Prrx1-driven LINC complex disruption in vivo reduces osteoid deposition but not bone

quality after voluntary wheel running

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Word count: 3277

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Abstract

The Linker of Nucleoskeleton and Cytoskeleton (LINC) complex serves to connect the nuclear envelope and the cytoskeleton, influencing cellular processes such as nuclear arrangement, architecture, and mechanotransduction. The role LINC plays in mechanotransduction pathways in bone progenitor cells has been well studied; however, the mechanisms by which LINC complexes govern *in vivo* bone formation remain less clear. To bridge this knowledge gap, we established a murine model disrupting LINC using transgenic Prx-Cre mice and floxed Tg(CAG-LacZ/EGFP-KASH2) mice. Prx-Cre mice express the Cre recombinase enzyme controlled by the paired-related homeobox gene-1 promoter (*Prrx1*), a pivotal regulator of skeletal development. Prx-Cre animals have been widely used in the bone field to target bone progenitor cells. Tg(CAG-LacZ/EGFP-KASH2) mice carry a lox-stop-lox flanked LacZ gene allowing for the overexpression of an EGFP-KASH2 fusion protein via cre recombinase mediated deletion of the LacZ cassette. This disrupts endogenous Nesprin-Sun binding in a dominant negative manner disconnecting nesprin from the nuclear envelope. By combining these lines, we generated a Prrx1(+) cell-specific LINC disruption model to study its impact on the developing skeleton and subsequently exercise-induced bone accrual. The findings presented here indicate Prx-driven LINC disruption (PDLD) cells exhibit no change in osteogenic and adipogenic potential compared to controls *in vitro* nor are there bone quality changes when compared to in sedentary animals at 8 weeks. While PDLD animals displayed increased voluntary running activity andPrrx1(+) cell-specific LINC disruption abolished the exercise-induced increases in osteoid volume and surface after a 6-week exercise intervention, no other changes in bone microarchitecture or mechanical properties were found.

Key Words: Paired-related homeobox gene-1 (Prrx1), Mechanical Signals, Mesenchymal Stem Cells, Mechanobiology, LINC, Bone

<u>Introduction</u>

Bone is a highly dynamic tissue influenced by both biochemical and mechanical stimuli to retain

proper structure and function [1]. While the anabolic effects of mechanical challenge (i.e.

weight-bearing exercise) on bone quality is well accepted, how Linker of Nucleoskeleton and

Cytoskeleton (LINC) complexes may affect bone progenitor cell response to these signals

remains underexplored.

LINC complexes serve as a physical link between the cytoskeleton and the nucleoskeleton,

facilitating the transmission of mechanical forces and signals between the extracellular matrix

and the nucleus [2]. LINC complexes are comprised of cytoskeletal nesprins (nuclear envelope

spectrin repeats) and perinuclear Sun (Sad1/Unc84) proteins with the N-terminal calponin

homology domains of nesprins binding to cytoskeletal F-actin microfilaments and the

evolutionarily conserved C-terminal KASH (Klarsicht/Anc-1, Syne Homology) domains binding

to Sun domains within the perinuclear space. Sun proteins directly engage with the intranuclear

lamina, completing the connection from the cytoskeleton to the nucleus [3-5]. Beyond their

structural role, LINC complexes have emerged as critical components in transducing

mechanical signals within cells [6].

Earlier mesechmal stem cell (MSC) *in vitro* studies have effectively illustrated the dynamic

involvement of LINC complexes within mechanotransduction pathways [6, 7]. For instance,

disabling LINC complexes through RNA interference against SUN1 and SUN2 proteins, or

transfecting cells with a dominant negative Nesprin KASH domain, leads to the suppression of

focal adhesion kinase (FAK) and Akt phosphorylation[7]. This, in turn, circumvents the

mechanical repression of adipogenesis when mesenchymal stromal cells are exposed to low-

magnitude, high-frequency signals [6]. While the role of LINC complexes in

mechanotransduction has been demonstrated *in vitro*, their role in orchestrating the mechanical

regulation of bone in an *in vivo* remains largely uncharted. The current study aims to implement

an *in vivo* strategy to investigate the ramifications of LINC complex disruption during mechanical

loading, specifically within bone progenitor cells. This was achieved by creating a cre/lox Prrx1-

driven LINC disruption (PDLD) murine model.

The paired-related homeobox gene-1 (*Prrx1*) is widely used to target bone progenitor cells as it

is expressed in early limb bud mesenchyme, playing a crucial role in regulating skeletal

development, and is found in adult undifferentiated mesenchyme and periosteum [8-11]. Thus,

using transgenic Prrx1-cre mice we are able to target skeletal tissues throughout development

and into adulthood. LINC disruption in Prx(+) cells was then achieved by crossing these mice

with floxed mice created by Razafsky and Hodzic that overexpress an EGFP-KASH2 fusion

protein upon Cre-recombination [12, 13]. This fusion protein binds to perinuclear Sun proteins in

a dominant negative manner, causing displacement of cytoplasmic nesprins into the

endoplasmic reticulum and thus, disrupting LINC connectivity between the nucleus and

cytoskeleton.

