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SP7 transcription factor ameliorates bone defect healing in low-density lipoprotein receptor-related protein 5-dependent osteoporosis mice

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Abstract: Loss-of-function variants in the low-density lipoprotein receptor-related protein 5 (LRP5) can lead to reduced bone formation, culminating in diminished bone mass. Our previous study reported SP7 transcription factor (SP7) binding sites on the LRP5 promoter and its pivotal role in upregulating LRP5 expression during implant osseointegration. However, the potential role of SP7 in ameliorating LRP5-dependent osteoporosis remained unknown. In this study, we used mice with a conditional knockout (cKO) of LRP5 in mature osteoblasts, which presented decreased osteogenesis. The in vitro experimental results showed that SP7 could promote LRP5 expression, thereby upregulating the osteogenic markers such as alkaline phosphatase (ALP), Runt-related transcription factor 2 (Runx2) and β-catenin ($P < 0.05$). For the in vivo experiment, the SP7 overexpression virus was injected into a bone defect model of LRP5 cKO mice, resulting in increased bone mineral density (BMD) ($P < 0.001$), volumetric density (bone volume (BV) / total volume (TV)) ($P < 0.001$) and decreased trabecular separation (Tb. Sp) ($P < 0.05$). These data suggested that SP7 could ameliorate bone defect healing in LRP5 cKO mice. Our study provides new insights into potential therapeutic opportunities for ameliorating LRP5-dependent osteoporosis.

Key words: Gene therapy; LRP5; SP7; Osteoporosis; Defect healing

1 Introduction

Osteoporosis, as a severe public health problem, is characterized by decreased bone density and reduced bone strength, eventually leading to skeletal dysfunction. Age, sex, hormones, physical activity, nutrition, hereditary factors, and environmental factors have all been reported to contribute to osteoporosis (Castrogiovanni et al., 2016; Cauley and Giangregorio, 2020; Munoz-Garach et al., 2020; He et al., 2023). Among these variables, genetic factors play a crucial

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role in the development of osteoporosis. Wnt/β-catenin signaling, the canonical branch of Wnt signaling, is a critical regulator in many skeletal physiological and pathological conditions (Baron and Kneissel, 2013; Knight et al., 2018), which has become one of the prime candidates for translational applications during bone regeneration (Leucht et al., 2019; Xu et al., 2022). Low-density lipoprotein receptor-related protein 5 (LRP5) is a coreceptor in the canonical Wnt signaling cascade that regulates bone metabolism (Katchkovsky et al., 2022). Previous studies have revealed the association between LRP5 mutations and human skeletal disorders, including osteoporosis-pseudoglioma syndrome (OPPG) caused by loss-of-function mutations in LRP5 (Gong et al., 2001). Additionally, genetic manipulation resulting in a gain-of-function of LRP5 induced a high bone mass phenotype in humans (Hofbauer et al., 2002; Little et al., 2002). The above evidence suggests that LRP5 is a highly desirable therapeutic target to ameliorate osteoporosis and promote bone regeneration. Our previous studies have also confirmed that LRP5 might be a potential therapeutic gene for enhancing bone regeneration during implant osseointegration (Jiang et al., 2017; Jiang et al., 2020).

In the past several years, the pharmacologic blockade of secreted inhibitors of WNT signaling
has received considerable attention for the purposes of LRP5-dependent osteoporosis therapy (Witcher et al., 2018). Nevertheless, the possibility of gene therapy to directly activate LRP5 warrants further investigation. Transcription factors directly interpret the genome and function as “master regulators” and “selector genes” to perform the first step in decoding the DNA sequence (Lambert et al., 2018). Transcription factors-based therapies have demonstrated great potential in achieving tissue regeneration including bone, cartilage and cardiac regeneration (Song et al., 2012a; Lee and Young, 2013; Rilo-Alvarez et al., 2021). The zinc finger protein SP7 is an indispensable transcription factor activating an array of genes involved in osteoblast differentiation within developing and mature bones (Fukuda et al., 2018). A previous study claimed that SP7 null mice lacked mature osteoblasts (Nakashima et al., 2002). Despite its significance in physiological homeostasis, the specific molecular functions of SP7 have yet to be fully elucidated (Hoshikawa et al., 2020; Wang et al., 2021). Similar to other SP family members, SP7 is initially posited to bind to GC-rich promoter/enhancer sequences to activate the osteogenic transcriptional network in osteoblasts (Hafner et al., 1995). However, evidence has emerged that the preference of SP7 for AT-rich promoter/enhancer sequences, distinct among SP proteins, is critical for osteoblast differentiation (Lui et al., 2022). Another recent study demonstrated that SP7 likely interacts with different enhancer DNA motifs at different osteoblast lineage stages to regulate enhancer activity (Wang, et al., 2021). Given its unique role in osteoblast differentiation, SP7 might be a promising therapeutic gene for tissue regeneration.

Wnt signaling, enhanced by activating mutations in LRP5, leads to the upregulation of SP7 expression (Lim et al., 2015). Conversely, SP7 expression is diminished in osteoblast precursor-specific β-catenin conditional knockout (cKO) mice and osteoblast-specific Wntless cKO mice (Hill et al., 2005; Zhong et al., 2012). Our recent study reported two SP7 binding sites on the rat LRP5 promoter, indicating a direct regulatory relationship between SP7 and LRP5. The important role of the SP7/LRP5 axis during early implant osseointegration has also been confirmed (Yu et al., 2022). Of note, it remains unknown whether SP7 regulates LRP5 expression to trigger a

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cascade of downstream signaling events to ameliorate LRP5-dependent osteoporosis *in vivo*. Thus, we hypothesized that SP7 could positively regulate LRP5 expression to restore osteogenesis in LRP5-dependent osteoporosis mice.

This study aimed to verify whether SP7 could regulate LRP5 expression *in vitro* and to investigate the potential role of SP7 in ameliorating bone defect healing in LRP5-dependent osteoporosis. Our findings provide novel insights into SP7 as a therapeutic target for osteoporosis treatment.

2 Experimental section

2.1 Mouse model generation and maintenance

LRP5$^{fl/fl}$ mice, B6N. FVB-Tg (BGLAP-Cre)1Clem/J (Oc-Cre) transgenic mice were purchased from The Jackson Laboratory (USA). B6/JGpt-Rosa26tm1 (CAG-LSL-Cas9-tdTomato)/Gpt (TdT) transgenic mice were obtained from Gem Pharmatech (Nanjing, China). To determine the genotype of transgenic mice, PCR analyses were conducted on genomic DNA extracted from mouse tails. The primers utilized for genotyping the floxed LRP5 knockout allele are listed in Supplementary Table 1. The mice were provided with a standard diet and housed under controlled climate with unrestricted access to food. All animal care and experimental procedures were approved by the Animal Research Committee of Zhejiang University (Hangzhou, China) and conducted following international standards. The animals were administered an intraperitoneal injection of alizarin (red) (30 μg/g; ScienCell, USA) at 10 days and calcein (green) (10 μg/g; Sigma-Aldrich, USA) at 3 days before being sacrificed. At 4, 8, 12, and 16 weeks, the male and female transgenic mice were harvested.

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2.2 Whole-mount skeletal staining

Skeletal staining allows the measurement of shapes and sizes of individual skeletal elements in their proper positions; therefore, it is a principal method for detecting skeletal changes. In addition, different staining makes it feasible to distinguish cartilage from bone, facilitating the determination of skeletal maturity rate (Rigueur and Lyons, 2014; Mead, 2020). To prepare the embryos for this process, they were subjected to brief scalding in hot tap water at 65℃ for 1 minute, after which the skin and viscera were removed. The embryos were then fixed in 95% ethanol for 1-2 days, followed by soaking in acetone for 2 days. Lastly, the embryos were submerged in alcian blue (300 mg alcian blue 8 GX in a mixture of 80 mL of 100% ethanol and 20 mL of glacial acetic acid) for cartilage staining for 1-2 days. They were then destained twice in 70% ethanol and incubated in 95% ethanol overnight. The 95% ethanol was subsequently removed and 2% KOH solution was added for 12-24 hours at room temperature until nearly all soft tissues disappeared. The next step involved the replacement of the 2% KOH solution with a solution of alizarin red (5 mg of alizarin red S in 100 mL of 1% KOH), in which the embryos were soaked for 12 hours at room temperature. Subsequently, the embryos underwent a series of clearing processes, including immersion in 1% KOH, followed by a mixture of 50% 1% KOH

and 50% glycerol, then a mixture of 50% ethanol and 50% glycerol. The embryos were finally transferred to 100% glycerol for preservation.

