

# The MicroRNA-23a Has Limited Roles in Bone Formation and Homeostasis In Vivo

J. PARK<sup>1,2\*</sup>, S. WADA<sup>1\*</sup>, T. USHIDA<sup>1</sup>, T. AKIMOTO<sup>1</sup>

\*These authors contributed equally to this work.

<sup>1</sup>Division of Regenerative Medical Engineering, Center for Disease Biology and Integrative Medicine, Graduate School of Medicine, University of Tokyo, Tokyo, Japan, <sup>2</sup>Department of Physical Education, Konkuk University, Seoul, Korea

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## Summary

Recent studies have demonstrated that some microRNAs (miRNAs) inhibit bone formation by inhibiting the translation of specific genes. Several *in vitro* studies have suggested that miR-23a inhibits osteogenic differentiation by suppressing the translation of Runx2, a transcription factor essential for osteoblastogenesis, and of Satb2, a member of the special AT-rich binding protein family. In the present study, we used a gain-of-function approach to determine the roles of miR-23a in bone formation and homeostasis *in vivo*. The miR-23a transgenic (Tg) mice grew normally and their body size and weight were similar to those of wild-type (WT) littermates. Bone structure and morphology were similar in Tg and WT mice. Furthermore, the numbers of osteoblasts and osteoclasts, as well as their activities in bone were similar between Tg and WT mice. Our results indicate that miR-23 has limited roles in bone formation and maintenance *in vivo* in mice.

## Key words

Non-coding RNA • Runx2 • Satb2 • Micro-CT

## Corresponding author

T. Akimoto, Division of Regenerative Medical Engineering, Center for Disease Biology and Integrative Medicine, Graduate School of Medicine, The University of Tokyo, 7-3-1 Hongo, Bunkyo, Tokyo 113-0033, Japan. Fax: +81-3-5800-9199. E-mail: akimoto@m.u-tokyo.ac.jp

## Introduction

Bone formation and maintenance are tightly

regulated by osteogenic signaling pathways and several transcription factors, which induce bone-specific transactivation of certain genes (Soltanoff *et al.* 2009). Several studies have provided insight into the posttranscriptional regulation of bone formation (Gaur *et al.* 2010) and osteogenic differentiation (Hassan *et al.* 2010, Zhang *et al.* 2011) by microRNAs (miRNAs).

miRNAs are small noncoding RNAs that regulate the translation of genes encoding proteins in higher organisms. miRNAs are involved in almost every biological process, including development, growth, differentiation, cell death, and homeostasis (Bartel 2009). It was predicted that there are about 2,000 miRNAs in humans. The identification of miRNAs associated with skeletal abnormalities has allowed the development of new approaches that can help us to understand bone homeostasis and to treat diseases (Li *et al.* 2009, Lian *et al.* 2012).

Mice with limb- or cartilage-specific deletion of the miRNA-processing enzyme Dicer exhibited a severe phenotype with reduced limb size but normal patterning (Harfe *et al.* 2005, Kobayashi *et al.* 2008). In addition, bone-specific deletion of Dicer resulted in a high bone mass phenotype (Gaur *et al.* 2010). These findings suggest that miRNAs play critical roles in bone formation and maintenance. However, the specific miRNA that regulates bone formation and maintenance has not been identified.

Several miRNAs were reported to regulate osteogenesis in studies using *in vitro* models of osteogenic differentiation (Li *et al.* 2009, Hassan *et al.*

2010). In particular, Hassan *et al.* (2010) reported that miR-23a inhibits Runx2 and Satb2 translation in terminally differentiated osteocytes, representing a possible feedback mechanism to attenuate osteoblast maturation (Hassan *et al.* 2010).

Although it is well established that miR-23a is involved in osteogenic differentiation *in vitro*, its roles in bone formation and in the regulation of bone turnover in the adult skeleton *in vivo*, are unknown. To address this issue, and to provide insight into the *in vivo* function of miR-23a in bone formation and homeostasis, we generated transgenic (Tg) mice overexpressing miR-23a. We used a gain-of-function approach to examine whether overexpression of miR-23a affects bone formation and maintenance *in vivo*.

## Materials and Methods

### Animal experiments

Adult (8-week-old) male C57BL/6 mice (Clea Japan, Inc., Tokyo, Japan) and miR-23a Tg mice were housed in a temperature-controlled room (21 °C) with a 12 h light/12 h dark cycle, and were provided with food and water *ad libitum*. The animal protocol was approved by the Animal Care and Use Committee of the University of Tokyo.