While there are several modalities for mechanical stimulation *in vivo*, exercise is considered a

potent modality that can trigger adaptive responses in bone tissue, enhancing bone density and

strength [14]. A variety of exercise models including forced/trained treadmill running,

voluntary/forced wheel running, swimming, and resistance training (loaded/unloaded ladder

climbing) have been utilized in rodent studies, all of which have been shown to improve bone

mass, bone strength, and bone mineral density [15] [16]. We chose voluntary wheel running for

the present study to reduce the amount of handling/environmental stress on the animals.

To interrogate the effect of disabling LINC complex function in Prx positive bone cell

progenitors, we created a LINC disruption model under the Prx-Cre driver and measured

primary cell differentiation potential *in vitro*, bone microarchitecture via micro-computed

tomography (micro-CT) and mechanical properties via 3-point bending at an 8-week baseline.

We then subjected a cohort of animals to either a running or non-running intervention starting at

8-weeks of age and lasting for 6 weeks with a 1-week acclimation period. Micro-CT and

biomechanical properties were also measured post-exercise to assess any effects of LINC

disruption on exercise induced bone accrual.

Materials and Methods

Animals

Mouse strains included B6.Cg-Tg(Prrx1-cre))1Cjt/J aka *Prx-Cre* (The Jackson Laboratory, Stock

Number: 005584)[8], Tg(CAG-LacZ/EGFP-KASH2) aka *KASH2* (Hodzic, Wash U)[12], and

B6.Cg-Gt(ROSA)26Sor[tm14(CAG-tdTomato)Hze]/J aka *Ai14* (generously provided by Dr. Richard

Beard)[17].

Hemizygous *Prx-Cre* mice were crossed with floxed *KASH2* mice to generate Prrx1-driven LINC

disrupted (PDLD) murine model. LINC disruption mechanism described by Razafsky and Hodzic

[12, 13]. Briefly, upon cre recombination, a LacZ containing lox-stop-lox cassette upstream of an

eGFP-KASH2 ORF is excised allowing for the overexpression an eGFP-KASH2 fusion protein

which saturates available Sun/KASH binding in a dominant-negative manner. Genotyping was

performed on tissue biopsies via real-time PCR probing for LacZ and Cre (Transnetyx, Cordova,

TN) to determine experimental animals and controls. Cre(+)/LacZ(+) animals were considered

experimental and all other genotypes were considered controls. Animals were housed in

individually ventilated cages under controlled conditions until placement in conventional cages

for the duration of the exercise intervention. *Ad libitum* access to food and water allowed.

Additionally, *Prx-Cre* mice were crossed with Ai14 RFP reporter mice to assess Prx-Cre activity

in skeletal tissue and bone marrow cells. All procedures approved by Boise State University

Institutional Animal Care and Use Committee. During sacrifice animals were first anesthetized

via Isoflurane inhalation followed by decapitation in this way efforts to alleviate suffering. Except

sacrifice animals were subjected to running procedures which did not cause any distress or did

not require the use of pain-relieving drugs.

Bone Marrow Cell Isolation, Expansion, and Differentiation

Bone marrow cells were isolated from tibiae and femora via centrifugation as previously

described [18]. Briefly, tibia and femur were dissected, cleared of all soft tissue, and centrifuged

at 12,000xg to remove the bone marrow. This bone marrow pellet was then resuspended in

media and plated in supplemented growth media (alpha-MEM +20% FBS, +100U/mL penicillin,

+100µg/mL streptomycin). Cells were washed with PBS after 48 hours to remove non-adherent

cells and allowed to proliferate to 50% confluency. At this confluency, cells were lifted, split onto

two separate plates to produce enough cells for assays, and allowed to proliferate to ~80%

confluency. Cells were then lifted and plated for differentiation assays.

For osteogenic assays (n=4 replicates/group), cells were plated in triplicate and seeded at 200K

per well on 6-well plates in normal growth media for 24 hours prior to switching to osteogenic

media (alpha-MEM with 20% FBS, 100U/mL penicillin, 100µg/mL streptomycin, 10mM beta-

glycerophosphate, 50µg/µL ascorbic acid) for 14 or 21 days.

For adipogenic assays (n=4 replicates/group), cells were plated in triplicate and seeded at 150K

per well on 6-well plates in normal growth media for 24 hours prior to switching to adipogenic

media (alpha-MEM with 10% FBS, 100U/mL penicillin, 100µg/mL streptomycin, 5µg/mL insulin,

0.1µM dexamethasone, 50µM indomethacin) for 7 days.