2.3 Isolation and culture of cells

Six- to eight-week-old WT mice were used to isolate the bone marrow mesenchymal stem cells (BMSCs). Briefly, the mice were sacrificed by decapitation under deep anesthesia with 3% pentobarbital sodium. To prepare the mice for analysis, their entire body was immersed in 75% ethanol for 1 minute. The tibias and femurs were then separated and a 2.5 mL syringe was used to aspirate the BMSCs from the bone marrows. Osteoblasts were isolated from the tibias and femurs of 3-week-old male WT and cKO mice by enzymatic digestion in a-MEM (Biological Industries, Israel) with 0.1% collagenase (Sigma-Aldrich, USA). BMSCs and osteoblasts were both cultured in basal medium comprising α-MEM containing 10% fetal bovine serum (FBS; Gibco, USA), 0.272 g/L L-glutamine (Sigma-Aldrich, USA), 1% penicillin (Gibco, USA), and 1% streptomycin (Gibco, USA).

2.4 Immunofluorescence microscopy

A total of 1×10^5 osteoblasts per well, derived from both WT and cKO mice, were seeded in 12-well plates and subjected to immunofluorescence assay. Following fixation with 4% paraformaldehyde, the nuclei of the samples were stained with 4',6-diamidino-2-phenylindole (DAPI; Solarbio, China) for 10-15 minutes. Subsequently, images were captured using a Zeiss Axio Observer A1 microscope (Germany).

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2.5 Flow cytometry

Passage 2 BMSCs with a density of $2x10^6$ cells/mL were suspended in ice-cold phosphate buffer saline (PBS) and incubated with the following antibodies: PE anti-mouse/rat CD29 antibody (102208; Biolegend, San Diego, CA), PE anti-mouse/human CD44 antibody (103008; Biolegend, San Diego, CA), PerCP/Cyanine5.5 anti-mouse/human CD11b antibody (101228; Biolegend, San Diego, CA), and PE anti-mouse CD45 antibody (147712; Biolegend, San Diego, CA). Flow cytometry (FCM) analysis was performed in a CytoFLEX LX multicolor analyzer (Beckman Coulter, Brea, CA, USA), and data analysis was conducted using FlowJo V10 (FlowJo, LLC, Ashland, OR, USA).

2.6 Construction and transfection of LRP5, SP7

In order to evaluate the potential regulatory effect of SP7 on LRP5, lentiviral vector interfering LRP5, interfering lentiviral vector negative control (LV5-NC), lentiviral vector overexpressing SP7, and overexpressing lentiviral vector negative control (LV3-NC) were prepared by GenePharma (Shanghai, China). BMSCs were characterized before experimentation. The FCM analysis of passage 2 BMSCs showed that BMSCs were positive for the stemness markers CD29 (99.98%) and CD44 (99%) but showed no expression of the negative markers CD11b (0.06%) and CD45 (0.22%) (Figure S1A−D). Then, BMSCs were seeded at a density of 3×10^5 cells/well in six-well dishes and divided into four groups according to the order of transfection with the lentivirus constructs: 1) Control group: transfected with LV5-NC first and

then with LV3-NC; 2) SP7+ group: transfected with LV5-NC first and then with lentiviral vector overexpressing SP7; 3) LRP5- group: transfected with lentiviral vector interfering LRP5 first and then with LV3-NC; 4) LRP5-/SP7+ group: transfected with lentiviral vector interfering LRP5 first and then with lentiviral vector overexpressing SP7.

2.7 ALP and Alizarin red S staining

The early osteogenic ability of BMSCs after transfection with the corresponding lentiviral vectors was evaluated through ALP staining while utilizing the BCIP/NBT alkaline phosphatase color development kit (C3206, Beyotime, Shanghai, China). The cells were fixed with 4% paraformaldehyde for 15 minutes, followed by complete coverage with the working solution for 30 minutes at room temperature. The working solution was subsequently discarded and the cells were rinsed three times with distilled water. The recorded results were subjected to analysis. Next, Alizarin red staining was performed to visualize the Ca nodules. After being cultured in an osteogenic culture medium (Cyagen Biosciences, Guangzhou, China) for 21 days, cells were fixed in 4% paraformaldehyde for 15 minutes and then stained with alizarin red (ScienCell, Carlsbad, USA) for one hour. The results were recorded by a scanner (LaserJet Pro, HP, USA).

2.8 Quantitative RT–qPCR

The total RNA of cultured cells was extracted using the TRIzol reagent (Invitrogen, Carlsbad, USA) following culturing in an osteogenic culture medium, and cDNA was synthesized using the PrimeScriptTM RT Reagent Kit (Perfect Real Time, TaKaRa, Dalian, China). The concentration of RNA was determined using the NanoDrop 2000 system (Thermo Fisher Scientific, USA). RT-qPCR was performed using an SYBR Green kit (TaKaRa, Japan) in an ABI ViiATM7 System (Applied Biosystems, Foster City, USA). The relative gene expression of genes was normalized to glyceraldehyde 3-phosphate dehydrogenase (GAPDH) using the $2^{-\Delta\Delta Ct}$ method. The utilized primer sequences are listed in Supplementary Table 2.

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2.9 Western blot analysis

The cells were cultured in an osteogenic induction medium for 7 days and then lysed in a combination of RIPA buffer (Beyotime, Shanghai, China) and 1 μL/mL protease inhibitor cocktail (Beyotime, Shanghai, China) for western blot analysis. Tris-glycine SDS-polyacrylamide gel electrophoresis (SDS-PAGE) was employed to separate proteins of equal amounts by utilizing a bicinchoninic acid (BCA) kit (Beyotime Biotechnology, China). Subsequently, the samples were transferred onto polyvinylidene fluoride (PVDF) membranes (Millipore, USA). The membranes were subjected to blocking using a blocking buffer consisting of 50 mM Tris-buffered saline (pH 7.4) with 5% skimmed milk and 0.1% Tween-20. After sectioning into small slices marked with indicators, various membranes were subjected to incubation with distinct primary antibodies at a temperature of 4℃ overnight. Subsequently, the membranes were washed four times for 10 minutes each with TBST and then exposed to HRP-conjugated goat anti-rabbit IgG (Goodbio Technology, China) for 1 hour. Afterwards, the membrane was washed four times for 10 minutes each with TBST and ultimately exposed using ECL solution (Applygen Technologies Inc., China) in a chemiluminescent detection system (Amersham Biosciences, UK). The intensities of the blots

were quantified using ImageJ software and normalized to those of GAPDH. The following primary antibodies were used: LRP5 (D80F2; Cell Signaling Technology, USA), SP7 (ab209484; Abcam, USA), β-catenin (ab32752; Abcam, USA), Runx2 (ab92336; Abcam, USA), and GAPDH (ab70699; Abcam, USA).

2.10 Surgery

Twelve-week-old male WT and cKO mice were divided into three groups as follows: 1) Control group: mice without the injection of SP7 lentiviral vector; 2) LVNC group: mice injected with 1 μL of LVNC into the prepared holes in the tibias; 3) SP7+ group: mice injected with 1 μL of the SP7 overexpressing lentiviral vector into the prepared holes in the tibias. In brief, all the included mice were anesthetized, and then bone defects were created on both sides of the anterior-proximal surfaces of the tibias using 1.2-mm dental stainless steel round drills by sequential drilling under cooled sterile saline irrigation. Subsequently, the muscles were meticulously sutured, with the LVNC and SP7+ groups having undergone lentivirus injection before muscle suturing. Alizarin (red) was intraperitoneally injected into individuals of each group at 10 days, followed by calcein (green) at 3 days before the animals were sacrificed. After a postoperative duration of 4 weeks, all animals from all groups were collected for analysis.