### Generation of Tg mice

The miR-23a Tg mice were generated as previously described (Wada *et al.* 2011). Briefly, pCXbG-miR-23a was linearized using *Sall-EcoRI* sites and was injected into C57BL6/J oocytes. Genotyping was carried out by polymerase chain reaction (PCR). Fluorescence microscopy was performed to confirm transgene expression in adult tissues. Tissue samples were harvested from the F2-3 generation of Tg mice and wild-type (WT) littermates (C57BL6/J background) at 8 weeks of age.

### MicroRNA analysis

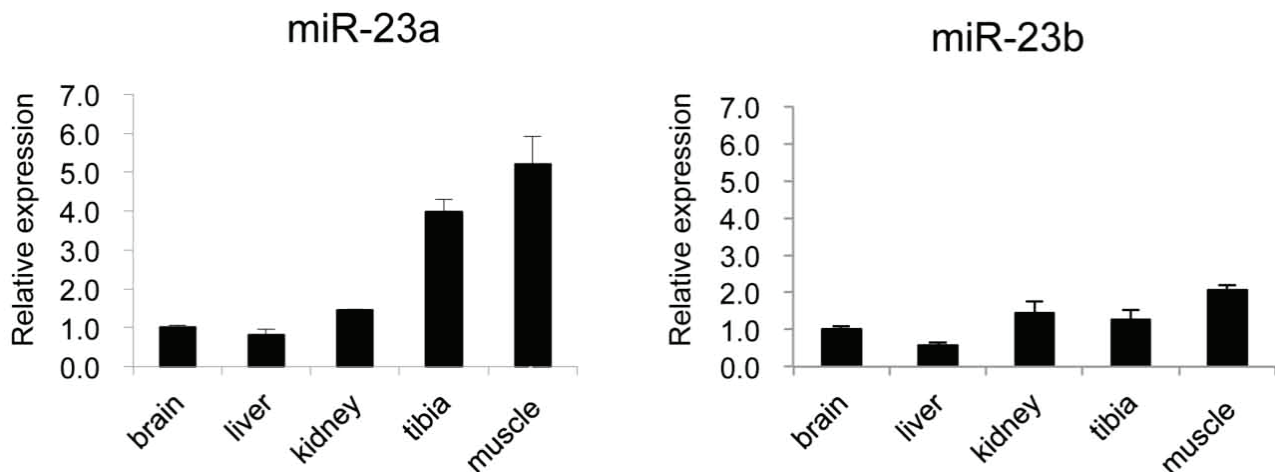
The TaqMan MicroRNA Reverse Transcription Kit and TaqMan MicroRNA assays (Applied Biosystems, Foster City, CA) were used for real-time PCR quantification of mature miRNA expression. Briefly, mature miR-23a was reverse-transcribed with specific reverse-transcription (RT) primers, quantified with a TaqMan probe, and normalized by U6 small nuclear RNA using TaqMan miRNA assays.

Total RNA (500 ng) was reverse-transcribed using specific RT primers for pri-miR-23a and ThermoScript RT (Invitrogen, Carlsbad, CA), as previously reported (Jiang *et al.* 2005). Briefly, 500 ng of total RNA, 1  $\mu$ l of 10  $\mu$ M oligo-dT primer, and 2  $\mu$ l of 10 mM dNTP were mixed and distilled water was added to a total volume of 12  $\mu$ l. The mixture was heated at 85 °C for 5 min and 57 °C for 5 min. After chilling on ice for 2 min, 4  $\mu$ l of 5 $\times$  cDNA synthesis buffer, and 1  $\mu$ l each of 0.1 M DTT, RNase inhibitor (ToYoBo, Osaka, Japan), and ThermoScript RT (15 U/ $\mu$ l) were added to the mixture. The contents were gently mixed and incubated at 57 °C for 60 min, and were heated at 85 °C for 5 min to terminate the reaction. To quantify pri-miR-23a, 1  $\mu$ l of the RT product was amplified by PCR using Ex Taq HS (TaKaRa Bio, Shiga, Japan) in a total reaction volume of 50  $\mu$ l using the following primers: forward 5'-AGC AAG AAT GCT CCA ATC TCA-3' and reverse 5'-TGG TAA TCC CTG GCA ATG TG-3'. The PCR conditions for pre-miR-23a consisted of 34 cycles of denaturation at 98 °C for 10 s, annealing at 57 °C for 15 s, and extension at 72 °C for 15 s. The PCR products were electrophoresed on 2 % agarose gels containing 0.00005 % ethidium bromide for 30 min. Fluorescent images were acquired under ultraviolet light using an LAS3000 imager (FujiFilm Corp., Tokyo, Japan).