Immunofluorescence staining and microscopy

Nesprin-1, Nesprin-2, Sun-1, and Sun-2 staining was performed on bone marrow cultures from

12-week Prx-Cre(+)/eGFP-KASH2(+) and aged-matched control mice (n=2/group). After

isolation and culture as described above, cells were rinsed with PBS, fixed in 4%

paraformaldehyde, permeabilized with 0.3% Triton buffer and blocked with 5% goat serum

(Jackson ImmunoResearch 005-000-001) prior to being tagged with a primary antibody.. After

primary antibody tagging, cells were incubated with an anti-rabbit secondary antibody (1:300

AlexaFluor 594nm goat anti-rabbit, Invitrogen A11037), nuclei were stained with Hoechst 33342

(Invitrogen™ R37605) and visualized via fluorescent microscopy (Zeiss LSM 900). No

additional staining was needed to visualize endogenous eGFP. Following primary antibodies

were used, Sun-1 (Sigma Aldrich, HPA008346), Sun-2 (Abcam, ab87036), Nesprin-2

(ImmuQuest, IQ565), Nesprin-1 (Millipore Sigma, MABT843).

Oil Red O and Alizarin Red Staining

After 7 days in adipogenic media, cultures were stained against Oil Red O as described

previously [19]. Briefly, cells were rinsed with PBS, fixed in 10% neutral buffered formalin for 30

mins at room temperature, and washed with deionized water. Cultures were then incubated in

100% propylene glycol, stained with 0.5% Oil Red O in propylene glycol, and finally incubated in

85% propylene glycol. Unbound dye was removed by rinses with tap water until clear and

images were taken. Oil Red O stain was then eluted with 100% propan-2-ol and optical

absorbance values were read on a microplate spectrophotometer (ThermoFisher Multiskan GO)

at 510nm.

After 14 days in osteogenic media, cells were rinsed in PBS, fixed with 70% ethanol, and

stained with 40mM Alizarin Red solution for visualization of calcium deposits. The stain was

then eluted using 10% w/v cetylpyridium chloride (CPC) and diluted 4-fold to avoid absorbance

saturation. Absorbance values were read on a microplate spectrophotometer (ThermoFisher

Multiskan GO) at 562nm.

Western Blot

Lysates were prepared using radio immunoprecipitation assay (RIPA) lysis buffer (150mM NaCl,

50mM Tris HCl, 1mM EDTA, 0.24% sodium deoxycholate,1% Igepal, pH 7.5) to protect the

samples from protein degradation NaF (25mM), Na_3VO_4 (2mM), aprotinin, leupeptin, pepstatin,

and phenylmethylsulfonylfluoride (PMSF) were added to the lysis buffer. Western protein

amounts were normalized to 15µg through BCA Protein Assay (Thermo Scientific, #23225).

Lysates (20µg) were separated on 10% poly-acrylamide gels and transferred to polyvinylidene

difluoride (PVDF) membranes. Membranes were blocked with milk (5%, w/v) diluted in Tris-

buffered saline containing Tween20 (TBS-T, 0.05%). Blots were then incubated overnight at 4°C

with appropriate primary antibodies. Following primary antibody incubation, blots were washed

and incubated with horseradish peroxidase-conjugated secondary antibody diluted at 1: 5,000

(Cell Signaling) at RT for 1h in 5% milk in TBST-T. Chemiluminescence was detected with ECL

plus (Amersham Biosciences, Piscataway, NJ). Following antibodies were used, Sun-1 (Sigma

Aldrich, HPA008346), Sun-2 (Abcam, ab87036, eGFP (abcam, ab184601)

Exercise Regimen

Eight-week old male PDLD or control mice were randomly assigned to a voluntary wheel

running exercise intervention, upright running wheel (Kaytee Silent Spinner Exercise Wheel), or

a non-running control group without access to a running wheel (n=10-12 mice/group). Animals

were allotted a one-week acclimation period in these new cages followed by a six-week tracked

exercise intervention. All mice were individually housed and running metrics including elapsed

time, total distance, average speed, and maximum speed were measured with a cyclocomputer

(CatEye Velo 7) and recorded daily. Ad libitum access to food and water was allowed. Body

mass and food intake was also tracked weekly.

Micro-computed tomography

Proximal tibiae (n=10-12 mice/group) stored frozen in PBS soaked gauze prior to scanning and

were scanned immersed in PBS using an x-ray microtomograph (SkyScan 1172F). Settings as

follows: power of 55kV/181mA, a voxel size of 10.33μm^3, and 230ms integration time. The

volume of interest for trabecular quantitative analysis started 10 slices distal to the proximal

physis extending 1 mm. The cortical volume of interest started 2.15mm distal to the physis,

extending another 0.5mm. Image reconstruction was performed with NRecon software (Bruker).

After any necessary image reorientation, quantitative analysis was performed with CTAn

(Bruker) and 3D image rendering was performed with CTVol. Reported variables and

nomenclature used according to ASBMR guidelines [20].

