Increased *Let-7g* leads to the differentiated phenotype of Dicer-deficient mouse ESCs. Furthermore, the *let-7* family has a variety of effects on neuronal lineage progression cells. It induces neuronal differentiation and is elevated in differentiated neuronal cultures. They can also act as tumor suppressors and lead to the differentiation of APL cells. Moreover, *let-7f-1* induced by lycopene causes apoptosis.

The *miR-10* family also has a wide variety of implications after RA induction. For example, reduced *miR-10a* is linked to atherosclerosis and can be a diagnostic tool. Furthermore, *miR-10a* promotes the differentiation of mouse embryonic stem cells into smooth muscle cells. *miR-10a* is also found in T cells and stabilizes iTregs that prevents their development

into helper T cells. In addition, *miR-10a* level is low in breast cancer cells but is overexpressed in metastatic pancreatic adenocarcinoma cells.

*miR-17* is generally decreased by RA. It is involved in the regulation of the MAPK signaling pathway, synaptic plasticity, and other markers of neuronal differentiation in neuroblastoma SH-SY5Y cells. It is also decreased in APL cell differentiation and in breast cancer cells. In addition, reduced levels of *miR-17* also promotes the macrophage inflammatory responses such as infiltration, phagocytosis, and pro-inflammatory cytokine secretion. *miR-17-92* also functions cooperatively with *miR-106b-25* to regulate mice spermatogonia differentiation.

Since miRNA can target many genes and pathways, it would be challenging to use them for disease treatment and prevention. Additionally, certain miRNAs such as *miR-452* has opposite effects based on the tumor types. Additional studies are required to dissect their functions and human relevance.

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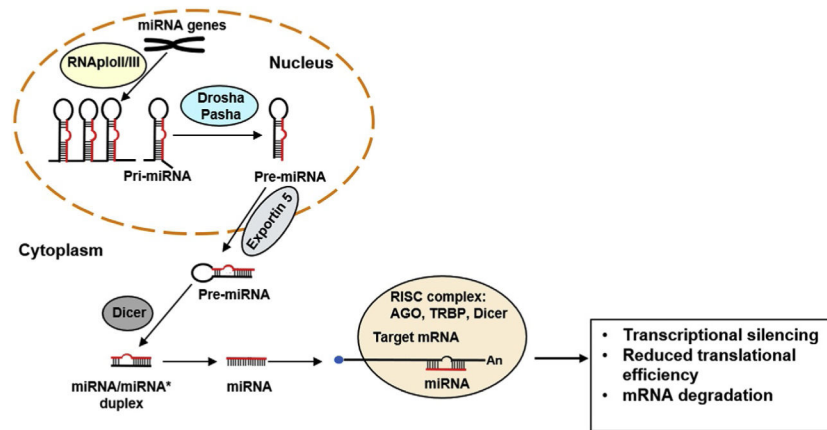


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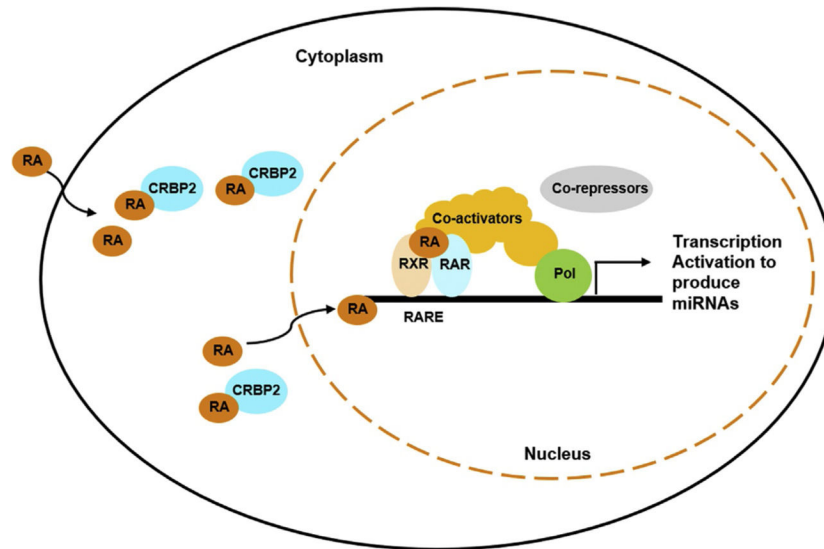
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**Fig. 1.** miRNA Biogenesis. miRNA is transcribed into pri-mRNA, which is converted to pre-miRNA by the protein complex Drosha-Pasha. Pre-miRNA is then transported out of the nucleus via the protein exportin 5. The endoribonuclease dicer cleaves pre-miRNA to form a miRNA duplex. Then, unwinding of the two strands and asymmetric assembly of one strand into RISC (RNA-induced silencing complex) occurs. The RISC complex acts via transcriptional silencing, reduced translational efficiency, or mRNA degradation.



**Fig. 2.** Retinoic acid and its receptor-mediated gene expression. RA is transported into the cell and bind to CRBP2 (cellular RA binding protein). In the nucleus, RA binds to nuclear receptors RXR and RAR heterodimer, which recognizes the RA receptor responsive element (RARE) located on the target gene, to regulate gene expression. The transcriptional activation requires the recruitment of coactivators and the departure of co-suppressors. Once miRNA is produced, it can silence the RA receptors, the transcriptional co-regulators, or other specific targets to modulate the effects of RA.