



Published in final edited form as:

*Bone*. 2021 February ; 143: 115757. doi:10.1016/j.bone.2020.115757.

## miRNAs in osteoclast biology

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### Abstract

MicroRNAs (miRNAs) are a class of short RNA molecules that mediate the regulation of gene activity through interactions with target mRNAs and subsequent silencing of gene expression. It has become increasingly clear the miRNAs regulate many diverse aspects of bone biology, including bone formation and bone resorption processes. The role of miRNAs specifically in osteoclasts has been of recent investigation, due to clinical interest in discovering new paradigms to control excessive bone resorption, as is observed in multiple conditions including aging, estrogen deprivation, cancer metastases or glucocorticoid use. Therefore understanding the role that miRNAs play during osteoclastic differentiation is of critical importance. In this review, we highlight and discuss general aspects of miRNA function in osteoclasts, including exciting data demonstrating that miRNAs encapsulated in extracellular vesicles (EVs) either originating from osteoclasts, or signaling to osteoclast from divergent sites, have important roles in bone homeostasis.

### Keywords

miRNA; Osteoclast; Extracellular vesicles; Differentiation

## 1. Introduction

The continual maintenance of bone mass through the life-span involves balancing the coordinated activities of bone formation (via the osteoblasts) and bone resorption (via the osteoclasts) [1]. These activities are largely orchestrated by the osteocyte, which is a mature, osteoblastic, matrix-embedded cell type [2–4]. As the organism ages or during physiological or environmental stressors (i.e. glucocorticoid use, estrogen depletion, cancer metastases),

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Declaration of competing interest  
The authors have nothing to disclose.

alterations in how these cell-types communicate can lead to an unbalancing of the processes of bone resorption and bone formation resulting in significant bone loss [5,6]. This compromised state of bone homeostasis is categorized in a disease called osteoporosis, which is characterized by the local destruction of bone tissue leading to lowered bone mass or compromised bone quality, leading to the increased risk of life-debilitating events such as fracture [6,7]. This condition is responsible for approximately 2 million fractures per year and is positively associated with morbidity and mortality, mostly in the elderly population [8]. Therefore, understanding how these processes are regulated at the molecular level is of critical importance and will uncover new avenues to target therapeutics to improve, or even prevent, the negative consequences of osteoporosis.

Although the regulation of normal and pathologic bone metabolism is multi-factorial and involves coordination of all bone-related cell types, in this review we will focus on the state of knowledge regarding the function and biology of miRNAs as they related to the osteoclast cell lineage.

## **2. Osteoclast functions in bone metabolism**

### **2.1. General osteoclast function and clinical relevance**

Osteoclasts are multinucleated, bone-resorbing cells derived from the myeloid lineage and are crucial to normal skeletal development and homeostasis. The functional importance of osteoclasts has been elucidated in large part through the study of osteopetrosis, a class of diseases characterized by increased bone density caused by defective bone resorption [9]. There are several forms of osteopetrosis, depending on the specific causal mutations, and severity of disease ranges from mild bone sclerosis to fatality during infancy. In addition to increased bone density, patients can experience cranial or optic nerve compression, extramedullary hematopoiesis, anemia, and immunodeficiency. Despite increased bone density, impaired bone remodeling also leads to higher risk for pathological fractures in osteopetrotic patients. Patients can exhibit dental abnormalities, impaired tooth eruption and osteomyelitis [10]. Similar to genetic mutations that disrupt resorption, pharmacologic anti-resorptive therapies used in the treatment of osteoporosis or cancer-induced bone disease, such as bisphosphonates and denosumab, induce side effects by decreasing the number of functional osteoclasts. Most commonly, these drugs are associated with significant reductions in new bone formation due to the reduction in bone remodeling and have also been associated with medication related osteonecrosis of the jaw [11] and atypical femoral fractures [12].

### **2.2. Osteoclast differentiation**

Differentiation of osteoclasts, which has been reviewed thoroughly [13–16], primarily requires two cytokines; macrophage colony stimulating factor (MCSF) that promotes proliferation and survival, and receptor activator of nuclear factor kappa-B ligand (RANKL) that induces differentiation. RANKL is produced by osteoblasts and osteocytes to stimulate bone resorption and initiate remodeling, at specific skeletal sites [17–19]. Osteoclast differentiation is further regulated by the expression of osteoprotegerin (OPG), a decoy receptor for RANKL, which inhibits the activation of osteoclast differentiation [20]. The