Three-point Bend Mechanical Testing

Bone strength was evaluated using 3-point bending on the tibias [21-23]. Tibias were rehydrated

in PBS for at least 24 hours prior to performing biomechanical testing. Biomechanical testing

was performed using a 3-point bending test fixture with an Instron Universal Testing System

model 5967. Due to the asymmetric nature of the tibia cross section, the biomechanical test

was optimized to place the most uniform cross section of the tibia between the spans, which

was set to 7.00 mm. This resulted in a region just below the trochanter and the distal end of the

tibia. A downward displacement of 0.02mm/s was applied until failure. Force and deflection data

was collected and analyzed in using MATLAB in order to determine the mechanical properties

of the bone(i.e. linear flexural stiffness, maximum yield force, and maximum force) according to

previously published methods [24, 25].

Histology

Tibias from 6-week voluntary running (n=8/grp) were MMA-embedded, thin sections were

deplasticized in acetone and stained via a modification of the von Kossa / MacNeal's (VKM)

Tetrachrome protocol.[26] For VKM-stained slides, mineralized bone was stained using the Von

Kossa silver method and the unmineralized tissue was counter-stained with MacNeal's

tetrachrome. Histomorphometric analysis was performed using the OsteoMeasure high

resolution digital video system (OsteoMetrics Inc., Decatur, GA). Standard nomenclature was

used according to the Histomorphometry Nomenclature Committee of the American Society of

Bone and Mineral Research.[27] Measurements included: osteoid volume per bone volume

(OV/BV), osteoid surface per bone surface (OS/BS), osteoblast surface per bone surface

(Ob.S./BS.), number of osteoblasts per bone perimeter (N.Ob./B.Pm.), and number of

osteoblasts per osteoblast perimeter (N.Ob./Ob.Pm.).

RNA-sequencing

Total RNA was extracted using RNAeasy (Qiagen) for three samples per group. Total RNA

samples were sent to Novogene for mRNA sequencing and analysis. Briefly, index of the

reference genome was built using Hisat2 v2.0.5 and paired-end clean 2 reads were aligned to

the reference genome using Hisat2 v2.0.5. featureCounts v1.5.0-p3 was used to count the

reads numbers mapped to each gene. And then FPKM of each gene was calculated based on

the length of the gene and reads count mapped to this gene. FPKM, expected number of

Fragments Per Kilobase of transcript sequence per Millions base pairs sequenced. Differential

expression analysis was performed using the DESeq2 R package (1.20.0). DESeq2 provides

statistical routines for determining differential expression in digital gene expression data using a

model based on the negative binomial distribution. The resulting P-values were adjusted using

the Benjamini and Hochberg's approach for controlling the false discovery rate. Genes with an

adjusted P-≤0.05 found by DESeq2 were assigned as differentially expressed. Genes with

significant differential gene expression were further analyzed with DAVID[28] for pathway

analysis. Pathways with a Benjamini ≤0.05 were selected, results were presented in Tables S1

and S2.

Statistical Analysis

Results are expressed as mean ± standard deviation. Normality was tested via Shapiro–Wilk

test. Significance was determined by 2-tailed unpaired student's t-test or 2-way ANOVA with

Tukey post-hoc test (Graphpad Prism version 10.2.0).

<u>Results</u>

Expression of EGFP-KASH2 fusion protein physically disrupts LINC complex in Prrx1 positive

cells

We crossed Prx-Cre(+) mice with the Ai14 RFP reporter line to visualize Cre activity in skeletal

tissues and bone marrow cells. P7 pups were placed in an *in vivo* fluorescent scanner (IVIS®

Spectrum) and notable red fluorescent in the appendicular skeleton and calvaria was visible

(Figure 1A), consistent with previous reports [29]. This confirms Cre recombinase activity is

present in Prrx1(+) tissues. We then isolated bone marrow from these animals at 12 weeks and

successfully visualized RFP containing cells within the bone marrow (Figure 1B) providing

evidence for the presence of Prrx1-Cre activity in bone marrow.

A Prx-driven LINC disruption (PDLD) model was then generated by crossing hemizygous Prx-

Cre(+) mice with floxed Tg(CAG-LacZ/EGFP-KASH2) mice. The mechanism for LINC disruption

in this model relies on Cre recombinase mediated excision of the lox-stop-lox LacZ cassette in

the *KASH2* mice allowing for the overexpression of an eGFP-KASH2 fusion protein. This fusion

protein then binds to perinuclear Sun proteins, displacing nesprins from the nuclear envelope.