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2.11 Micro-computed tomography

Fully fixed samples were used for the micro-CT (Scanco Medical, Switzerland) scans. First, the sample was assembled in a cylindrical sample holder (diameter, 20.5 mm) with the long axis of the sample perpendicular to the X-ray source. The scanning parameters were set to 55 kV and 70 mA. We defined the regions of interest as the areas 0.5 mm proximally away from the growth plate to the distal 100 slices (10 μm per slice). Finally, the microarchitectural parameters were measured directly using the micro-CT Evaluation Program V4.4A (Scanco Medical).

2.12 Specimen preparation and histomorphometric analysis

The dissected samples were fixed in 4% paraformaldehyde for 2 days, then embedded in 0.5 M ethylenediaminetetraacetic acid disodium solution for 3 weeks at room temperature for demineralization. Next, HE, Masson, TRAP, Oil red, IHC, and immunofluorescence staining were performed according to standard procedures, and images of HE, Masson, TRAP, Oil red, and IHC were captured under a microscope (Laika, Germany). The immunofluorescence staining images were captured using a confocal laser scanning microscope (Nikon A1, Japan). The TRAP, Oil red, and IHC scores were calculated using ImageJ 1.53a.

2.13 Three-point bending test

In order to assess the biomechanical properties of femurs obtained from twelve-week-old male WT and cKO mice, a small animal bone strength test instrument (YLS-16A; Corp., Yanyi Jinan, P.R. China) was utilized to conduct a three-point bending experiment. The freshly dissected femurs were promptly subjected to this test using two end support points and one central loading point. Biomechanical measurements were obtained from the load-deformation curves, with the maximum load (N) being recorded.

2.14 Hard tissue sectioning

The samples were dehydrated in a graded ethanol series (70–100%) and embedded in methyl methacrylate after microCT scanning. Slices of the samples were made using a high-speed precision microtome (Leica 2500E; Germany) and ground to a final thickness of 40 mm. Next, the images of samples were observed and captured under a light microscope (Laika, Germany).

2.15 Statistics

Statistical analysis was conducted using unpaired, two-tailed Student's *t* test for comparisons between groups using Prism (GraphPad). The level of statistical significance was set at a *P* value < 0.05.

3 Results

3.1 Generation of the LRP5-related osteoporosis mouse model and identification of the Oc-Cre-mediated recombination

In order to explore the potential SP7 therapy strategy for LRP5-dependent osteoporosis, an LRP5-related osteoporosis mouse model was generated by crossing a floxed LRP5 ($LRP5^{fl/fl}$) mouse strain with a transgenic mouse that expresses Cre recombinase under the control of the osteocalcin promoter (B6N.FVB-Tg (BGLAP-Cre)1Clem/J, Oc-Cre) for specific recombination in osteoblasts. To demonstrate the specificity and efficiency of Oc-Cre-mediated recombination, we crossed the established B6N.FVB-Tg (BGLAP-Cre)1Clem/J (Oc-Cre) with the B6/JGpt-Rosa26tm1(CAG-LSL-Cas9-tdTomato)/Gpt (TdT) to generate the Oc-Cre; TdT reporter mouse model (Fig. 1A). The genotypes were identified by DNA horizontal electrophoresis (Fig. 1B). When constitutively activated, TdT-marked osteolineages express Oc-Cre, including bone surface osteoblasts, osteocytes and osteoprogenitor cell features while delaying Oc-Cre expression until postnatally restricting TdT targeting committed osteoblasts and osteocytes. The histological analysis of frozen sections from femurs and mandibles confirmed the presence of TdT+ cells (Fig. 1C). Next, to verify the specificity and efficiency of Cre-mediated recombination, osteoblasts were isolated from $LRP5^{fl/fl}$, TdT (WT) and Oc-Cre, $LRP5^{fl/fl}$, and TdT (cKO) mice. The fluorescence imaging of osteoblasts from WT and cKO male mice (Fig. 1D) and the FCM analysis of osteoblasts from cKO male mice (Fig. 1E) confirmed the specificity and efficiency of Cre-mediated recombination.

The immunohistochemical results showed that LRP5 was hardly expressed in the femur tissues of cKO mice and its downstream molecule β-catenin was also reduced compared with that in WT mice (Fig. 1F). In addition, RT–qPCR revealed that the mRNA expression levels of LRP5 were significantly decreased in osteoblasts from cKO mice compared with those from WT mice (Fig. 1G). Western blot analysis showed that the protein expressions of LRP5 were decreased in osteoblasts from cKO mice compared to WT mice (Fig. 1H). These results further proved the successful knockout of LRP5 in the osteolineages.

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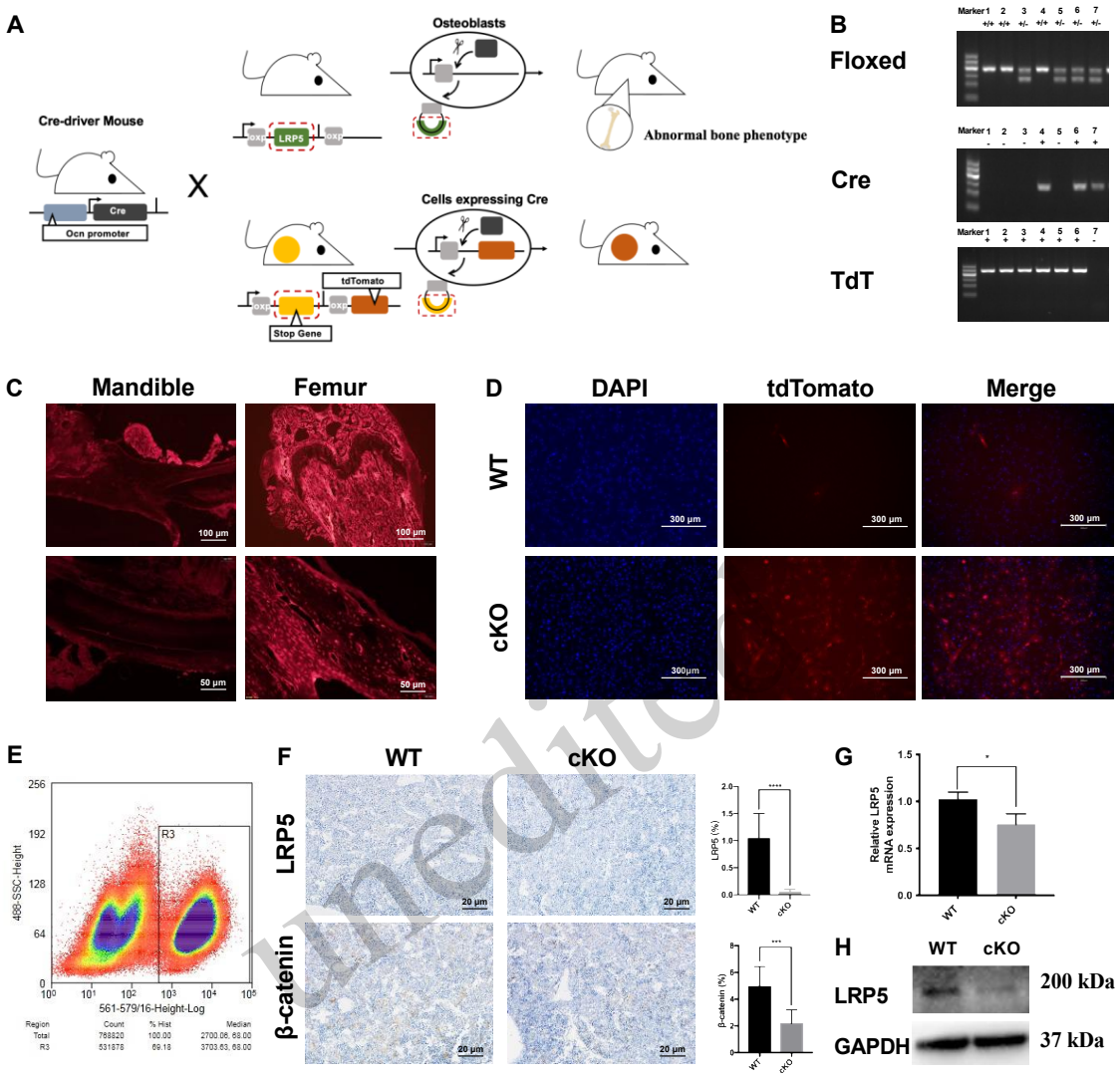

