Role of microRNAs in progenitor cell commitment and osteogenic differentiation in health and disease (Review)

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Abstract. MicroRNAs (miRNAs) are considered ‘micro-managers of gene expression’ and awareness of their fundamental role in the control of biological functions is constantly increasing. Bone formation and homeostasis are complex processes involving the differentiation and interaction of various cell types. Several miRNAs have been shown to be involved in different pathways and stages in the regulation of normal and abnormal bone formation and turnover. This present review focuses on the involvement of miRNAs in terms of their effect on the commitment of bone marrow mesenchymal stem cells towards osteogenesis, adipogenesis and chondrogenesis, respectively. The miRNAs involved in regulating osteoblast, chondroblast and osteoclast activity, are also taken into consideration, as are their interactions. miRNA expression levels, which may differ significantly in healthy versus pathological conditions, can be readily monitored and represent useful biomarkers. Several studies have suggested that miRNAs offer potential as useful biomarkers of bone pathologies, including osteoporosis and osteosarcoma. The development of efficient methods of delivering miRNA mimics or miRNA inhibitors into specific cells remains a challenge for novel therapeutic applications in the field of personalized medicine.

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1. Introduction

Skeletal development is a multistep process during which mesenchymal progenitor cells (MSCs) undergo proliferation and differentiation, giving rise to cartilage and bone cells. Bone is produced by two distinct processes. In the endochondral ossification process, which occurs in long bones and vertebrae, MSC-derived chondrocytes produce a cartilage template, which is subsequently replaced by a mineralized matrix, deposited by the bone-making cells, MSC-derived osteoblasts. The intramembranous ossification process, which occurs in skull bones and clavicle formation, relies instead on the direct differentiation of condensed MSCs into osteoblasts. The bone modeling occurring during development and the life-long process of remodeling are controlled by several factors, including systemic hormones, bone morphogenetic proteins (BMPs), fibroblast growth factors (FGFs) and secreted signaling factors, including Wnt. Various signaling molecules can trigger intracellular responses by modulating the expression of transcription factors, which are essential for MSC chondrogenic/osteogenic commitment; these include Runx-related transcription factor 2 (RUNX2), SRY-box 9 (SOX9), osterix (OSX) and activating transcription factor 4 (ATF4). Bone plasticity allows continuous adjustments to the mechanical demands solicited by skeletal functions. The leading effectors of bone remodeling are osteoblasts, osteocytes (mature osteoblasts within the mineralized matrix) and osteoclasts (large multinucleated cells suited to bone resorption due to their ability to secrete hydrochloric acid and proteases which degrade the mineralized matrix). Interactions occurring between these three cell types contribute to their reciprocal regulation and determine bone homeostasis in physiological conditions. Osteoclast differentiation is induced by the osteoblastic product, receptor activator of nuclear factor-κB (RANK)
There is increasing interest in the promising potential applications of miRNAs as diagnostic biomarkers and as molecular targets for therapeutic options in the treatment of bone disorders. miRNAs can be isolated from cells or bone specimens; they can also be retrieved from circulatory biofluids, including plasma or serum, as they are secreted from cells in exosomes or encapsulated within microvesicles. The present review examines and discusses the role of selected miRNAs, which have been consistently recognized in previous studies to affect the activity of various bone cell types in physiological and pathological conditions (7-9).

2. Role of miRNAs in commitment determination of MSCs

Bone cells progenitors, MSCs, are multipotent stem cells capable of differentiating into adipocytes, chondrocytes or osteoblasts. A mutually inhibitory association exists between osteogenic and adipogenic commitment. Alternative cell fate decisions are regulated by multiple signaling pathways. Increasing evidence indicates that miRNAs affect decisions concerning the fate of bone marrow MSCs. These can operate by silencing components of the Wnt or BMP signaling pathways at the post-transcriptional level, and by modulating the expression of key transcription factors, including RUNX2 (10-12). Chondrocytes arise from mesenchymal cell aggregation and differentiation. Growth factors, cellular interactions and extracellular matrix (ECM) elements are involved in the differentiation process by inducing chondrocyte-specific gene expression of SOX9, COL2A1, aggrecan, COL10A1 and parathyroid hormone-related protein (13). In this scenario, miRNAs are important in chondrocyte differentiation. In particular, miR-30a has been shown to be significantly upregulated during the chondrogenic differentiation of rat MSCs; it targets delta-like 4 gene, a ligand of the Notch signaling family (14). miR-140, which targets A disintegrin and metalloproteinase with thrombospondin motif 5, a metalloproteinase which degrades aggrecan, is expressed at a high level during the chondrogenesis of MSCs, in addition to increased expression levels of SOX9 and COL2A1 (15). By contrast, miR-455-3p has been shown function as an early activator of chondrogenesis, by targeting the gene expression of RUNX2 (16). The miRNAs involved in the adipogenic osteogenic and chondrogenic switch, respectively, in addition to their targets, are shown in Fig. 2.