To confirm this model disrupts LINC function via displacement of LINC complex elements

nesprin1, nesprin-2 , sun-1 and sun-2 , we flushed bone marrow from 12-week old PDLD and

control animals (N=4/group) to check for cells expressing endogenous eGFP localized to the

nuclear envelope, indicating the overexpression of the eGFP-KASH2 protein. We additionally

immunostained these cells with an anti-nesprin1, nesprin-2 (Figure2), sun-1 and sun-2 (Figure

3) antibodies and secondary fluorophore to confirm their detachment or decreased expression

from the nuclear envelope. As seen in Figure 2 and 3, there is a clear nuclear halo of eGFP

fluorescence in PDLD mice compared to no eGFP visualized in controls, we also confirmed the

eGFP expression via bone marrow flushing followed by western blotting agans eGFP (Fig.S1A).

Shown in Figure 2, nesprin-1 and nesprin-2 stainings do not show a clear nuclear localization

pattern (nuclear halo) in PDLD mice compared to the clear nuclear positioning seen in controls

indicating successful displacement of nesprins from the nuclear envelope where eGFP is

present. Shown in Figure 3 and Fig. S1B, sun1 and sun 2 show a slight decrease in PDLS

animas. These data provide evidence of successful LINC disruption in cells expressing eGFP.

Prrx1-driven LINC disruption does not change adipogenic and osteogenic differentiation

potential from LINC-intact controls

To determine the differentiation potential of LINC disrupted cells, bone marrow was flushed from

tibia and femur of 12-week male PDLD and negative control mice (n=4) and plated for

osteogenic/adipogenic differentiation assays (Figure 4). After 7 days, adipogenic cultures were

stained with Oil Red O and eluted stain was quantified via spectrophotometry at 510nm. After

14 days, osteogenic cultures were stained with Alizarin Red and eluted stain was quantified via

spectrophotometry at 562nm.

Relative absorbance values of Oil Red O dye from PDLD adipogenic cultures was 24.8% lower

than adipogenic LINC-intact controls (p=0.15) and 120.4% greater than undifferentiated controls

(p<0.05). Relative absorbance values of Alizarin Red stain from PDLD osteogenic cultures was

5.0% less than that of LINC intact osteogenic controls (p=0.8), and 531.4% greater than

undifferentiated LINC-intact controls (p<0.01). This suggests a trend towards diminished

adipogenic differentiated potential in PDLD cells compared to LINC-intact controls, but no

appreciable difference in osteogenic potential.

To exclude the possibility of these cells not surviving the marrow extraction we first confirmed

that eGFP-KASH expressing LINC-deficient cells were present in our cultures after marrow

extraction. Shortly, we harvested cells from female Prx-Cre(+)/Ai14(+)/eGFP-KASH2(+) animals

that express eGFP and tdTomato in Prx(+) cells. Cells were visualized for green and red

fluorescence. Average cell counts from 24 representative images with 683 total cells yielded

98.07 ± 7.2% red cells and 86.3 ± 14.52 % green cells indicating that eGFP- KASH2 expressing

cells were present in our cultures (Fig. S2 A/B). Next to confirm participation of LINC-deficient

cells in osteogenic nodules we have differentiated these cultures into osteogenic lineage and

stained with calcein blue. Our results in Fig.S2 C confirms that Prx-Cre(+)/eGFP-KASH2(+) cells

were present within calcein blue stained nodules. Finally, it is worth noting that the duration of *in*

vitro studies involving KASH overexpression is relatively short (1-2 days to 1 week), while the

animals in this study express the dominant negative KASH proteins chronically from conception.

To test the possible effect of acute versus chronic KASH protein expression, we utilized

transient transfection with a previously published dominant negative form of the nesprin-1 KASH

domain (DNK) [30, 31]. RNA-seq and qPCR results from transient DNK transfection show

decreased osteogenic gene transcripts *in vitro* when compared to empty mCherry plasmid

transfected controls (Fig.S3*).* Pathway analysis were provided in Tables S1 and S2 indicates

decreased collagen production was decreased in DNK expressing groups.

Bone microarchitecture unchanged in PDLD mice compared to LINC-intact controls at 8-week

baseline

Prior to starting a cohort on the exercise intervention, we established baseline bone

microarchitecture measurements via micro-computed tomography (micro-CT) using an 8-week

cohort of mice covering all four possible genotypes (n=3/grp): Prx-Cre(+)/EGFP-KASH2(+), Prx-

Cre(+)/EGFP-KASH2(-), Prx-Cre(-)/EGFP-KASH2(+), Prx-Cre(-)/EGFP-KASH2(-). There was

no significant difference found between genotypes (Fig. S4), so Prx-Cre(+)/EGFP-KASH2(+)

mice remained our experimental model while all other genotypes were indiscriminately used as

controls.