Fig. 1 The specificity and efficiency of Oc-Cre-mediated recombination was confirmed. (A) The Cre x Cre-reporter breeding strategy used in this study. (B) The genotypes were identified by DNA horizontal electrophoresis identification. (C) Histological analysis of frozen sections from femurs and mandibles of cKO mice. (D) Dual fluorescence imaging of osteoblasts from WT and cKO male mice. (E) FCM analysis of osteoblasts from cKO male mice. (F) Immunohistochemical staining and quantification of LRP5 and β-catenin from femoral sections of WT and cKO male mice. (G) According to RT-qPCR analysis, the relative mRNA expression of LRP5 was decreased in osteoblasts from cKO mice compared to WT mice. (H) Western blot analysis showed decreased protein expressions of LRP5 in osteoblasts from the cKO mice compared to WT mice. ***: $P < 0.001$, ****: $P < 0.0001$.

3.2 Characterization of morphological phenotypic changes in Oc-Cre; LRP5$^{fl/fl}$ mice.

As a first attempt to evaluate the skeletal development of the two genotypes of mice, we measured the weight and length of female and male specimens at 4 weeks of age (Fig. 2A-B). The body length of cKO mice was slightly decreased compared with that of WT mice, but the difference was not statistically significant. Furthermore, the two genotypes showed no significant difference in body weight. Newborn mice did not present any obvious systemic developmental

defects, which were difficult to distinguish by the naked eye in littermate WT mice (Fig. 2A). We used alcian blue and alizarin red S whole skeleton staining to examine the development of craniofacial and axial skeletons in cKO mice; cKO neonatal mice had shorter long bones and smaller skulls and mandibles (Fig. 2C). Furthermore, cKO exhibited the phenotype of wide sutures, unclosed fontanelles and wide cranial sutures. These data revealed that both intramembranous ossification and endochondral ossification were inhibited in cKO mice.

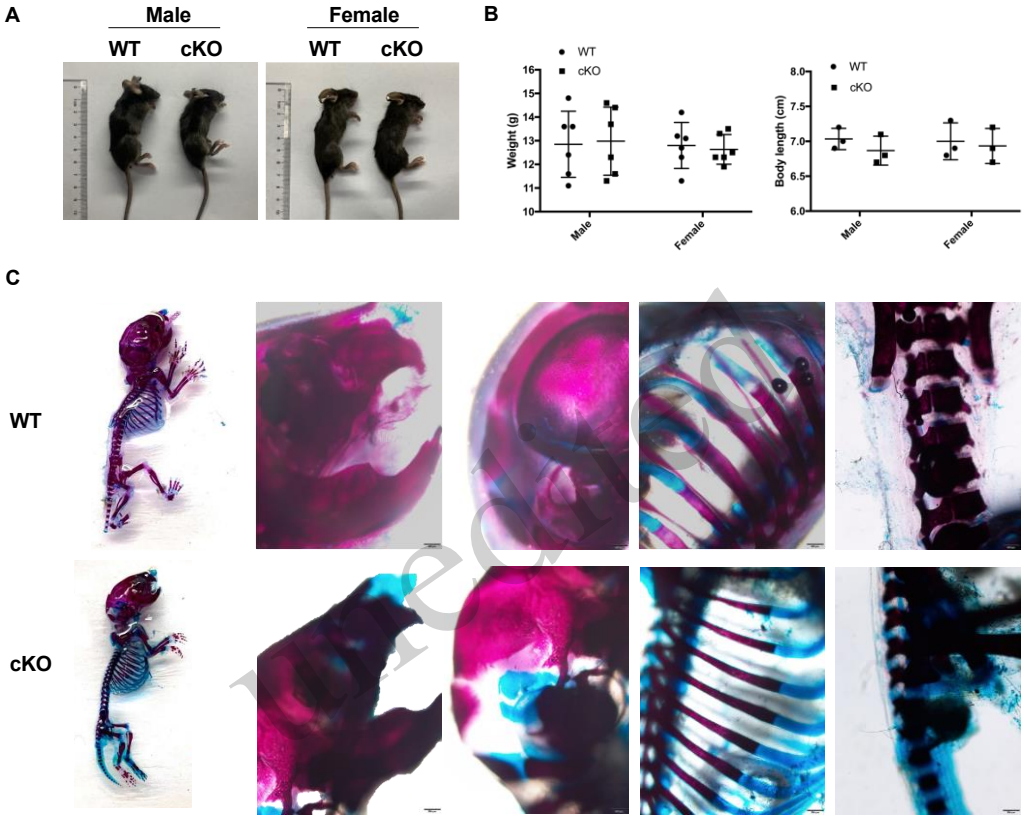

Fig. 2 Characterization of morphological phenotypic changes in Oc-Cre and LRP5$^{fl/fl}$ mice. (A) and (B) Weight and length measurement of WT and cKO 4W female/male mice. (C) Whole-mount skeletal staining of WT and cKO newborn mice.

3.3 Oc-Cre-mediated deletion of LRP5 led to decreased bone mass.

The histomorphometry of femoral metaphysis was performed to observe osteogenesis and adipogenesis in mice (Fig. 3A). The number and area of trabeculae in the bone marrow cavity of cKO mice were significantly reduced, as shown by HE and Masson staining. As a marker of bone resorptive activity, TRAP expression was elevated in cKO mice. Additionally, the proportion of fat in the medullary cavity was increased in these mice (Fig. 3A-B). The fluorochrome labeling of bone 10 and 3 days before sacrifice revealed a progressive pattern of bone formation and mineralization (Fig. 3D). Further morphometric analysis of the femoral bone by micro-CT (Fig. 4A-B) detected a significant decrease in the trabecular number in cKO mice compared with that in WT littermates. The volumetric density (bone volume (BV) / total volume (TV)), bone mineral density (BMD), and trabecular number (Tb. N) were significantly reduced in the proximal tibiae

of 4-, 8-, and 12-week-old cKO mice compared with those in age- and sex-matched WT mice, while trabecular separation (Tb. Sp) was markedly increased.

Using the above detection methods, we could confirm that the BMD and bone mass of cKO mice were significantly lower than those of WT mice. The biomechanical properties of mouse femurs in different groups were analyzed using the three-point bending test (Fig. 3D). Compared with that in WT mice, the elastic modulus of cKO mouse femurs was reduced, lowering the bending ability of the femurs in this mouse type. The bone yield and fracture strength were also diminished, with statistical significance. Therefore, the lack of LRP5 in bone tissue was considered to potentially cause bone loss and reduce bone fragility.

RT–qPCR indicated that the mRNA expression levels of LRP5 and the expression of downstream genes, including β-catenin, Runx2, and SP7, were significantly decreased in osteoblasts from cKO mice compared with those from WT mice (Fig. 4C). Western blot analysis showed decreased protein expressions of LRP5, β-catenin, Runx2, and SP7 in osteoblasts from cKO mice compared to WT mice (Fig. 4D), which suggested that LRP5 played a vital role in bone homeostasis via an LRP5/β-catenin/Runx2/SP7 regulatory loop. Correspondingly, alkaline phosphatase (ALP) activity was decreased in osteoblasts from WT mice (Fig. 4E).