### Micro-computed tomography of trabecular and cortical bone

Bone morphology and microarchitecture were assessed by high-resolution micro-computed tomography ( $\mu$ CT) (inspeXio SMX-90CT; Shimadzu, Tokyo, Japan) as previously described (Harada *et al.* 2011). The proximal tibia and diaphysial tibia were scanned at an X-ray energy of 70 keV, with an integration time of 0.12 s and voxel size of 0.025 mm/pix. Three-dimensional (3D) reconstruction of mineralized tissue was performed using the TRI-BONE system (Ratoc System Engineering, Co., Ltd., Tokyo, Japan).

For the trabecular bone region of the proximal tibia, we determined trabecular bone volume (BV/TV, %), trabecular thickness (Tb.Th,  $\mu$ m), trabecular number (Tb.N, 1/mm), trabecular separation (Tb.Sp, mm), and structure model index (SMI) (Hildebrand and Rüeggsegger 1997). For the cortical bone region in the tibial diaphysis, we assessed medullary volume/total bone volume (MV/TV, %), cortical bone volume/total bone volume (CV/TV), and cortical thickness (Ct.Th,  $\mu$ m).



**Fig. 1.** Expression of miR-23a and miR-23b in brain, liver, kidney, tibia, and muscle of miR-23a Tg and WT mice. The expression levels of mature miR-23a and miR-23b were measured by real-time TaqMan RT-PCR, and were normalized to the expression of U6 with the  $2^{-\Delta\Delta Ct}$  cycle threshold method. Values are presented relative to the expression level in brain. Data are presented as the mean  $\pm$  SEM ( $n=3$ ). Tg, miR-23a transgenic mice; WT, wild-type mice

#### Histology and quantitative histomorphometry

Femoral width and length was measured using calipers. Femoral length was measured from greater trochanter to medial condyle. Femoral width was measured at the point of the half of femoral length. Quantitative histologic analysis, and quantitative static and dynamic histomorphometry were assessed as previously described (Hiruma *et al.* 2013). The histomorphometric measurements of the secondary spongiosa of the proximal tibia included trabecular BV/TV, Tb.Th, Tb.N, Tb.Sp, eroded surface/bone surface (ES/BS, %), osteoid surface/bone surface (OS/BS, %), osteoblast surface/bone surface (Ob.S/BS, %), osteoclast surface/bone surface (Oc.S/BS, %), osteoblast number/bone surface (Ob.N/BS,  $\text{mm}^{-1}$ ), osteoclast number/bone surface (Oc.N/BS,  $\text{mm}^{-1}$ ), and multiple osteoclast number/bone surface (Mu.Oc.N/BS,  $\text{mm}^{-1}$ ).

#### Measurement of alkaline phosphatase (ALP) and tartrate-resistant acid phosphatase (TRAP) activities

ALP and TRAP activities were measured as previously described with minor modifications (Bessey *et al.* 1946, Lau *et al.* 1987). After completely removing the bone marrow and blood from the cortical region of the femur, the bone fragments were grinded in a mortar on dry ice and homogenized in a buffer consisting of 10 mM 2-amino-2-hydroxymethyl-1,3-propanediol, 0.9 % NaCl, and 1 % Triton X-100. After centrifugation, the protein content of the supernatant was determined by the Lowry method (Lowry *et al.* 1951).

ALP activity was determined as the release of

*p*-nitrophenol (*p*NP) from *p*-nitrophenol phosphate (*p*NPP). First, 1 ml of a mixture of 10 mM *p*NPP, 100 mM 2-amino-2-methyl 1,3-propanediol-HCl (pH 10.0), and 5 mM  $\text{MgCl}_2$  was incubated at 37 °C. Then, 10  $\mu\text{l}$  of the extracted protein was added and incubated at 37 °C for 10 min, followed by the addition of 66  $\mu\text{l}$  of 1 N NaOH to stop the reaction.

TRAP activity was determined using 10 mM *p*NPP in citrate buffer (pH 5.5) containing 200 mM NaCl and 80 mM L(+)- $\text{Na}_2\text{C}_4\text{H}_4\text{O}_6$ . Samples were incubated at 37 °C for 60 min and 66  $\mu\text{l}$  of 1 N NaOH was added to stop the reaction.