Each mouse from this cohort was weighed and both tibiae and femora were harvested from Prx-

Cre(+)/EGFP-KASH2(+) and control (n=10/group). Each tibia was cleared of soft tissue for

micro-CT analysis. We noted no change in body weight in PDLD mice vs. control recorded at

21.59 ± 1.7 g and 21.20 ± 0.77 g (p=0.68) respectively. A trend towards decreased bone

microarchitecture with a 5.6% decrease in BV/TV (p=0.30), 5.3% decrease in trabecular

thickness (p=0.19), and 6.10% decrease in cortical bone area (p=0.12) in PDLD mice was

observed between control and PDLD mice (Figure 5).

Prrx1-driven LINC disrupted mice run longer, farther, and faster than controls

A second cohort of 8-week male mice were given voluntary access to a running wheel (or no

wheel and allowed a one-week acclimation period before beginning the six-week tracked

exercise intervention. Tracked running metrics including elapsed time, average distance,

average velocity, and max speed were recorded daily (Figure 6). Our data indicate that PDLD

mice ran significantly longer, farther, and faster than their LINC intact counterparts with an

average run time of 169.2 ± 6.8 mins compared to 146.6 ± 9.4 mins (p<0.001), an average

distance of 2.35 ± 0.16 km compared to 1.82 ± 0.1 km (p<0.0001), and an average velocity was

0.53 ± 0.05 km/hr for PDLD mice and 0.48 ± 0.02 km/hr for controls (p<0.05).

LINC disruption does not significantly affect bone microarchitecture or mechanical properties in

PDLD mice subjected to six-week running protocol but decreases exercise-induced osteoid

deposition.

Bone microarchitecture was measured via micro-CT to assess any effects of LINC disruption on

exercise-induced bone accrual in the proximal tibial metaphysis and diaphysis for trabecular and

cortical parameters, respectively. There was no notable difference in trabecular bone fraction

(BV/TV), trabecular thickness (Tb.Th.), trabecular separation (Tb.Sp.), trabecular number

(Tb.N), total cortical tissue area (Tt.Ar.), or cortical thickness (Ct.Th.) between any of the

groups. There was, however, a 10.5% decrease ($p < 0.05$) in cortical bone area (Ct.Ar.) in

PDLD+Ex compared to sedentary LINC-intact controls and a 6.15% decrease ($p < 0.05$) in

cortical area fraction (Ct.Ar./Tt.Ar.) in PDLD+Ex compared to PDLD-Ex. No significant changes

in measured bone mechanical properties were noted (Figure 7). Representative micro-CT

images for trabecular and cortical architecture of control and PDLD animals with and without

exercise were presented in Figure S6.

Tibias from 6-week voluntary running (n=8/grp) were MMA-embedded and stained via a

modification of the von Kossa / MacNeal's (VKM) Tetrachrome protocol.[26] Shown in Fig.8,

analysis indicate that voluntary running exercise significantly increases osteoid volume (OV/BV,

252%, $p < 0.01$) and osteoid surface (OS/BS, 235% , $p < 0.05$) in control animals, suggesting that

exercise increases organic portion of the bone matrix that forms prior to the maturation. In

PDLD mice however this response to voluntary running exercise was completely abolished,

decreasing averaged osteoid volume by 17-fold (OV/BV, $p < 0.0001$) and that osteoid surface by

9.7-fold in exercised PDLD animals when compared to exercised control animals. Non-

exercised osteoid measures of control animals were not significantly different from non-

exercised PDLD mice. While no exercise effect was observed on osteoblast measures under

exercise and PDLD conditions, exercised PDLD mice showed a modest decrease of

Osteoblasts surface per bone surface (Ob.S./BS) when compared to both non exercised (42%,

$p < 0.0.5$) and exercised (50%, $p < 0.0.5$) control mice.   Similarly, osteoblast number per bone

perimeter (N.Ob./Ob.Pm) of PDLD exercise mice showed a small decrease (60%, $p < 0.05$) when

compared to non-exercised control.   No changes in of osteoblasts per osteoblast perimeter

(N.Ob./Ob.Pm.) were found.

Discussion

While the *in vitro* role of LINC complex in mechanotransduction pathways in bone progenitor

cells has been relatively well studied [32-45], its function *in vivo* remains underexplored. Here

we sought to elucidate if LINC complex disruption in *Prx(+)* cells influences bone marrow

stromal cell phenotype and compromises bone tissue quality throughout development and

during bone response to voluntary wheel running. After successfully generating a LINC

disruption mouse model under the Prrx1-Cre driver, we found no change in osteogenic and

adipogenic differentiation potential in PDLD cells, nor did we find any bone architecture changes

in PDLD mice at an 8-week baseline. While histology outcomes found that exercise-induced

osteoid volume and surface was abolished in PDLD animals, there were no remarkable

differences in bone microarchitecture or mechanical properties between PDLD mice subjected

to a six-week exercise intervention compared to LINC intact animals or sedentary controls.