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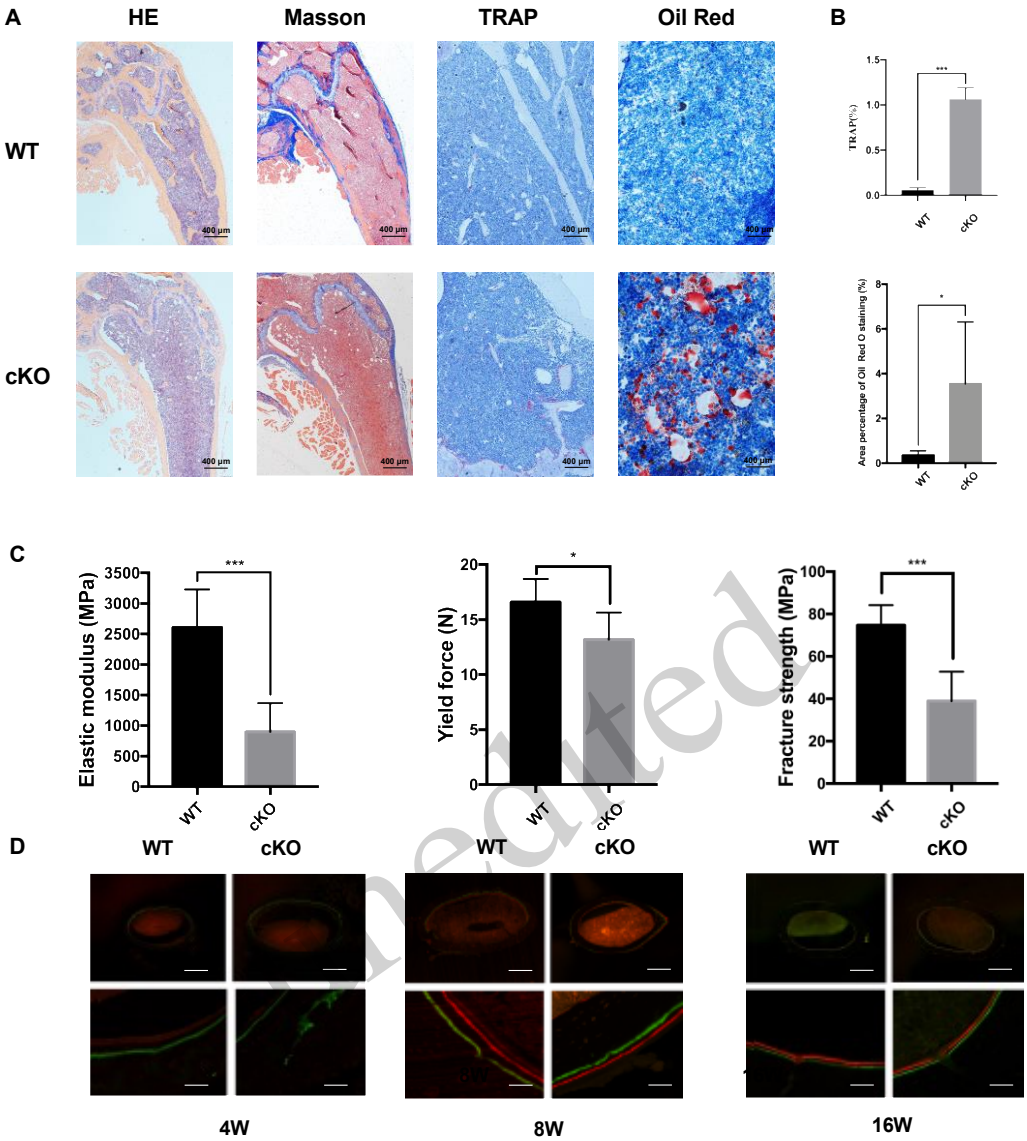

Fig.3 The deletion of LRP5 in Ocn+ osteoblasts resulted in bone impairment and marrow adiposity. (A) HE, Masson, TRAP, Oil red staining of femoral sections from WT and cKO male mice. Area percentage of TRAP and Oil red staining in the distal marrow per tissue area. (B) Three-point bending experiment to evaluate the biomechanical properties of mouse femurs from WT and cKO male mice. The elastic modulus, bone yield strength and fracture strength of cKO mice femurs were significantly reduced. (C) The images of fluorochrome labeling in the bone marrow of tibial defects from 4W, 8W, 16W WT and cKO male mice. *: $P < 0.05$, ***: $P < 0.001$.

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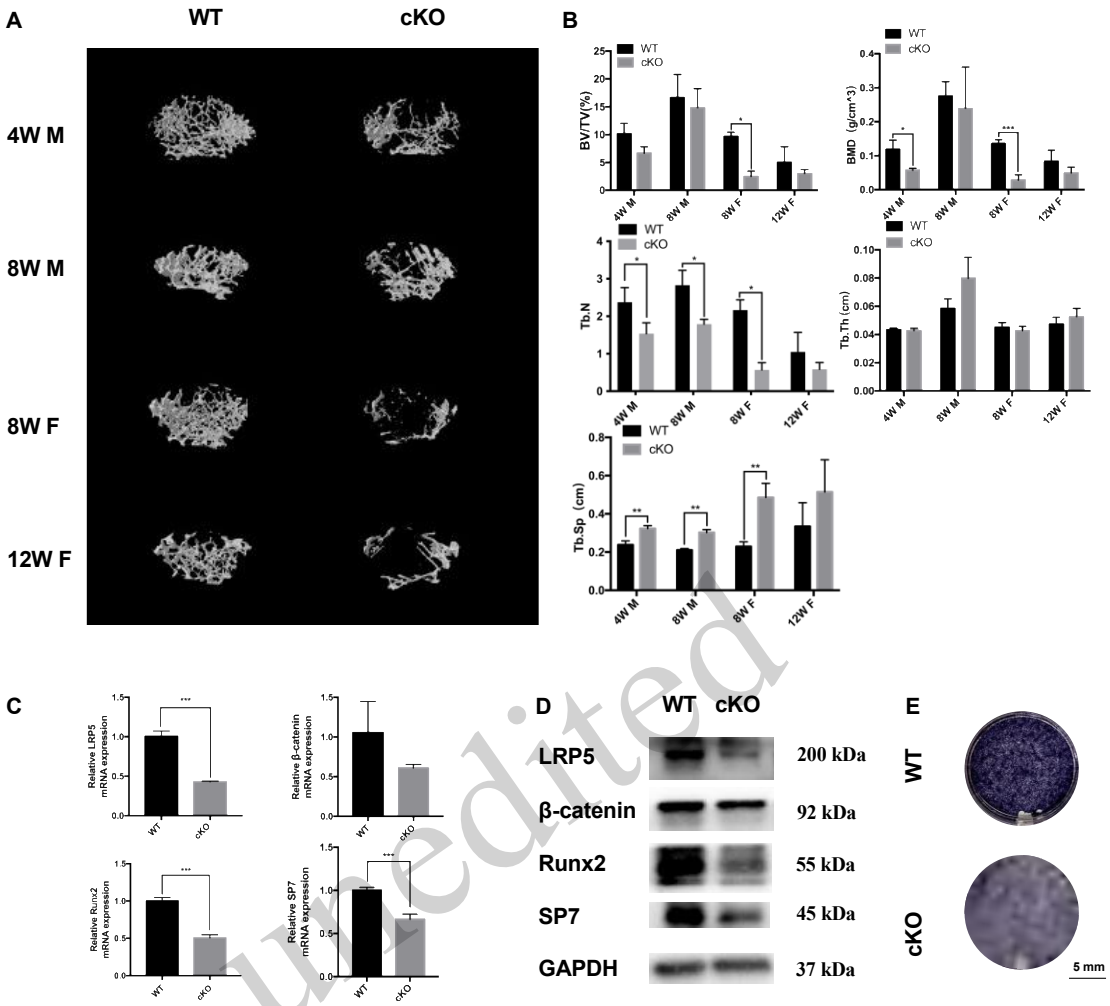