In both assays, the absorbance was measured (ARVO MX; PerkinElmer, Waltham, MA) at 405 nm. ALP and TRAP activities for each sample were calculated using a *p*NP standard curve and were normalized to the total protein concentration.

#### Statistics

Data are presented as the mean  $\pm$  standard error. Statistical significance ( $P<0.05$ ) was determined by Student's *t*-test for comparisons between two groups or by analysis of variance followed by Dunnett's test for comparisons between multiple groups.

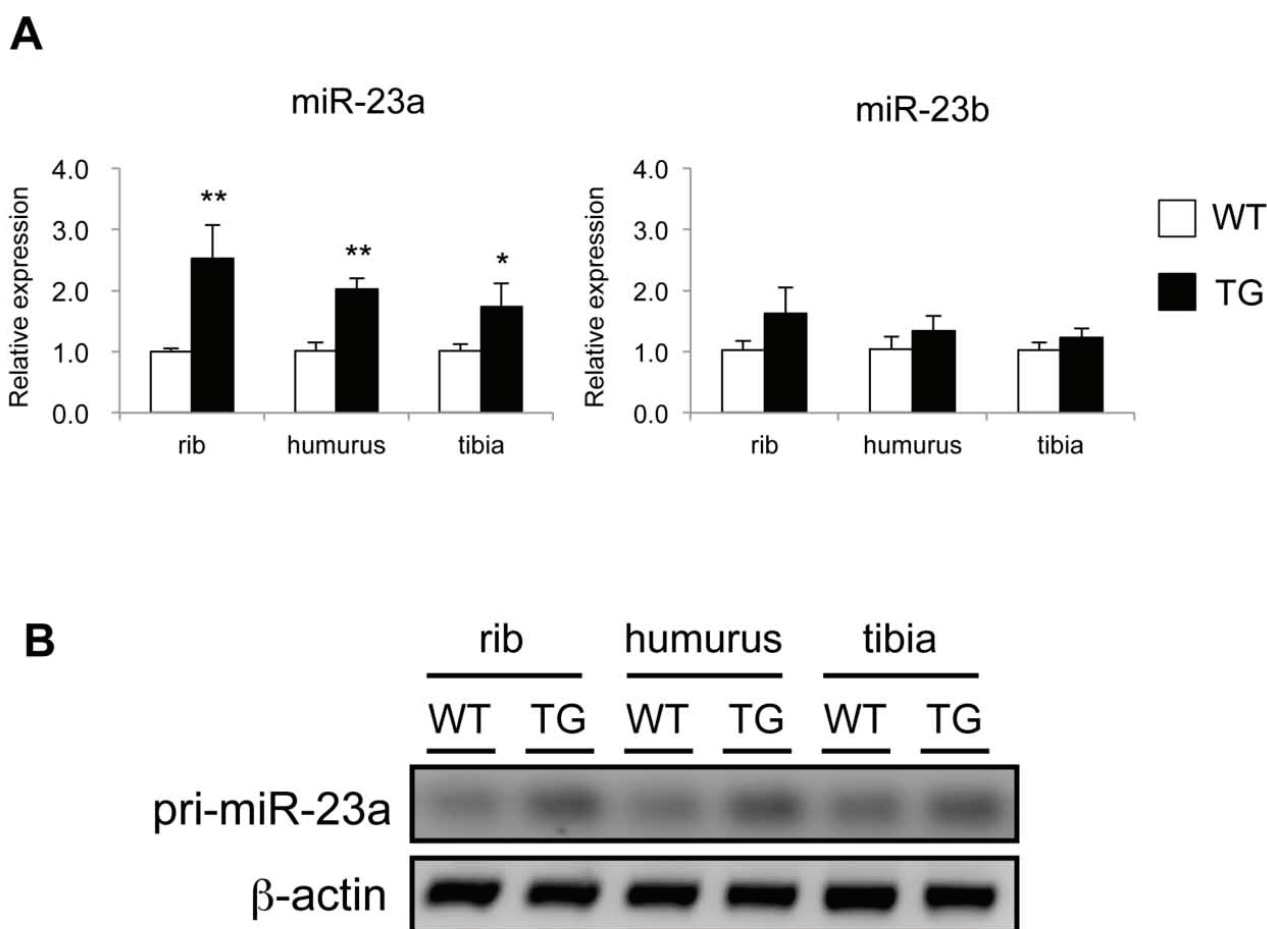
## Results

#### Tissue expression of miR-23

We first measured expression levels of miR-23a and miR-23b in various tissues from Tg mice (Fig. 1). Skeletal muscle had the highest expression level of miR-

23a of all tissues tested. The expression level of miR-23a was higher in bone than in brain, liver, or kidney. Skeletal muscle also had the highest expression level of miR-23b,

but the differences in miR-23b expression levels among the tissues were quite small. These results suggest that miR-23a has some roles in bone.