Studies involving LINC complex disruption via KASH overexpression *in vitro* show decreases

osteogenic activity in human bone marrow mesenchymal stem cells by reducing Runx2 via

increased histone acetylation [47]. We recently reported that LINC disruption also decreases

adipogenic potential *in vitro* [48]. Despite this evidence, our results indicate no change in

adipogenic and osteogenic potential of these cells when extracted from bone marrow. To

exclude the possibility of these cells not surviving the marrow extraction we first confirmed that

eGFP-KASH expressing LINC-deficient cells were present in our cultures after marrow

extraction and next we ensured that LINC-deficient cells were participating in osteogenic

nodules (Fig. S2). Finally, to test possible the of acute versus chronic effects of KASH protein

expression, we utilized transient transfection with a previously published dominant negative

form of the nesprin-1 KASH domain (DNK) [30, 31]. The DNK plasmid utilized contains a

mutated form of the nesprin-1 KASH domain where the eGFP-KASH2 fusion protein contains a

mutated form of the nesprin-2 KASH domain. While KASH inserts come from different nesprin

isoforms the KASH domain is highly conserved between nesprin isoforms and results should be

comparable. [49] RNA-seq and qPCR results from transient DNK transfection show decreased

osteogenic gene transcripts *in vitro* when compared to empty mCherry plasmid transfected

controls (Fig.S3). While it is not clear why we did not see any effect on cell phenotypes from

animals, pathway analysis in DNK expressing cells show decreased levels of collagen

deposition related genes (Table S1), which support the decreased osteoid volume and surface

measures in PDLD animals (Fig.8). However, beyond osteoid measure we did not see any other

skeletal effects in animals, therefore, it is possible bone cells in our animals may have adapted

to this chronic expression of eGFP-KASH fusion protein and respond differently when compared

to acute expression of Nesirin-1 KASH domain.

Prrx1 is a well-established marker for early limb bud development [8, 9], and this study provides

valuable insights into the impact of LINC disruption across various developmental stages, from

embryogenesis through adolescence into adulthood. Interestingly, our findings suggest that this

disruption has no significant influence on the differential potential of bone marrow cells or whole

bone structural or mechanical properties. One possible explanation for this observation is that

cells with LINC disruption might be selectively excluded from the population of bone-forming

cells, possibly directed towards apoptotic pathways. Previous reports indicated a function of

nesprin-2 in apoptotic cells where nesprin-2 binds to Bax and the binding increases in apoptotic

cells[50] which may support this phenomenon. However, it's worth noting that we do detect

Prx1-Cre activity in adult bone marrow cell aspirates, indicating that these cells are still present

in the adult skeletal system. Yet, their precise function and role in bone biology remain unclear.

Some studies propose that cells originating from the Prx1 lineage may not be actively involved

in the homeostatic mechanisms or bone remodelling [29]. This raises questions about the

specific contributions of these cells within the intricate landscape of bone development and

maintenance, prompting further investigation into their functions and potential implications for

bone health.

Voluntary wheel running studies also with a six-week intervention but using older (16 week)

female mice found increased trabecular quality and quantity post-exercise in animals on a

regular diet [51] [52]. While bones of male mice also shown to respond to voluntary wheel

running [53] [54] [55], other studies using male mice reported minimal effects of exercise on

bone after 10 or 21 weeks of voluntary wheel running [56, 57]. Compared to reported daily

running metrics in these studies (ranging from 4-10 km/day), our mice ran less on average (2.1

km/day). The reason for this is unknown, but may have affected our outcomes. Furthermore, our

mice were 8-weeks old when placed in the exercise intervention, which is before the 12-week

reported age of skeletal maturity [56, 58]. Therefore, it is possible that mechanical challenge

provided by voluntary wheel running did not affect the ongoing bone growth in these mice and

thus were not able to alter osteoblast numbers (Fig.8). Further indicated in Figure 8 however,

we found however that voluntary running exercise significantly increases osteoid volume

(OV/BV) and osteoid surface (OS/BS) in control animals indicate that exercise increases organic

portion of the bone matrix that forms prior to the maturation after 6wk of voluntary running at

16wk of age. In PDLD mice however this response to voluntary running exercise was

completely abolished suggesting Prrx1+ cells may play a role in immature bone deposition.

Further studies using different modalities of LINC disruption (i.e. SUN & Nesprin depletion

models) or the use of different mesenchymal/osteochondroprogenitor cre drivers (i.e. Dermo1 or

Sox-9) would shed further light on the impact of impaired mechanotransduction in skeletal

stem/progenitor cells.

Acknowledgements

This study was supported by AG059923, AR075803, P20GM109095, NSF1929188 and NSF 2025505 to GU and AR074473 to WRT. The author(s) declare no competing interests financial or otherwise.

Author Contributions: All authors have read and approved the final submitted manuscript.