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Fig. 4 Relative expression of LRP5 in osteoblasts and expression changes of canonical Wnt signaling target genes. (A) Representative images of micro-CT reconstruction of trabecular bone structure in the distal femoral head. (B) Quantitative micro-CT analyses of metaphysis region of distal femurs. (C) According to RT-qPCR analysis, the relative mRNA expressions of LRP5, β-catenin, Runx2, and SP7 were decreased in osteoblasts from cKO mice compared to WT mice. (D) Western blot analysis showed the protein expressions of LRP5, β-catenin, Runx2, and SP7. (E) ALP staining was performed to evaluate the osteogenic ability of osteoblasts from cKO mice compared to WT mice on osteogenic day 7. *: *P* < 0.05, **: *P* < 0.005, *: *P* < 0.001.**

3.4 Role and mechanism of the SP7/LRP5 signaling axis in the osteogenesis of osteoblasts.

Our recent study reported a direct regulatory relationship between SP7 and LRP5 (Wang, et al., 2021). To study the role of SP7/LRP5 signaling axis in the osteogenesis of osteoblasts, we constructed cell models *in vitro* using lentiviral vectors to inhibit or overexpress related genes. ALP activity, detected by ALP staining and semiquantitative methods (Fig. 5A-B), was increased in the SP7+ group and decreased in the LRP5- group. When co-transfected with LRP5- and SP7+ viruses, the ALP activity was significantly increased compared with that in the LRP5- group. Similarly, mineralized nodules were increased after SP7 overexpression, and LRP5 inhibition decreased the number of mineralized nodules. SP7 overexpression prevented LRP5 inhibition and increased the number of mineralized nodules on Day 21. Furthermore, the results of RT–qPCR

and western blot indicated that the expression levels of LRP5, β-catenin and osteogenic markers Runx2 and SP7 were significantly repressed in the LRP5 group (Fig. 5C-D). SP7 overexpression significantly rescued the decreased expression of osteogenic genes caused by LRP5 interference. To explore the regulation between SP7 and LRP5, sequences were analyzed using the JASPER program (Khan et al., 2018). LRP5 regulatory elements share homology to known SP7 binding sites (Fig. 5E). The findings suggested that SP7 might be a direct transcriptional regulator that promoted LRP5 gene expression, and SP7 could be a promising therapeutic gene to ameliorate LRP5-dependent osteoporosis.

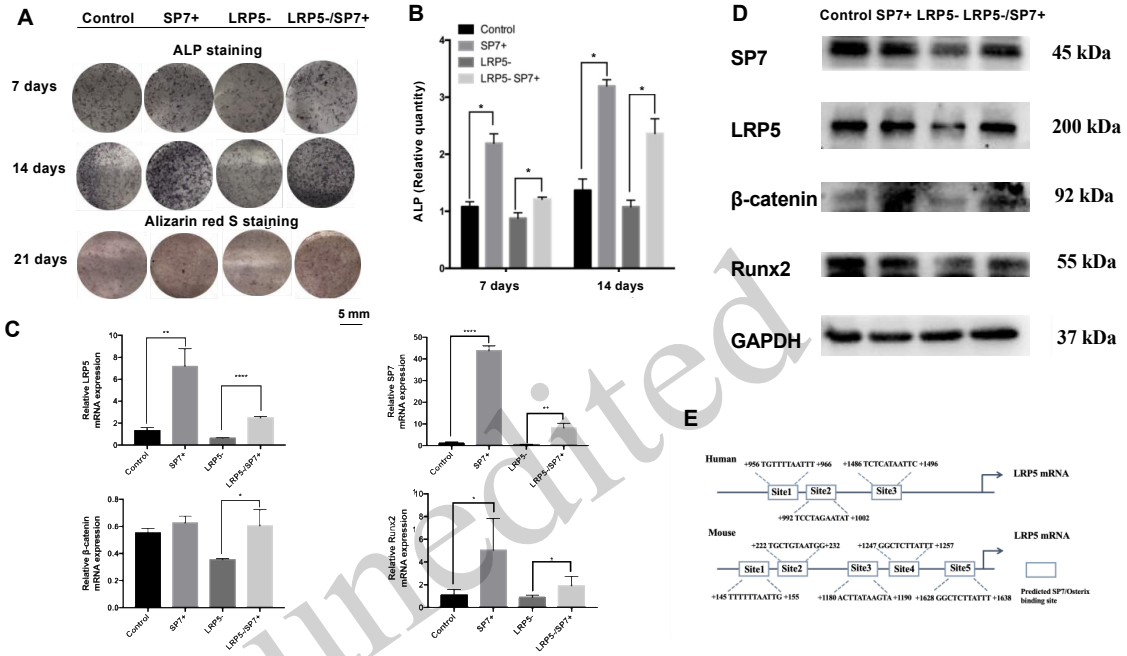

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Fig. 5 SP7 promoted LRP5 gene expression, thereby upregulating the osteogenic transcriptional network. (A) ALP staining was performed to evaluate the early osteogenic ability of mouse BMSCs on osteogenic day 7 and day 14 after cotransfection of LRP5- and SP7+. Alizarin red S staining was carried out to visualize the Ca nodules of mouse BMSCs on osteogenic day 21 after the co-transfection of LRP5- and SP7+. (B) The ALP activity of the LRP5-/SP7+ group was significantly increased compared to the LRP5- group. (C) RT-qPCR analysis of relative mRNA expression of SP7, LRP5, 2, β-catenin, and Runx2 on osteogenic day 7 after co-transfection of LRP5- and SP7+ in mouse BMSCs. (D) Western blot analysis showed the protein expressions of SP7, LRP5, Runx2, β-catenin, and on osteogenic day 7 after the co-transfection of LRP5- and SP7+ in mouse BMSCs. (E) Prediction of binding sites using the JASPER program. *: $P < 0.05$, **: $P < 0.005$, ***: $P < 0.001$.

3.5 SP7 viral therapy improved defect healing in adult mice lacking LRP5 *in vivo*.

In order to verify whether SP7 overexpression viral therapy can ameliorate osteogenesis in LRP5-dependent osteoporosis *in vivo*, a tibial defect model was constructed. The SP7 overexpressing virus was transfected into WT and cKO mice defect sites (Xiang et al., 2017). Micro-CT analysis was performed to evaluate new bone formation in the defect areas of each group at 4 weeks after surgery (Fig. 6A-B). The BMD and BV/TV of the WT: SP7+ group were higher than those of the WT: Blank and WT: LVNC groups, but the difference was not statistically significant. The BMD and BV/TV of the cKO: SP7+ group were significantly higher than those of the cKO: Blank and cKO: LVNC groups. To investigate the rates of mineralized bone formation

in the defect areas of each group, alizarin and calcein were administered for fluorochrome labeling 10 days and 3 days before sacrifice (Fig. 6C). The MAR of the WT: SP7+ group was higher than that of the WT: Blank and WT: LVNC groups, but the difference was not statistically significant. The MAR of the cKO: SP7+ group was significantly higher than that of the cKO: Blank group but not significantly different from that of the cKO: LVNC group (Fig. 6D). These results indicated that SP7 therapy could improve tibial defect healing in mice lacking LRP5 *in vivo*, indicating the potential value of SP7 as a therapeutic gene for osteoporosis.