3. miRNAs which promote adipogenesis and inhibit osteogenesis

miR-204 and miR-211 behave as endogenous repressors of RUNX2, the master regulator of MSC osteogenic commitment (12). miR-17-5p and miR-106a target BMP2 mRNA, which promotes osteogenic differentiation (17). miR-30e targets LDL receptor-related protein 6 (LRP6), a member of the Wnt canonical pathway co-receptor group (LRP5/LRP6/Frizzled) (18). miR-637 is known to target OSX, a key regulator of osteoblastic maturation acting downstream of RUNX2 (19).

4. miRNAs which promote osteogenesis and inhibit adipogenesis

miR-21 targets SRY-box 2 (SOX2), one of the four genes which promote induced pluripotent stem cells, and sprouty homolog 2 (SPRY2), a negative regulator of the extracellular signal-regulated kinase-mitogen-activated protein kinase signaling pathway (20,21). In MSCs overexpressing miR-21, osteogenic markers, including RUNX2 and osteonectin (OCN), are also overexpressed (22). This suggests a dual action of miR21 on progenitor cells, namely the suppression of pluripotency and promotion of osteogenic differentiation. miR-22 is also present in bone marrow progenitors; its expression decreases during adipogenic differentiation and increases during osteogenic differentiation (23). miR-22 and miR-2861 target histone deacetylase 6 (HDAC6) and histone deacetylase 5 (HDAC5), respectively. These histone deacetylases act as transcriptional co-repressors of RUNX2 (24). miR-3960, which is clustered with miR-2861 and encoded by the same transcript, targets homeobox A2 gene, another RUNX2 inhibitor (25). miR-20a promotes osteogenic differentiation by targeting pexisome proliferator activated receptor γ2, a positive regulator of adipocyte differentiation (26).

5. miRNAs which regulate osteoblast activity

The miRNAs involved in regulating osteoblast activity are listed in Table I. OsteomiRNAs, or bone-regulating miRNAs, can act as stimulators and repressors of osteogenesis. Among the stimulators, miR332 appears to increase the expression of OSX by targeting transducer of ERBB2, 2 (TOB2), which belongs to the TOB family of antiproliferative proteins; it facilitates the deadenylation and degradation of mRNAs, including OSX (27). By contrast, miR-181 promotes osteogenesis by targeting miRNAs coding for members of the transforming growth factor-β (TGF-β) signaling pathway, namely TGF-β receptor 1 and TGF-β-induced, which negatively regulate osteoblastogenesis (28). miR-29 exerts a positive regulatory effect on osteoblast differentiation, enhancing Wnt signaling,
and Dickkopf-related protein 1 (DKK1), a Wnt inhibitor, is among its targets (10). miR-335-5p also targets DKK1 (29). miR-26-a promotes osteogenesis by targeting glycogen synthase kinase 3β, a member of the β-catenin destruction complex (30). The miRNAs which target RUNX2 and OSX, respectively, act as negative regulators of osteogenesis; among others, these include the above-mentioned miR-204 and miR-211, which downregulate RUNX2, whereas miR-138...
and miR-143 target OSX (31,32). A negative regulator of bone formation is miR-214, which targets ATF4, a transcription factor modulating the gene expression of osteocalcin (33). miR-483-5p and miR-320-a downregulate insulin-like growth factor 2 (IGF2) and RUNX2, respectively, which inhibits osteoblastic function (34). Finally, miR-182 negatively regulates osteoblast proliferation by targeting Forkhead box protein O1 (FOXO1), a regulator of bone mass (35); miR-155 has been demonstrated to inhibit mouse osteoblast differentiation by suppressing the expression of small mothers against decapentaplegic family member 5 (SMAD5) (36).