**Fig. 2.** Expression of miR-23a in the bones of miR-23a Tg mice. **(A)** The expression levels of mature miR-23a and miR-23b were measured by real-time TaqMan RT-PCR. **(B)** Precursor miR-23a (pre-miR-23a) was quantified by semi-quantitative PCR ( $n=4$ ). Values are relative to the expression in the rib of WT mice. \*  $P<0.05$  and \*\*  $P<0.01$  vs. WT mice. Data are presented as the mean  $\pm$  SEM ( $n=4-5$ ). Tg, miR-23a transgenic mice; WT, wild-type mice

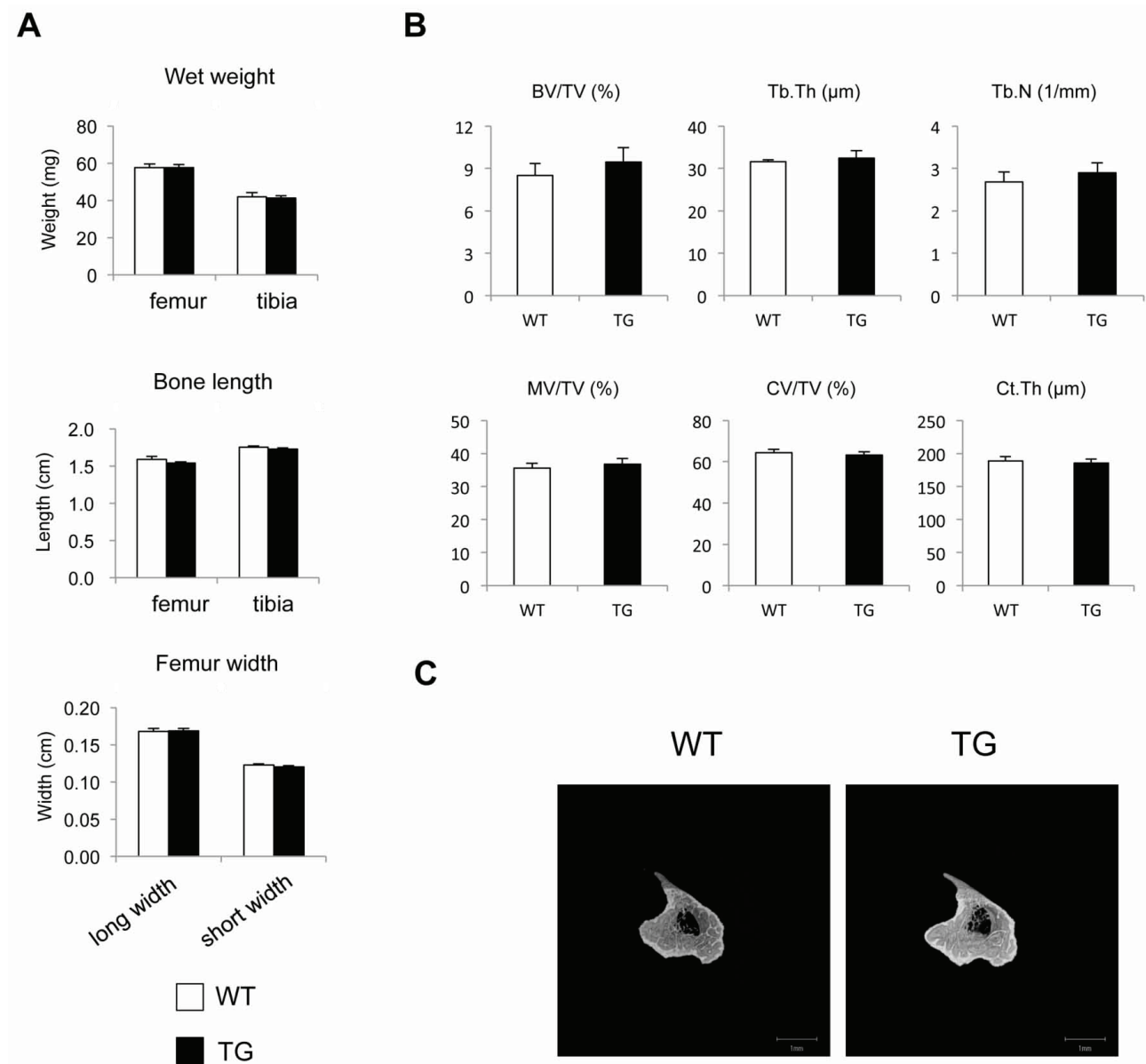
#### Skeletal growth in miR-23a Tg mice

The expression of mature miR-23a in bone was about 2 times higher in Tg mice than in WT littermates, whereas the expression of mature miR-23b was not significantly different between these genotypes (Fig. 2A). We confirmed that the expression of primary miR-23a (pri-miR-23a) was also increased in Tg mice (Fig. 2B). The Tg mice were born in normal Mendelian ratios and were fertile. The skeletal development of Tg mice during embryogenesis was macroscopically normal (data not shown). Postnatally, the Tg mice grew normally, and their body size and weight were similar to those of WT littermates. The bone weight and bone length were also similar between the two genotypes (Fig. 3A). Femur width was not significantly different

between Tg and WT mice (Fig. 3A).