binding of RANKL to the cell surface receptor RANK on osteoclast progenitors activates intracellular signaling pathways that stimulate nuclear factor kappa-light-chain-enhancer of activated B cells (NFkB), FOS and nuclear factor of activated T-cells, cytoplasmic 1 (NFATc1) transcription factors [13]. Osteoclast differentiation induces expression of additional proteins crucial for cell fusion (i.e. dendrocyte expressed seven transmembrane protein [DCSTAMP]) [21,22] and adhesion to the bone surface (integrin subunit alpha V [ITGAV] and integrin subunit beta 3 [ITGB3]) [23]. RANKL activation of mature osteoclasts together with integrin signaling induces morphological changes in order to resorb bone. The actin cytoskeleton is rearranged to form the actin ring and seal off a zone between the basal membrane and the bone surface [24]. This space becomes the resorption lacunae, which is acidified through secretion of H<sup>+</sup> and Cl<sup>-</sup> ions. In addition, fusion of lysosomal vesicles creates the characteristic osteoclast ruffled border while delivering enzymes to aid in digestion of the bone matrix [25]. The processes involved in cell fusion, adhesion, as well as vesicular trafficking are highly dependent on G protein signaling [26], which, in part, underlie the sensitivity of these cells to nitrogenous bisphosphonates [27]. By resorbing bone, osteoclasts help to shape bones during skeletal development, as well as create the bone marrow cavity required for hematopoiesis and B lymphocyte differentiation [28]. Following skeletal maturation, bone resorption continues to be essential for the maintenance of bone quality, removing weakened or damaged bone so that it can be replaced by new bone [29].

There is much evidence that osteoclasts promote subsequent osteoblast differentiation and bone formation at sites of bone resorption, a process known as the “coupling” of bone resorption to bone formation [30,31]. It is well established that osteoclast-mediated bone resorption precedes bone formation during bone remodeling. Further, serum markers of resorption closely correlate with markers of bone formation, and pharmacologic disruption of resorption (i.e. anti-resorptive therapy) leads to a concomitant reduction in bone formation [32].

During bone resorption, osteoclasts release bone-derived factors, including transforming growth factor-β (TGFB) [33] and insulin-like growth factor-1 (IGF1) [34] that may act in an autocrine or paracrine manner within the bone microenvironment to promote subsequent cycles of bone formation. However, as evidenced in osteopetrosis patients that maintain osteoclast numbers (“osteoclast-rich” osteopetrosis) with defective bone resorption but normal or increased bone formation, the presence of osteoclasts themselves promote bone formation [35,36]. Thus, osteoclasts are thought to also secrete factors, dubbed “clastokines” [37] that may signal to the bone microenvironment to promote angiogenesis [38] and osteoblast differentiation [35,39,40]. In addition to secreted factors, there is evidence that osteoclast-membrane bound proteins may directly interact with osteoprogenitors to regulate osteoblast differentiation. This interaction has been suggested for osteoclast-derived EFNB2 to promote osteoblast differentiation through osteoprogenitor-expressed EPHB4 [41]. Likewise, osteoclast expression of RANK can activate bidirectional signaling in osteoprogenitors downstream of membrane bound RANKL [42].

### 2.3. Osteoclasts and T-lymphocyte activation

Osteoclasts also have roles in modulating immune responses, specifically through regulation of T lymphocyte activation. Similar to other myeloid-derived immune cells (i.e. macrophages, dendritic cells), osteoclasts can express class I/II major histocompatibility complex (MHC) molecules and co-activators for antigen presentation and activation of T cell responses [43]. Kiesel et al. reported that murine osteoclasts induced FOXP3 expression in CD8+ T cells; these cells lacked cytolytic activity, suggesting activation of a T-regulatory (Treg) cell response [44]. Certain osteoclast progenitor and osteoclast populations have been shown to have myeloid suppressor function [45,46]. More recently, dendritic cell-derived inflammatory osteoclasts in a mouse model of colitis were described to activate inflammatory CD4+ T cell responses in contrast to activation of Treg responses in healthy mice [47]. Further study has shown that these inflammatory osteoclast populations show further functional heterogeneity, with differential effects on T cell activation. The ability of osteoclasts to prevent T lymphocyte activation, even in the setting of inflammation, may be crucial to skeletal homeostasis, especially considering the potential for immune responses to collagen peptides generated during bone resorption [48].