### 6. miRNAs which regulate chondrocyte activity

The miRNAs involved in regulating chondrocyte activity are listed in Table II. The differentiation process in chondrocytes is followed by proliferation, hypertrophy, terminal differentiation, mineralization and programmed cell death. Of note, miR-140 (mentioned above) is involved in cartilage homeostasis; it has been shown that miR-140-knockout mice developed osteoarthritis (37). miR-let7, expressed in various tissues, is required for chondrocytes proliferation in normal conditions (38). The downregulation of miR-let7, obtained by Lin28a inhibitor, reduces chondrocytes proliferation and growth. These effects may be interpreted as consequences of the overexpression of two miR-let7 target genes, namely cell division cycle 34 and E2F transcription factor 5. Therefore, miR-let7, together with miR140, regulates the skeletal development by acting on chondrocyte proliferation and homeostasis (38). miR-199a and miR-214, which are generated from the RNA transcript Dnm3os and expressed in mesenchymal cells and chondrocytes, contribute to correct skeletal development. In particular, the upregulation of miR-199 has been observed upon chondrocytic differentiation (39). miR-195 can inhibit chondrocyte proliferation, by acting on the G-protein coupled receptor kinase interacting protein-1; COX2, cyclooxygenase 2; OSX, osterix; ATF4, activating transcription factor 4; GIT1, G-protein coupled receptor kinase interacting protein-1; HIF, hypoxia inducible factor; SP1, specificity protein 1; SIRT1, sirtuin 1.

### 7. miRNAs which regulate osteoclast activity

An important function in bone homeostasis is bone resorption. Various evidence supports the idea that miRNAs are involved in bone resorption, as they may act on osteoclastic proliferation, differentiation and survival (Table III). Among the positive regulators of osteoclastogenesis is miR-223, which targets nuclear factor IA (NFIA), a negative regulator of macrophage colony-stimulating factor receptor (44). miR-148-1 has been demonstrated to stimulate osteoclastogenesis by targeting transcription factor MafB, a transcriptional repressor of RANKL (45). miR-31 is upregulated during osteoclast differentiation in murine bone marrow cells; its target, RhoA, is a GTPase involved in cytoskeletal reorganization, which can affect osteoclast formation (46). Similarly, miR-21 is...
miR-124-3p targets the osteoclastic receptor RANK (48). miR-218 and miR-503 is a negative regulator of osteoclastogenesis, as it target the programmed cell death 4 (Pdcd4) gene (47). By contrast, miR-21-5p is a marker of RANKL-induced osteoclastogenesis, targeting the upregulated in osteoclast precursors and is identified as a factor 6.

Examples of miRNAs which modulate osteoclast activity. ↑, positive effect on osteoclastogenesis; ↓, negative effect on osteoclastogenesis.

<table>
<thead>
<tr>
<th>miRNA</th>
<th>Target gene</th>
<th>Regulatory effect on osteogenesis</th>
</tr>
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<tbody>
<tr>
<td>miR-223</td>
<td>NF1A</td>
<td>↑</td>
</tr>
<tr>
<td>miR-148a</td>
<td>MAFB</td>
<td>↑</td>
</tr>
<tr>
<td>miR-31</td>
<td>RhoA</td>
<td>↑</td>
</tr>
<tr>
<td>miR-21-5p</td>
<td>PDCD4</td>
<td>↑</td>
</tr>
<tr>
<td>miR-503</td>
<td>RANK</td>
<td>↓</td>
</tr>
<tr>
<td>miR-218</td>
<td>NFATC1</td>
<td>↓</td>
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<tr>
<td>miR-124-3p</td>
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<tr>
<td>miR-125a</td>
<td>TRAF6</td>
<td>↓</td>
</tr>
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</table>