#### Bone morphology of Tg mice

We next assessed the bone morphology and microarchitecture of Tg mice using  $\mu$ CT. We scanned the proximal and diaphysial tibia, and determined BV/TV, Tb.Th, Tb.N, MV/TV, CV/TV, and Ct.Th. The results are shown in Figure 3B and 3C. The cortical bone and total bone volumes in WT mice were  $0.21\pm 0.03$  and  $0.21\pm 0.04$  mm<sup>3</sup>, respectively, while those in Tg mice were  $0.32\pm 0.05$  and  $0.33\pm 0.05$  mm<sup>3</sup>, respectively. The SMI was  $2.34\pm 0.66$  and  $2.90\pm 0.07$  in WT and Tg mice, respectively. There were no significant differences in any bone morphologic factors between Tg and WT mice.



**Fig. 3.** Bone morphology of miR-23a Tg mice. **(A)** Bone weight, bone length, and femur width in Tg and WT mice. **(B)** Bone morphology and microarchitecture were assessed by  $\mu$ CT. **(C)** Representative  $\mu$ CT images of the proximal tibia in WT and Tg mice. Data are presented as the mean  $\pm$  SEM ( $n=5-6$ ). Tg, miR-23a transgenic mice; WT, wild-type mice; BV/TV, trabecular bone volume/total bone volume; Tb.Th, trabecular thickness; Tb.N, trabecular number; MV/TV, medullary volume/total bone volume; CV/TV, cortical bone volume/total bone volume; Ct.Th, cortical thickness

#### Histomorphometry of Tg mice

We next assessed whether overexpression of miR-23a affected the histomorphometric characteristics of bone (Fig. 4A, B). The histomorphometric measurements of the secondary spongiosa of the proximal tibia revealed no differences in the parameters BV/TV, Tb.Th, Tb.N, Tb.Sp, ES/BS, OS/BS, Ob.S/BS, Oc.S/BS, Ob.N/BS, Oc.N/BS, or Mu.Oc.N/BS between Tg and WT mice (Fig. 4A, B).