## 3. miRNA biology

### 3.1. General miRNA biogenesis and function

MicroRNAs (miRNAs or miRs) are a specialized family of small, non-coding RNA molecules (~19–25 nucleotides in length) that regulate gene expression through post-transcriptional degradation and/or translational repression of mRNAs [49,50]. They mediate this effect through specific base-pairing interactions with “seed” sequences (7–8 nucleotides) primarily located within the 3′ untranslated region (UTR) of target mRNAs [51]. Since the interaction between the miRNA and mRNA-UTR utilizes only short stretches of sequence information, most miRNAs can interact with and influence the expression of many mRNAs simultaneously (often numbering in the 100 s) [52–54]. Interestingly, this miRNA pathway of gene expression regulation has been uncovered in organisms throughout evolutionary history, suggesting this regulatory mechanism is highly conserved and is a deeply embedded biological regulatory mechanism [55,56]. They have been implicated in essentially all biological processes and in nearly every tissue, including in the development, homeostasis and aging of the skeleton [57–64].

### 3.2. Osteoclast phenotypes of disrupted miRNA processing

Many excellent reviews on the biosynthetic pathways of miRNA biogenesis and processing can already be found in the literature [49–51,56], therefore an extensive review will not be included here. However, the importance of the miRNA regulatory pathway in bone biology can be illustrated by examining the effects of conditional deletion of one of the important molecules involved in the production of mature miRNAs, namely DICER1. Briefly, DICER1 is a member of the RNase III family of enzymes, which serves to process pre-miRNAs that have been exported to the cytoplasm by trimming off the terminal loop resulting in a mature, double-stranded miRNA molecule that then is loaded in the RNA-induced silencing complex (RISC) and eventually leads to RNA silencing [65]. Gene silencing of DICER1 in osteoclast precursors results in an impairment of osteoclastic gene expression and function in vitro,

including decreases in osteoclastogenesis and bone resorption [66]. Conditional deletion of DICER1 in osteoclast precursors, using *Cd11b-Cre*, results in a mild form of osteopetrosis characterized by decreases in overall osteoclast number [66]. Similarly, conditional DICER1 deletions using cathepsin K (*Ctsk*)-Cre, which is active in more mature osteoclastic cells, also results in a decrease in osteoclast number and leads to higher bone mass phenotype [67]. In a broader sense, deletion of DICER1 in osteoblast cells (using various osteoblastic promoters such as *Coll1a1*, *Bglap*, *Osx* and *Runx2*) also affects bone homeostasis in various capacities [60,68,69]. These prior reports provide proof-of-principle arguments that loss of miRNA function in bone cells, including in osteoclasts, is important for the proper maintenance of bone homeostasis. Therefore, understanding how miRNAs regulate various cellular activities of osteoclasts is important.

#### 4. miRNA functions in various aspects of osteoclast formation

During the course of osteoclastogenesis, many miRNAs are differentially expressed and regulate osteoclast differentiation and function (reviewed by Hrdlicka et al. and Lozano et al. [70,71]). In this section, we will highlight some of the miRNAs that are important in each stage of osteoclast differentiation (summarized in Fig. 1 and Table 1) and validated using in vivo studies.

##### 4.1. Role of miRNAs in osteoclast differentiation

As a master regulator of osteoclastogenesis, NFATc1 is a critical component of osteoclast differentiation. There are several miRNAs that regulate osteoclast differentiation by targeting *Nfatc1* mRNA. MiR-124 regulates RANKL-dependent and -independent osteoclast differentiation by suppressing *Nfatc1* expression [72–74]. MiR-214 and miR-21 promote osteoclastogenesis by targeting the PTEN/PI3K/AKT pathway [75,76], while downregulating osteoclastogenesis by blocking the NFKB pathway [77]. MiR-125a dramatically suppresses osteoclastogenesis in human CD14+ peripheral blood mononuclear cells (PBMCs) through a novel tumor necrosis factor (TNF) receptor-associated factor 6 (*Traf6*)/*Nfatc1*/miR-125a regulatory feedback loop [78]. Overexpression of miR-193–3p has an osteoprotective effect in ovariectomized (OVX) mice by suppressing NFATc1 pathways [79]. MiR-301b knockout mice exhibited markedly increased bone mass by reducing osteoclastogenesis by directly targeting cylindromatosis (*Cyld*) leading to phosphorylated NFKB pathway. Further, these authors found that OVX-induced osteoclastogenesis was abrogated by osteoclastic miR-301b ablation [80]. MiR-218 negatively modulates osteoclast differentiation by downregulating the NFKB pathway and targeting TNF receptor superfamily member 1A (*Tnfrsf1a*) [81]. In addition, myeloid lineage restricted expression of miR-218 enhanced trabecular bone volume and decreased osteoclast number in vivo and protected from OVX-induced bone loss by targeting sirtuin 1 (*Sirt1*) and NFKB pathway signaling [82].