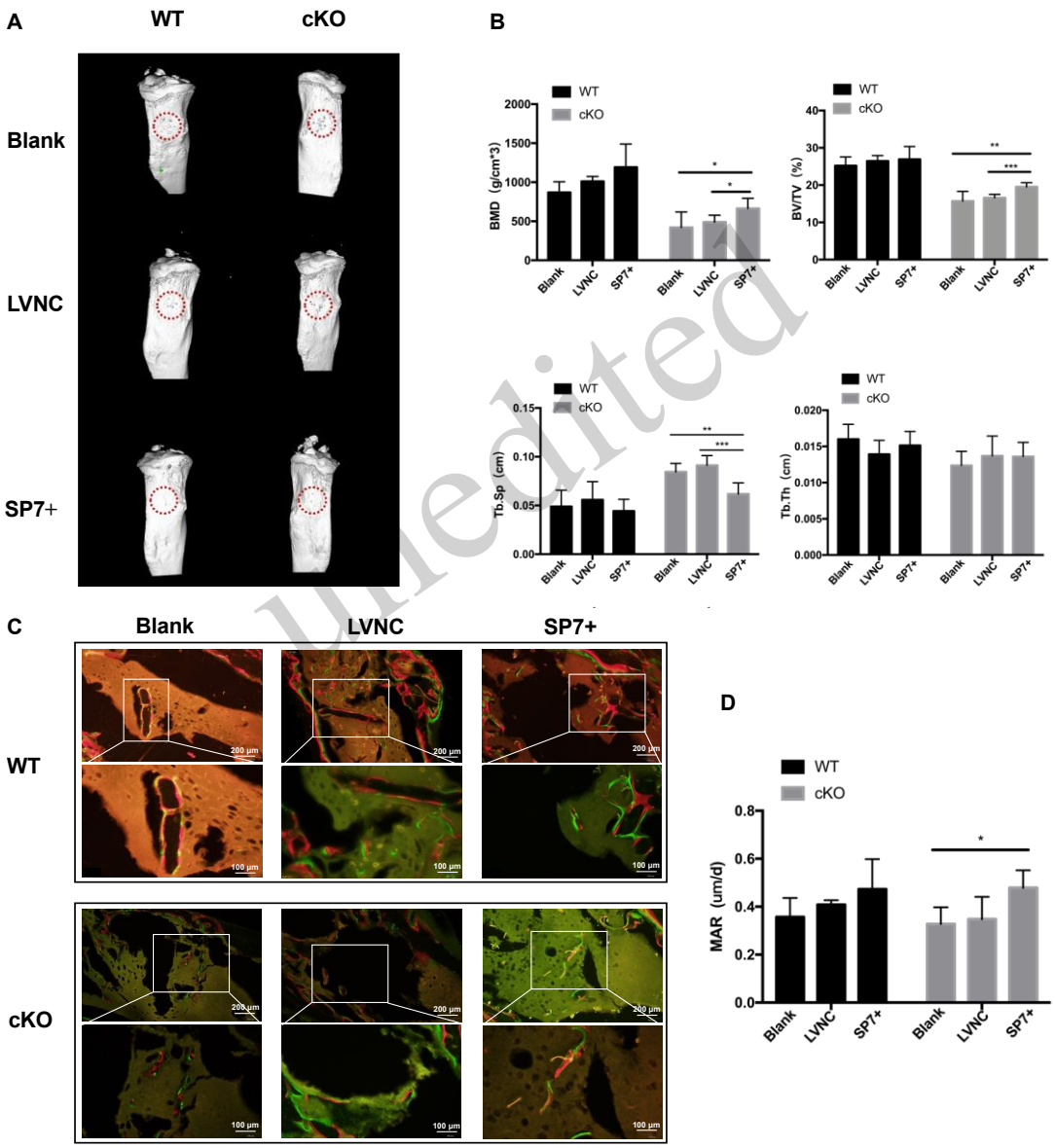

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Fig. 6 SP7 viral therapy improved tibia defect healing in adult mice lacking LRP5 *in vivo*. (A) The representative images of micro-CT reconstruction from six groups were observed and recorded 4 weeks after surgery. (B) Quantitative micro-CT analyses of the area of tibial defects from six groups. (C) Images of fluorochrome labeling in the area of tibial defects from six groups. The MAR of the WT: SP7+ group was significantly higher than that of the cKO: Blank group, but not significantly different from that of the cKO: LVNC group. *: $P < 0.05$, **: $P < 0.005$, ***: $P < 0.001$

4 Discussion

Emerging evidence points to SP7 as a vital transcription factor in the osteogenic differentiation of osteoblasts and bone healing. SP7 gene delivery has been reported to effectively induce bone differentiation (Tu et al., 2007; Wang et al., 2013; Kim et al., 2021) and the BMSC-associated osseointegration of implants (Xu et al., 2009). However, no studies have yet evaluated the role and underlying mechanisms of SP7 therapy in ameliorating osteogenesis for LRP5-dependent osteoporosis *in vivo*. Our study demonstrated that the viral delivery of SP7 could ameliorate compromised osteogenesis attributed to LRP5 deficiency by directly upregulating the suboptimal expression of LRP5. Moreover, we presented evidence on that defect healing was impaired in cKO mice, and local administration of the SP7 overexpression virus markedly enhanced the formation of new bone during the bone defect repair process in adult mice lacking LRP5 (Fig.7).

Consistent with previous results (Cui et al., 2011), abnormal bone tissues and impaired bone quality were found in cKO mice in the present study. We also established that bone defect healing was impaired due to LRP5 deficiency. A recent study reported similar activation of Wnt signaling within mesenchymal cells during bone defect healing in adult mouse skeletons (He, et al., 2023). Thus, Wnt signaling is considered essential for both skeletal development and postnatal bone regeneration. The phenotype of LRP5 cKO mice corroborated our *in vitro* observation that the loss of LRP5 in mature osteoblasts led to the low expression of osteogenic-related genes. Of note, the expression of SP7 was also reduced in LRP5 cKO mice.

Considerable progress has been made regarding our understanding of functional links between LRP5 and SP7. Our recent study indicated that bidirectional regulation between SP7 and LRP5 is involved in circRNA422-mediated early osseointegration of the implant (Yu, et al., 2022). In this paper, to investigate the potential role of SP7 therapy in ameliorating LRP5-dependent osteoporosis, we locally injected SP7 lentivirus into the tibia defect sites of WT and cKO mice. *In vivo* experiments revealed that the SP7 overexpression viral therapy promoted the formation of new bone during bone defect repair. The identification of the robust effects of SP7 overexpression virus in cKO suggests that LRP5-related diseases characterized by a relative or absolute decrease in bone formation might reap significant bone-building benefits from SP7 therapy. Therefore, SP7 overexpression viral delivery may ameliorate osteoporosis caused by the insufficient expression of LRP5, providing a novel therapeutic avenue for diseases characterized by a relative or absolute decrease in bone formation. We further analyzed the sequences from mouse or human samples using the JASPER program (Khan, et al., 2018) and could predict that the LRP5 regulatory element and SP7 binding site were homologous. However, it remains to be determined how the precise genomic binding sites of SP7 are specified to LRP5 and how SP7 binding ultimately relates to the regulation of LRP5 transcription.

Transcription factors are used for therapy either in a protein form or encoded in suitable gene vectors (plasmid DNA and mRNA in viral vector) (Kootstra and Verma, 2003; Ledo et al., 2020). In this study, the local delivery of SP7 was achieved by local administration of SP7 mRNA overexpression virus in the tibia defect area. mRNA gene therapy has been reported as a promising

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alternative leading to a higher level of tissue regeneration (Wang et al., 2020; Wisitrasameewong et al., 2022). Compared to the delivery of DNA, recombinant proteins and peptides, mRNA therapy is considered more efficient and suitable in non-dividing cells, since mRNA is directly translated inside the cytoplasm (Wisitrasameewong, et al., 2022). However, the instability and immunogenicity of mRNA largely limit its application *in vivo (Kimelman Bleich et al., 2012; Schlake et al., 2019).* In future studies, effective approaches to increase the stability and translatability of SP7 mRNA and decrease the high immunogenicity of this kind of therapy need to be explored. The introduction of modified nucleosides into the *in vitro* transcribed mRNA has been proven to be effective in solving the above problems (Kariko et al., 2005). Furthermore, a systemic treatment approach remains to be explored to deliver SP7 mRNA targeting whole-body bone tissue in LRP5-dependent osteoporosis mice. A recombinant adeno-associated virus 9 (rAAV9) has been reported to be highly effective for transducing osteoblasts in the bone (He, et al., 2023). Thus, the systemic delivery of SP7 targeting osteoblasts might be achieved via rAAV9 or improved rAAV9 in future work.