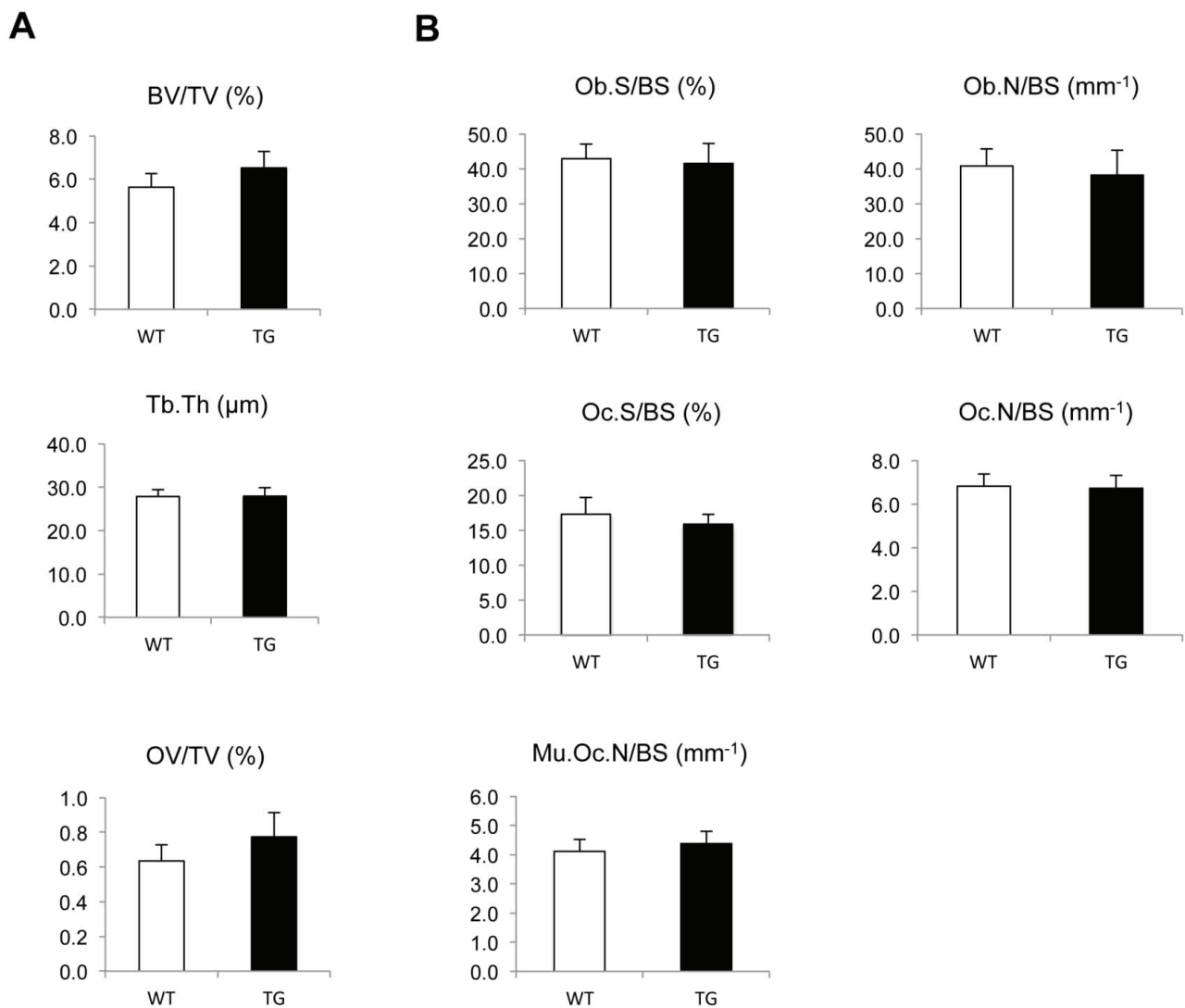
#### Osteoblast and osteoclast activities in Tg mice

We finally assessed osteoblast and osteoclast

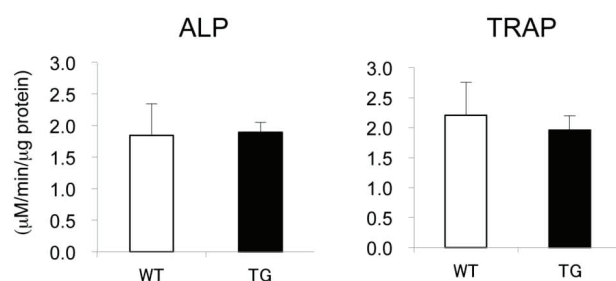
activities in Tg mice. As shown in Figure 5, there were no differences in ALP or TRAP activities between Tg and WT mice.

#### Discussion

The present results show that miR-23a-mediated control of gene expression has limited roles in bone formation and homeostasis *in vivo*, based on the morphology, microarchitecture, and histology of bone in miR-23a Tg mice.



**Fig. 4.** Bone histochemistry of miR-23a Tg mice. Bone morphology and microarchitecture were assessed histologically. Data are presented as the mean  $\pm$  SEM ( $n=5-6$ ). Tg, miR-23a transgenic mice; WT, wild-type mice; BV/TV, bone volume/total volume fraction; Tb.Th, trabecular thickness; Tb.N, trabecular number; Tb.Sp, trabecular separation; ES/BS, eroded surface/bone surface; OS/BS, osteoid surface/bone surface; Ob.S/BS, osteoblast surface/bone surface; Oc.S/BS, osteoclast surface/bone surface; Ob.N/BS, osteoblast number/bone surface; Oc.N/BS, osteoclast number/bone surface



**Fig. 5.** Osteoblast and osteoclast activities in miR-23a Tg mice. ALP and TRAP activities were measured by colorimetric assays. Data are presented as the mean  $\pm$  SEM ( $n=5-6$ ). Tg, miR-23a transgenic mice; WT, wild-type mice; ALP, alkaline phosphatase; TRAP, tartrate-resistant acid phosphatase