During early osteoclast differentiation, the miR-29 family is critical for osteoclast precursor commitment by directly targeting nuclear factor I/A (*Nfia*), G-protein coupled receptor 85 (*Gpr85*) and *CD93* [83]. Contrary to this result, in human PBMCs, miR-29b overexpression inhibits osteoclast formation [84]. However, our unpublished data using global expression of

miR-29 decoy, which down-regulates the miR-29 activity, indicates that expression of miR-29 in multiple organs and cells (e.g., osteoclasts and osteoblasts) makes it difficult to determine the role of miR-29 in bone as these mice, which express miR-29 decoy globally, did not exhibit alteration of bone mass (Lee and Delany, unpublished data).

#### 4.2. miRNAs regulating pre-osteoclast maturation and fusion

As described earlier in this review, committed osteoclast precursors differentiate into multinucleated giant cells by fusion. Osteoclast fusion is regulated by the Rho-GTPase family members ras homolog family member A (RHOA), cell division cycle 42 (CDC42) and rac family small GTPase 1 (RAC1), as well as the miR-29 family, miR-7b, miR-26a and let-7e. The miR-29 family regulates actin remodeling by targeting the Rho-GTPase Cdc42 and SLIT-ROBO-GTPase activating protein-2 (SRGAP2) [83]. DCSTAMP, which is a critical for osteoclast fusion, has been reported to be a target for miR-7b [85,86], while upregulated miR-26a inhibits DCSTAMP protein expression during osteoclast differentiation by suppressing connective tissue growth factor/CCN family 2 (*Ctgf Ccn2*) expression [87]. MiR-30a attenuates osteoclastogenesis via suppression of DCSTAMP/FOS/NFATc1 signaling pathways [88].

#### 4.3. miRNAs regulating osteoclast function, survival and apoptosis

MiR-365 and miR-186 negatively regulates matrix metalloproteinase (*Mmp9*) and *Ctsk*, respectively, to modulate osteoclastic bone resorption [89,90]. MiR-27a has been reported to be involved in regulating estrogen-inhibited osteoclast bone resorption by targeting peroxisome proliferator-activated receptor gamma (*PPAR $\gamma$* ) and adenomatous polyposis coli (*APC*) [91]. Global deletion of miR-146a in mice exhibited no distinct trabecular or cortical bone phenotype with high bone turnover (increased osteoblast and osteoclast numbers). However, miR-146a deletion protects OVX-induced bone loss by causing impaired osteoclast bone resorption [92]. MiR-21 global knockout mice exhibit decreased osteoclast function and number in vivo and result in increased trabecular bone volume [93], while overexpression of miR-100-5p suppressed in vivo bone resorption by targeting fibroblast growth factor (*Fgf21*) [94]. In mice that have osteoclast-specific overexpression of miR-214 using the acid phosphatase 5, tartrate resistant (*Acp5*) promoter, trabecular bone volume is significantly decreased due to enhanced bone resorption by targeting activating transcription factor 4 (*Atf4*) mRNA (an important transcription factor for osteoblast differentiation) [75,95]. In addition, miR-128 deletion in osteoclast lineage using *LysM-cre* reveals a dramatic increase in trabecular bone volume, and an accompanying reduced bone resorption which prevents OVX-induced bone loss [82]. These authors also found that miR-128 specifically targets *Sirt1* mRNA post-transcriptionally. Downregulation of miR-17 activates bone resorption by stabilizing protein tyrosine phosphatase receptor type O (*Ptp-oc* or *Ptpro*) mRNA and thereby downregulating EPHA4 receptor signaling, indicating the involvement in coupling [96]. Further, downregulation of miR-155 inhibits bone resorption [97], while upregulation of miR-106b inhibits bone resorption [98]. MiR-145 agomir treatment inhibits osteoclast activity in OVX mice by downregulating *Smad3* expression [99], while miR-31 antagomir treatment significantly reduces bone resorption by controlling cytoskeleton organization by targeting RhoA [100]. miR-193-3p agomir treatment of OVX mice markedly reduces OVX-induced bone loss/resorption by inhibiting *Nfatc1* expression and its



downstream osteoclastic target proteins CTSK, ACP5 and carbonic anhydrase 2 (CAR2) [79].