8. Role of miRNAs in the pathological osteogenic commitment of progenitor cells

Altered patterns of miRNA expression have been shown in bone-related pathologies, which may jeopardize progenitor cell commitment and osteogenic differentiation. miR-29b is known to have an important regulatory role in osteoblast differentiation, as it targets COL1A1 and SPARC (osteonectin) mRNAs (51). As osteoblasts mature, miR-29b attenuates the expression of collagen genes, allowing the organization of collagen fibrils for subsequent mineralization. Of note, the downregulation of miR-29b has been reported in two distinct genetic bone disorders, osteogenesis imperfecta (OI) and osteopetrosis (OPT). OI is an ‘osteoblast disease’, characterized by varying degrees of bone fragility and skeletal deformities. Kaneto et al (52) reported that, in patients with OI, heterozygosity for causative COL1A1 gene mutations led to the reduced mRNA expression of COL1A1, and the levels of miR-29b were severely reduced. The authors suggested that the miR-29b control of collagen protein accumulation in the ECM depends on the levels of its target and hypothesized that the low mRNA levels of COL1A1 observed in OI cells at various stages of osteogenic differentiation were not sufficient for the induction of miR-29b. OPT is considered an ‘osteoblast disease’. In peripheral blood mononuclear cells (PBMCs) from patients with OPTA2, a survey of aberrantly expressed miRNAs showed that miR-29b was among the most significantly downregulated (53). A previous study demonstrated that miR-29b promotes osteoclastogenesis; its knockdown in murine pre-osteoclasts inhibited differentiation (54). Due to their important effects on bone marrow progenitor cell differentiation, misregulated miRNAs may profoundly affect primary and metastatic bone tumors. It has been demonstrated that the upregulation of miR-135b is involved in the impaired osteogenic differentiation of MSCs derived from patients with multiple myeloma (55). The study also demonstrated that impaired osteogenic differentiation overlapped with a marked downregulation of osteogenic markers, including BSP, COL1A1 and OPN. The authors suggested that miR-135b inhibited osteogenic differentiation by targeting SMAD5 mRNA and possibly other strategic target mRNAs. Bone metastasis, frequently occurring in late stages of breast and prostate cancer, disrupts normal bone remodeling. The involvement of miRNAs in the control and fate of bone metastasis has been reviewed extensively (56,57). miRNA profiles can be of diagnostic and prognostic value, and they may become therapeutic agents in the near future.

Osteosarcoma (OS) is a common malignant bone tumor in children and young adults. Surgery and chemotherapy failure occur in certain patients with OS. Therefore, biomarkers for active disease are required in order to monitor relapses and to predict prognosis in subjects who have a poor response to multi-agent chemotherapy. Several studies have investigated the role of circulating miRNAs as possible biomarkers with various, sometimes contradictory, findings (58-61). In particular, miR21 (Fig. 2) emerges consistently as a significant marker for poor prognosis, when its expression levels in the plasma of patients with OS and cancer cells are compared with those found in controls (62-64). miR-199a, which has been shown to be dysregulated in several types of tumor, has been found to be underexpressed in osteosarcoma cells and patient samples. Keremu et al (65) demonstrated that cisplatin-resistant OS cells treated with agomir199 were sensitized to cisplatin. Further investigations in this field may lead to the identification of other miRNA markers for more precise and timely prognosis, and to miRNAs therapeutic applications for osteosarcoma.

9. Altered miRNA expression levels in osteoporosis

Osteoporosis is a common age-related degenerative disease associated with bone loss and low-traumatic fractures. Bone fragility in postmenopausal osteoporosis originates from an imbalance in bone homeostasis, caused by increased osteoclastic activity and a progressive decline in osteoblastic proliferation (66). Due to the importance of miRNAs in the regulation of bone remodeling, several studies have investigated osteoporosis-related changes in their expression (Table IV). In several studies specific miRNAs, selected on the basis of previous reports, were isolated from serum samples of osteoporotic patients (OP) and age/sex matched healthy controls, reverse transcribed and then analyzed using reverse transcription-quantitative polymerase chain reaction analysis (67-72). In another study, total RNA was extracted from fresh femoral trabecular bone obtained from OP and
control groups, and hybridized to a miRNA array containing >1,900 miRNAs (34). Biostatistical analyses were performed in all experiments in order to identify significant (P<0.05) differences in miRNA expression between cases and controls. Several limitations in these studies do not allow the obtaining of univocal miRNAs signatures of osteoporosis. Notably, the patient/control groups in each study were small and different; differences in miRNA expression between cases and controls.

Several limitations in these studies do not allow the obtaining of univocal miRNAs signatures of osteoporosis. Notably, the patient/control groups in each study were small and different; in addition, miRNAs were different and non-randomly selected. However, consistent findings stand out from the plethora of data. Significant differences in the expression of specific miRNAs produced either by osteoblast or osteoclast cells, as described above, and in Tables I and III, respectively, appear to be essential in osteoporosis. Table IV illustrates how osteoblast micRNAs, which target essential positive effectors of osteogenic commitment, including miR30e, miR214, miR483-5p, miR182 and miR320a, are overexpressed in patients with osteoporosis, compared with matched healthy controls, whereas other miRNAs, including miR335-5p, which targets DKK1, are underexpressed in OP. Certain findings conflict with previously reported data. Yavropoulou et al (72) found serum levels of miR214-3p, a negative regulator of osteoclastogenesis (Table III) and miR2861, a positive regulator of osteoblastogenesis (Fig. 2) to be higher in postmenopausal women with a low bone mineral density (BMD), compared with those in women with a normal BMD. The authors hypothesized a compensatory mechanism of enhanced osteogenesis in response to menopause-induced bone loss, in order to justify their conflicting findings.