Several *in vitro* studies have shown that miR-23a suppresses the protein expression of Runx2 and Satb2 by directly binding to their 3' untranslated regions (Hassan *et al.* 2010, Zhang *et al.* 2011). According to these earlier observations, we hypothesize that overexpression of miR-23a in mice would delay osteocyte maturation in the mineralized matrix and would adversely affect bone structure, including its architecture, morphology, and histology. However, contrary to our original hypothesis, we found that the bone morphology of miR-23a Tg mice was normal, and was similar to that of their WT littermates. Furthermore, the histological analysis showed that the numbers of osteoblasts and osteoclasts, as well as their activities, were similar in both genotypes. These

findings indicate that miR-23a plays limited roles in bone formation and homeostasis *in vivo*.

Runx2 is a runt-related transcription factor that is involved in the earliest stages of bone formation. Runx2 is also expressed in pre-chondrocytes (Enomoto *et al.* 2000). In humans, a mutation in one allele of Runx2 was found in patients with cleidocranial dysplasia, a skeletal disorder (Lee *et al.* 1997, Mundlos *et al.* 1997). A similar phenotype was observed in mice with a mutation in one allele of this gene (Otto *et al.* 1997). Transgenic mice with a dominant-negative form of Runx2 exhibited transient osteopenia, confirming the importance of Runx2 in postnatal bone formation (Ducy *et al.* 1999). We expected to see an Runx2 loss-of-function phenotype in miR-23a Tg mice, if the expression of miR-23a was sufficient to inhibit Runx2 protein expression *in vivo*.

It has been shown that miR-23a also targets Satb2, a member of the special AT-rich binding transcription factor family, which interact with nuclear matrix attachment regions and activate transcription (Hassan *et al.* 2010). Of note, Satb2 directly interacts with Runx2 to enhance its activity (Dobrev *et al.* 2006). Deletion of Satb2 in mice and mutations in Satb2 in humans revealed that Satb2 is involved in osteoblast differentiation and craniofacial development (Dobrev *et al.* 2006, Leoyklang *et al.* 2007, Britanova *et al.* 2006). Overexpression of miR-23a in MC3T3-E1 cells inhibited osteogenic differentiation by inhibiting Runx2 and Satb2 protein translation (Hassan *et al.* 2010, Zhang *et al.* 2011). Osteoblast numbers and activities in Tg mice were similar to those in WT mice, suggesting that overexpression of miR-23a did not affect osteogenic differentiation *in vivo*.

It was reported that the expression of miR-23a increases during osteogenesis (Hassan *et al.* 2010, Zhang *et al.* 2011). We also confirmed the induction of miR-23a in MC3T3-E1 cells, as an *in vitro* model of osteogenic differentiation (data not shown). It was speculated that the increased expression of miR-23a during osteogenesis attenuates the osteoblast-like activity of osteocytes in a mineralized matrix (Hassan *et al.* 2010). It is unclear why our *in vivo* data do not support the results of *in vitro* studies. One reason for this difference may be the vector system used to express the miRNAs. Stein's group

(Zhang *et al.* 2011, 2012) and Lian's group (Hassan *et al.* 2010) used a lentiviral vector system to express miR-23a *in vitro*, whereas we used a conventional plasmid vector system to generate Tg mice.

Another possibility is that the mild phenotype of the Tg mice arises from insufficient transgene expression. The expression of mature miR-23a in our Tg mice was about two times higher than that in WT littermates, while the expression of pri-miR-23a was much higher in Tg mice. We used an expression vector containing the chicken  $\beta$ -actin promoter and cytomegalovirus enhancer, a  $\beta$ -actin intron, and a bovine globin poly-adenylation signal to drive pre-miR-23a expression. This construct was used to generate Tg mice that express the target transgene throughout the body, and expression was maintained from pre-implantation of the embryo to adulthood (Okabe *et al.* 1997). It should also be noted that, although we used conventional mice to induce miR-23a expression and gain overall control of its expression, we are unable to rule out the possibility that other regulatory factors acted in a compensatory manner.

### Conflict of Interest

There is no conflict of interest.

### Acknowledgements

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### Abbreviations

ALP, alkaline phosphatase  
miRNA, microRNA  
Runx2, Runt-related transcription factor 2  
Satb2, Special AT-rich sequence-binding protein 2  
Tg, transgenic  
TRAP, tartrate-resistant acid phosphatase  
UTR, untranslated region  
WT, wild-type

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