Several studies implicate the critical role of miR-29 in bone. miR-29a overexpressing transgenic mice driven by a phosphoglycerate kinase 1 (*Pgk1*) promoter show significantly impaired bone resorption in vivo and a reduction in glucocorticoid-induced osteoclastic erosion [101]. Similar results that miR-29a protects glucocorticoid-induced bone loss, have been reported in rats [102]. Interestingly, our data indicated that miR-29-3p has a differential role in conditions of homeostasis versus inflammation, as its expression in myeloid cells impairs bone resorption and enhances trabecular and cortical bone volume by increasing calcitonin (CALCR) and CTSK expression, while miR-29-3p targets *Tnfrsf1a* mRNA during TNF-induced inflammation (Delany and Lee, unpublished).

Some miRNA have been implicated in osteoclast apoptosis and fas cell surface death receptor (FAS)/FAS ligand (FASL) interactions have been reported to be critical [103]. MiR-21 promotes cell survival targeting *FasI* [104]. Mice deficient for miR-21 globally exhibited increased trabecular bone volume by decreasing osteoclast activity without altering osteoblast or bone formation [93]. Another miRNA, miR-29b which has been known to be expressed in multiple organs and cells, enhances osteoclast survival by targeting B-cell lymphoma 2 (BCL2) modifying factor (*Bmf*) [105]. In addition, overexpression of miR-539 accelerated osteoclastic apoptosis in an osteoporotic rat model [106].

## 5. miRNAs in human bone diseases

### 5.1. miRNAs in osteopetrosis

Osteopetrosis in humans is commonly caused by genetic mutations to genes affecting osteoclast differentiation (e.g., TNF superfamily member 11 [*TNFSF11*]) or osteoclast resorptive function (e.g., T-cell immune regulator 1, ATPase H<sup>+</sup> transporting V0 subunit A3 [*TCIRG1*] or chlo-ride voltage-gated channel 7 [*CLCN7*]). While miRNAs have been shown to contribute to the regulation of osteoclast differentiation and function as discussed, there have been no causal miRNA-specific mutations identified in human osteopetrotic patients. However, it remains possible that disruption of miRNAs in response to osteopetrotic mutations could contribute to disease pathogenesis. Using PBMCs from healthy versus osteopetrotic patients (*CLCN7*, rs387907576: A > G), Ou et al. identified 123 differentially expressed miRNAs [107]. The most abundant miRNA was miR-23a, which is suppressor of osteogenic differentiation. In contrast, osteopetrotic PBMCs showed a significant decrease in miR-29b-3p, which stimulates osteoblast differentiation. It is possible that these miRNAs are dysregulated in response to increased bone formation relative to impaired resorption exhibited by these patients. The authors further detected 117 computationally predicted miRNA-protein target pairs that were reciprocally expressed in the osteopetrotic PBMCs. Of these pairs, miR-320a and ADP ribosylation factor 1 (ARF1) were further evaluated due to the known relationship between ARF family members and *CLCN7*. MiR-320a was significantly decreased in the osteopetrotic PBMCs, leading to increased ARF1 protein, potentially to compensate for insufficient *CLCN7* [107]. While it is unlikely that these specific miRNAs play a causal role in osteoclast dysfunction contributing to osteopetrosis, it

is possible that this bioinformatics strategy could be further used to identify novel therapeutic targets.

## 5.2. miRNAs in osteoporosis

Osteoporosis, in contrast to osteopetrosis, is a disease of low bone mass caused by excess bone resorption as compared to bone formation. While osteopetrosis is caused by mutations specifically affecting bone resorption, osteoporosis can result from altered osteoclast activity or changes to the osteoblast lineage. In a study designed to identify miRNAs associated with elevated osteoclast resorption in postmenopausal osteoporosis, Wang et al. performed a miRNA expression array on circulating monocytes derived from women with either high or low bone mineral density. They identified miR-133a as a potential biomarker for osteoporosis [108]. It remains unclear whether miR-133a has a functional effect on osteoclasts and will require further experimentation.

## 5.3. Potential for miRNA-based clinical therapies

There has been some investigation into potential miRNA-based therapies to promote bone formation in conditions such as osteoporosis; however, most of these studies have aimed to use miRNAs to modulate osteoblast differentiation and bone formation and not in osteoclast functions. Song et al. showed that endothelial cell-derived exosomes delivering miR-155 modulate osteoclastogenesis in vitro and prevented OVX-induced bone loss. These endothelial cell-derived exosomes showed improved localization to bone as compared to osteoblast lineage-derived exosomes, suggesting that these exosomes could have therapeutic potential for targeting the osteoclast lineage to treat osteoporosis [109]. More research is needed to identify miRNA-dependent pathways that could modulate the function of osteoclasts in particular in these human bone diseases.