10. miRNAs as potential therapeutic targets for osteoporosis

As the dysregulation of miRNAs appears to contribute considerably to bone pathologies, including osteoporosis, several approaches aiming to correct such dysregulation have been applied to model systems. One type of approach consists in the delivery of pro-osteoblastic miRNAs in order to promote osteogenesis; another is the silencing of endogenous pro-osteoclastic miRNAs. The design of biologically sTable RNA molecules and their efficient delivery represent the main requirements in the two approaches. Zhang et al (73) designed a two-stage delivery system. A hyperbranched polymer vector containing miRNA26-a was encapsulated in polyactic-co-glycolic acid (PLGA) microspheres; these biodegradable PLGA microspheres were attached to 3D scaffolds, which were then implanted into mice. miRNA26-a had previously been demonstrated to promote osteogenesis (Table I). Zhang et al (73) showed that long-term miR26-a delivery locally rescued the osteogenic capacity in osteoporotic mice. By contrast, Liu et al (74) described a successful strategy to knock down pro-osteoclastic miRNA148-a (Table III). Downregulation/silencing of single miRNAs can be achieved by means of antagonomiRs, specifically engineered oligonucleotides complementary to the miRNA target. Liu et al (74) encapsulated antagonimR148-a in (D-Asp8)-modified liposomes, which favorably bind to bone-resorption surfaces, thus targeting osteoclasts. The therapeutic effect of antagonimR148-a was assessed upon delivery to ovariectomized (OVX) mice, which are animal models for the postmenopausal status. Encouraging results were derived from bone metabolism marker measurements and the observed attenuated decrease of BMD in the treatment group. In another study, Chen et al (48) demonstrated an opposite effect of antagonimR503 upon injection in OVX mice. miRNA503 inhibits osteoclastogenesis by targeting RANK, as described above (Table III) and the authors found it was dramatically downregulated in postmenopausal osteoporotic subjects. AntagomiR503-treated animals showed increased protein expression of RANK and bone resorption, whereas treatment with exogenous agomiR503 inhibited bone resorption and prevented bone loss. The above cited studies suggest that certain miRNAs are important in the pathogenesis of postmenopausal osteoporosis, due to their various effects on osteoblast or osteoclast activities. Exogenous agomiRNAs (potentiators), or exogenous antagonimRNAs (inhibitors) appear to be novel therapeutic tools against osteoporosis, a disabling disease which affects ~200 million individuals worldwide (75).
11. Conclusions

The role of miRNAs as modulators of gene expression and, consequently of physiological and pathological tissue functions, is attracting increasing attention. Referred to as ‘micromanagers of gene expression’, miRNAs regulate a substantial region of the human genome. Experimental in vivo and in vitro studies have shown how miRNAs complex inter-actions affect bone development and homeostasis. Excreted miRNAs, recovered from blood or other body fluids, repre-sent useful biomarkers for skeletal disorders; experiments in animal models suggest that antagomiRNAs or miRNA mimics may function as novel therapeutic tools. The exploita-tion of miRNA analysis as a molecular diagnostic tool is an interesting concept; however, important issues require consid-eration, including sample-to-sample biological variability and modulation of miRNAs in similar phenotypes. Although certain miRNAs have been observed consistently in different experimental conditions, their stimulatory or inhibitory effects on osteoblast and osteoclast differentiation remain to be fully elucidated. For example, miR-335-3p is upregulated in the commitment of MSCs to the osteogenic lineage, however, its levels are reduced during osteoblast maturation (76). As another example, miR-223 is expressed in mononuclear osteoclast precursors and has been shown to enhance osteoclast differentiation (77). By contrast, in PBMCs or RAW264.7 cells, the overexpression of miR-223 inhibits osteoclast forma-tion (6). Therefore, these findings define the role of miRNAs in maintaining bone homeostasis by modulating osteoblast and osteoclast commitment or maturation; however, complement ary evaluations are advisable in order to interpret correctly those findings concerning the elevation or reduction of specific miRNAs. Finally, an awareness of the roles and functions of miRNAs is a pre-requisite for the development of promising tools in personalized medicine. A number of issues remain, including how to optimize miRNA stability and delivery systems efficiency, and how to reach a specific tissue, specific cell population and specific mRNA target. As individual miRNAs may target numerous mRNAs, adverse collateral effects require consideration. These challenges indicate the requirement for further basic investigations in the field.

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Competing interests

The authors declare that they have no competing interests.

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