In addition, the fat content in the bone marrow cavity of knockout mice was relatively increased and bone resorption was accelerated in cKO mice compared with their control littermates. Previous studies have reported that the upregulation of PPARG and the downregulation of Runx2 in osteoblasts induced the transdifferentiation of osteoblasts to adipocytes (Kim et al., 2016). Song L et al has further confirmed that the loss of Wnt/β-catenin signaling caused the transdifferentiation of osteoblasts to adipocytes (Song et al., 2012b). Hence, it is hypothesized that the inactivation of LRP5 in Ocn+ osteoblasts may potentially induce the transdifferentiation of osteoblasts into adipocytes, leading to augmented adiposity within the bone marrow. However, the mechanisms underlying increased marrow adiposity formation need to be explored in future studies.

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5 Conclusions

In summary, we observed that SP7 enhanced the bone defect healing process by upregulating insufficient LRP5 expression, and the physical and functional interaction between LRP5 and SP7 was confirmed. SP7 could promote LRP5 gene expression, thereby upregulating the osteogenic transcriptional network. Our results suggest that SP7-mediated LRP5 activation could serve as a foundation for the development of therapeutic strategies aimed at improving conditions related to osteoporosis and facilitating bone repair.

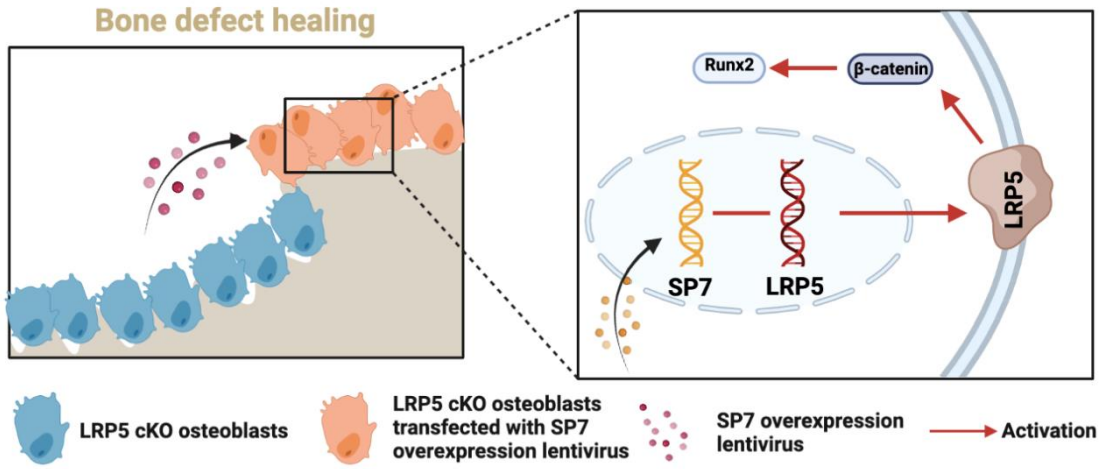

Fig. 7 Mechanisms of SP7-based therapy underlying bone defect healing in LRP5-dependent osteoporosis mice.

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Author contributions

Ying Wang, Guoli Yang, Yue Xi, and Qifeng Jiang performed the study concept; Wei Dai, Chaozhen Chen, and Yang Wang provided acquisition, analysis, and interpretation of data; Kaichen Lai, Xiaoyan Miao, and Zhiwei Jiang performed the development of methodology; Yue Xi and Qifeng Jiang performed statistical analysis and writing. All authors revised, read, and approved the final paper.

Compliance with ethics guidelines

Yue Xi, Qifeng Jiang, Wei Dai, Chaozhen Chen, Yang Wang, Xiaoyan Miao, Kaichen Lai, Zhiwei Jiang, Guoli Yang, Ying Wang declare that they have no conflict of interest.

All institutional and national guidelines for the care and use of laboratory animals were followed.

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Supplementary information:

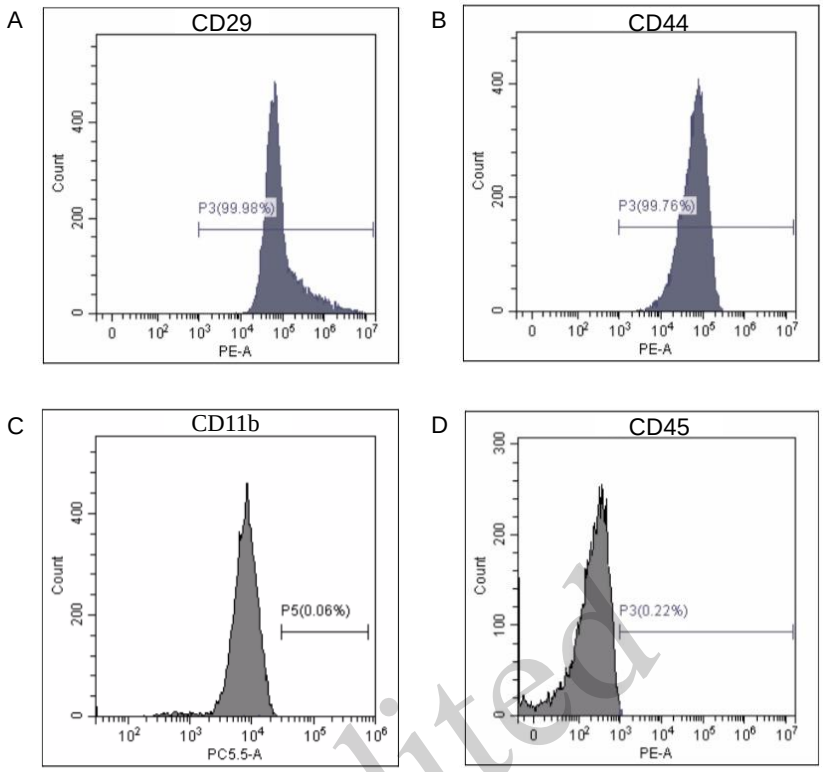

Figure S1. Characteristics of BMSCs. Flow cytometry analysis of cell marker expression on the surface of passage 2 BMSCs and showing that BMSCs were positive for CD29 and CD90 but negative for CD34 and CD45.

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Table 1. Primers used to identify the genotype of transgenic mice

Genes	Forward primer 5'-3'	Reverse primer 5'-3'
floxed LRP5 knockout allele	TGCTCTCCATTGGTTGTTCA	TTACCTGGGTCACCTGTCCT
Oc-Cre transgene	CAAATAGCCCTGGCAGATTC	TGATACAAGGGACATCTTCC
TdT transgene	CCCAAAGTCGCTCTGAGTTGTTA	TCGGGTGAGCATGTCTTTAATCT

Table 2. Primers used for RT-qPCR

Genes	Forward primer 5'-3'	Reverse primer 5'-3'
LRP5	*GAGCGAGGGTACATGTACTTTA*	*CACAGCTTTCGATTCGCTTTAG*
SP7	*GGAAAGGAGGCACAAAGAAGC*	*CCCCTTAGGCACTAGGAGC*
β-catenin	*AGGAATGAAGGCGTGGCAACATAC*	*GGCACCAATGTCCAGTCCAAGATC*
Runx2	*AGAGTCAGATTACAGATCCCAGG*	*TGGCTCTTCTTACTGAGAGAGG*
GAPDH	*GGAGCGAGATCCCTCCAAAAT*	*GGCTGTTGTCATACTTCTCATGG*