# 6. Involvement of miRNA-containing EVs in osteoclast biology

## 6.1. General EV biology

EVs are a broad collection of secreted, membrane-bound phospholipid particles involved in cellular communication with nearby cells (autocrine or paracrine) or distant cells (endocrine) through traversing the circulation [110]. They are formed intracellularly as intraluminal vesicles, are sorted and routed through the endosomal pathway and eventually released from the cell by budding off of the plasma membrane [111]. EVs are loosely categorized based on size of the particle, with exosomes and small EVs in the range of 30–200 nm in diameter, and larger vesicles in the range of 200–1000 nm (and even up to 5000 nm when considering apoptotic bodies) [112,113]. These particles can carry a veritable treasure trove of cargo, including proteins and various enzymatic activities, DNA and mRNAs, including non-coding RNAs such as lncRNAs and miRNAs [112]. Due to their nature for carrying cargo from their incipient cell to distant targets through the circulation, EVs have been used as biomarkers for both the detection and prognosis in many conditions and diseases [110,114], which will be covered elsewhere in this Special Issue. For more detailed information on the biogenesis and activities of EVs in various cellular contexts and disease states, a number of excellent reviews already exist [115–119] and therefore will not be covered in detail herein. Fig. 2 summarizes the involvement of EVs secreted from osteoclasts that affect multiple



other cell/tissue types and those EVs that affect osteoclast function (where the osteoclast is the target cell of the exogenous EV).

## 6.2. Osteoclast-secreted EVs

Osteoclasts secrete factors to promote the coupling of bone resorption to bone formation and until recently, these studies have focused primarily on secreted proteins. However it is plausible that osteoclast-derived miRNAs in EVs may also contribute to the coupling of resorption and formation, and as such serve as “EV-associated coupling factors”. One such miRNA is miR-214–3p, which has been found to be present in osteoclast-derived exosomes [95,120,121]. These miR-214–3p-containing exosomes have been demonstrated to target pre-osteoblastic cells in a paracrine fashion, and through direct interaction with and repression of *Atf4* mRNA, inhibits bone formation [122]. Similarly, exosomes derived from RANKL-induced, osteoclastic RAW 264.7 cells contain miR-23a-5p that downregulates *Runx2*, an essential transcription factor for bone formation [123], to inhibit osteogenic differentiation [124]. Osteoclast-derived exosomes also contain let-7a-5p, which targets the SMAD2/TGFB-induced pathway to inhibit chondrogenic differentiation and therefore promotes hypertrophic differentiation of chondrocytes [125]. Thus, it remains an exciting possibility that osteoclast-derived exosomes, which possess targeting for osteoprogenitors, may be loaded with anabolic miRNAs for therapeutic purposes to drive osteogenic responses.

## 6.3. Systemically-derived EVs affecting osteoclasts

Slightly more is known about systemically-derived EVs that target osteoclasts to influence the regulation of bone mass. Many of these miRNA-containing exosomes originate from tumor cells from various sources, and are often called “tumor-derived exosomes”, which can influence various aspects of osteoclastic activity, depending on their particular target mRNAs [126]. These miRNA-containing exosomes arise from diverse sources including breast cancer cells [127], prostate cancer cells [77,128], multiple myeloma plasma cells [129–131], osteosarcoma cells [132] and lung adenocarcinoma cells [133]. The particular miRNAs found in these tumor-derived exosomes often directly enhance osteoclastic activity to cause autolytic bone destruction and overall poor health of the bone leading to potentially life-threatening fractures (especially in these cancer patients). Other sources of EVs that directly target osteoclasts also existing, arising from such diverse sources as endothelial cells [109,134] and aging bone marrow stromal cells [135] (covered elsewhere in this Special Issue).

## 7. Conclusions and future directions

In the past few years knowledge concerning the functions of miRNAs both in osteoclast biology and the effects of miRNAs from EVs on osteoclasts has dramatically increased, although many significant gaps in our understanding still exist. A majority of these studies were conducted using in vitro or ex vivo (e.g., cell culture) systems. Indeed, more in vivo studies are necessary to confirm the functionality of miRNAs in a more biologically relevant system to greater understanding of their role(s) in bone homeostasis and for the potential for

the use of miRNAs (or encapsulated miRNAs in EVs) in therapeutic options for bone diseases such as osteoporosis and osteopetrosis.

## Acknowledgments

This work was supported by NIH grants R01 AR068275 (DGM), R01 AG063707 (DGM), P01 AG004875 (DGM), K01 AR070281 (MMW), R01 AR064867 (SKL).

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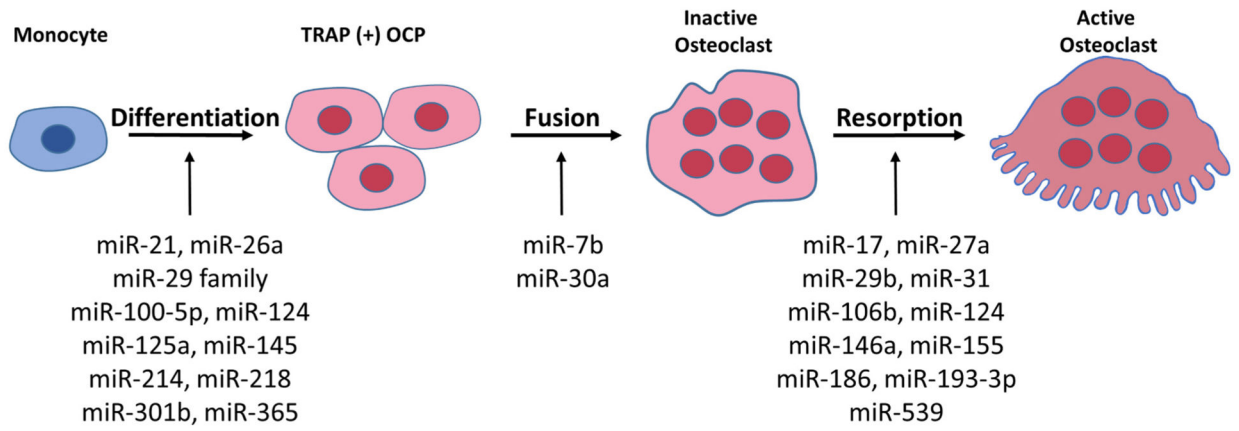
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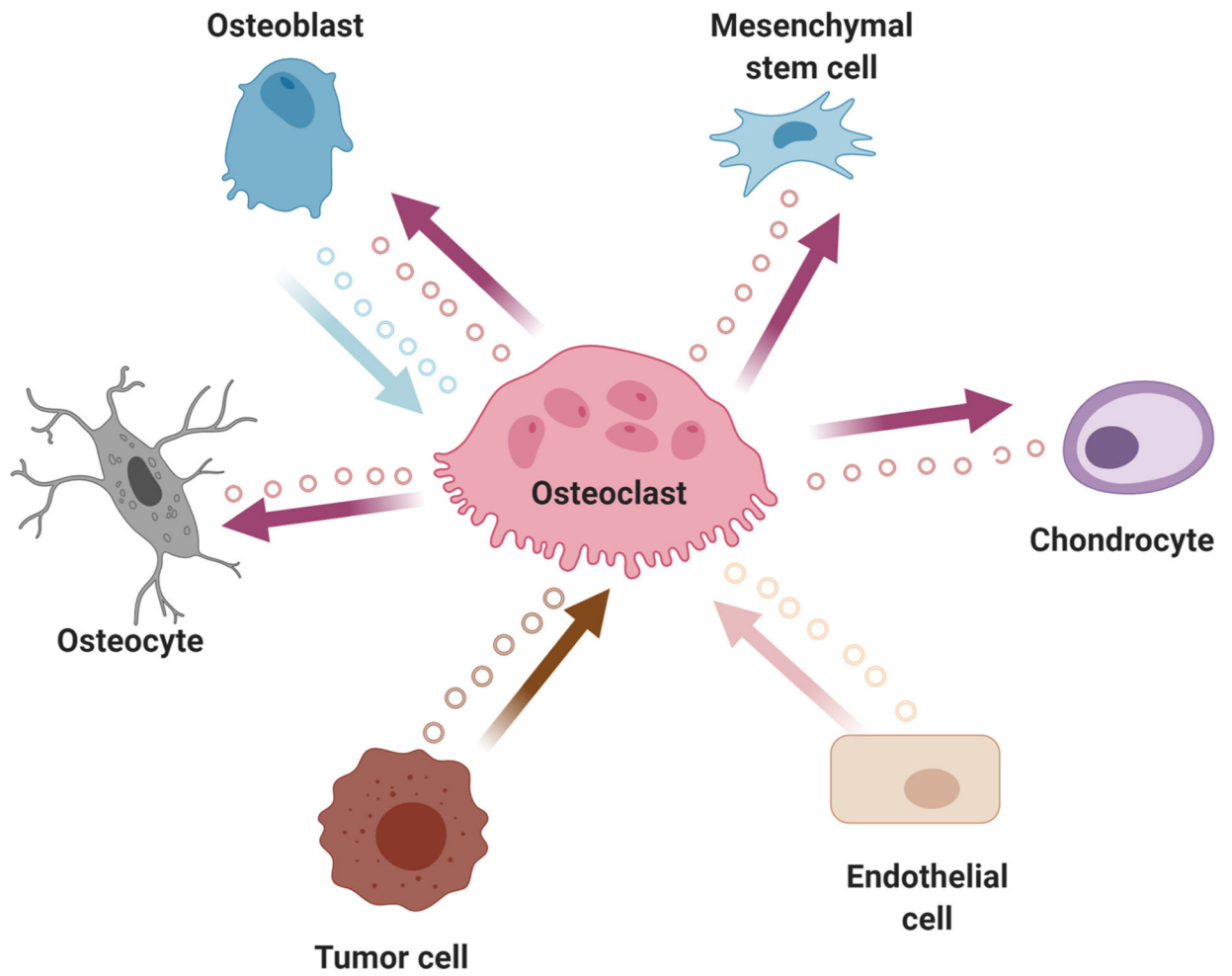


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**Fig. 1.** Depiction of miRNAs involved in the various stages of osteoclast differentiation.



**Fig. 2.** Depiction of extracellular vesicle (EVs; small circles) communication from osteoclasts to other distant cell lineages. Highlighted is the bi-directional EV communication between osteoclasts and osteoblasts.

**Table 1**

Summary of featured miRNA regulators of genes involved in osteoclast (Ocl) differentiation and function.

miRNA	Target mRNA(s)	Pathways/functions	Reference (s)
Positive regulators			
mmu-miR-21	<i>Pten, Spry1, Pcd4</i>	PI3K/AKT pathway, Ocl differentiation	[76,93,104]
mmu-miR-29 family	<i>Nfia, Gpr85, Cd93, Srgap2, Cdc42, Calcr</i>	Ocl differentiation	[83]
mmu-miR-31	<i>Rhoa</i>	Ocl differentiation, bone resorption	[100]
mmu-miR-128	<i>Sirt1</i>	NFKB pathway, Ocl differentiation	[82]
mmu-miR-146a	–	Bone resorption	[92]
mmu-miR-214	<i>Pten, Atf4</i>	PI3K/AKT pathway, NFKB pathway, bone resorption	[75,77,95]
mmu-miR-301b	<i>Cyld</i>	NFKB pathway, Ocl differentiation	[80]
Negative regulators			
mmu-miR-7b	<i>Dcstamp</i>	Ocl fusion	[85,86]
mmu-miR-17	–	EphA4 signaling, bone resorption	[96]
mmu-miR-26a	<i>Ctgf/Ccn2</i>	Ocl differentiation	[87]
mmu-miR-27a	<i>Pparg/Apc</i>	Ocl differentiation, bone resorption	[91]
hsa-miR-29b	–	Ocl differentiation, bone resorption	[84]
mmu-miR-30a	<i>Dcstamp</i>	FOS/NFATC1 pathway, Ocl differentiation, bone resorption	[88]
mmu-miR-100–5p	<i>Fgf21</i>	Ocl differentiation	[94]
mmu-miR-106b	<i>Rank1</i>	Bone resorption	[98]
mmu-miR-124	<i>Nfatc1</i>	Ocl differentiation	[72–74]
hsa-miR-125a	<i>Traf6</i>	NFATC1 pathway, Ocl differentiation	[78]
mmu-miR-145	<i>Smad3</i>	Ocl differentiation	[99]
mmu-miR-155	<i>Lepr</i>	AMPK pathway, bone resorption	[97]
mmu-miR-186	<i>Ctsk</i>	Bone resorption	[90]
mmu-miR-193–3p	<i>Nfatc1</i>	NFATC1 pathway, bone resorption	[79]
mmu-miR-218	<i>Tnfrsf1a</i>	NFKB pathway, Ocl differentiation	[81,82]
mmu-miR-365	<i>Mmp9</i>	Ocl differentiation	[89]
mmu-miR-539	–	AXIN-dependent Wnt signaling, Ocl apoptosis	[106]

*Pten*, Phosphatase and tensin homolog; *Pcd4*, programmed cell death 4; *Lepr*, Leptin receptor; *Ampk*, Adenosine monophosphate activated protein kinase.