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Figure Legends

Figure 1. Prx-Cre activity confirmed in bone marrow using Ai14 reporter animals A) IVIS®

Spectrum *in vivo* fluorescent scan of P7 pups from Prrx1-Cre/Ai14 cross indicating skeletal Cre

activity in Prx-Cre(+) mice (red) vs. no Cre activity in Prx-Cre(-) littermates (blue). **B)**

Representative image of bone marrow aspirates from 8-week male Prx-Cre(+)/Ai14 mice

indicating the presence of Prx-Cre(+) cells within the bone marrow space.

Figure 2. Prrx1-driven LINC disruption (PDLD) model characterization A) Bone marrow

aspirates from 12-week male Prrx1-driven LINC disrupted (PDLD) and control littermates.

Confirmation of eGFP expression localized to the nuclear envelope with nesprin displacement

compared to no eGFP visualization and intact nesprin localization to the nuclear envelope in

controls. Cells were manually counted and analyzed for nuclear localization of eGFP and/or anti-

nesprin 2 red fluorescence. In PDLD cultures: 72.4% of cells had green, but not red nuclear

localization; 17.7% has red, but no green nuclear localization; and 9.9% had both (n=141 cells

from 12 images). In control cultures: out of 12 images from two separate animals, there was no

appreciable green fluorescence from 121 cells with red fluorescent nuclear localization. **B)** Bone

marrow aspirates from 12-week male Prrx1-driven LINC disrupted (PDLD) and control littermates.

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image of bone marrow aspirates from 8-week male Prx-Cre(+)/Ai14 mice indicating the presence

of Prx-Cre(+) cells within the bone marrow space. **C)** Bone marrow aspirates from 12-week male

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and intact nesprin localization to the nuclear envelope in controls

Figure 4. Bone marrow aspirates from PDLD mice do not display differences in osteogenic and adipogenic differentiation potential compared to LINC intact controls. A) Schematic for differentiation assay timeline as described in Methods **B)** 4x images of Oil Red O staining after 7 days in adipogenic or normal growth media for 12 week male ODLD mice vs LINC intact controls (n=4/grp). **C)** Absorbance values for eluted Oil Red O stain read at 510nm. **D)** 4x images of Alizarin Red staining after 21 days in osteogenic or normal growth media. **E)** Absorbance values for eluted Alizarin Red stain read at 562nm. Results presented as mean +/- SD. Normality confirmed with Shapiro-Wilk test. Significance determined via ordinary one-way ANOVA. *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$

Figure 5. Bone microarchitecture and body mass not significantly different between PDLD and control mice at 8-week baseline. Trabecular measurements include bone volume fraction (BV/TV), trabecular thickness (Tb.Th.), trabecular spacing (Tb.Sp.), and trabecular number (Tb.N). Cortical measurements include total cross-sectional area inside the periosteal envelope (Tt.Ar.), cortical bone area (Ct.Ar.), cortical area fraction (Ct.Ar./Tt.Ar.), and average cortical thickness (Ct.Th.) Significance determined via non-parametric Student's t-test. *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$

Figure 6. PDLD mice run significantly longer, farther, and faster than controls. A) Exercise regimen timeline schematic **B)** Body mass steadily increased throughout exercise intervention with no significant difference between groups. **C)** No significant difference in food intake between groups. **D)** PDLD mice ran longer, farther, and faster than LINC intact controls. Running metrics tracked by cyclometer measuring elapsed time, average distance and average velocity. Significance determined via 2-way ANOVA for body weight and food intake and unpaired Student's t-test for elapsed time, average distance, and average velocity. *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$

Figure 7. Trabecular and cortical microarchitecture of proximal tibiae unaffected by LINC disruption after 6-week voluntary wheel running. Trabecular measurements include bone volume fraction (BV/TV), trabecular thickness (Tb.Th.), trabecular spacing (Tb.Sp.), and trabecular number (Tb.N). Cortical measurements include total cross-sectional area inside the periosteal envelope (Tt.Ar.), cortical bone area (Ct.Ar.), cortical area fraction (Ct.Ar./Tt.Ar.), and average cortical thickness (Ct.Th.) n=10-12 mice.group. Significance determined two-way ANOVA with Tukey post-hoct '*p<0.05, **p<0.01, ***p<0.001

Figure 8. Von kossa staining for proximal tibiae section in LINC-disrupted and LINC-intact animals after 6-week voluntary wheel running. Measurements included: osteoid volume per bone volume (OV/BV), osteoid surface per bone surface (OS/BS), osteoblast surface per bone surface (Ob.S./BS.), number of osteoblasts per bone perimeter (N.Ob./B.Pm.), and number of osteoblasts per osteoblast perimeter (N.Ob./Ob.Pm.). n=8 animal per group.*p<0.05, **p<0.01, ***p<0.001

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green KASH-GFP expressing cells were located in the blue Calcein Blue stained nodule region

Figure S3. RNA-seq Analysis of DNK and MC Expressing MSCs During Osteogenesis: (**A**)

Heatmap of FPKM values for mCherry tagged dominant negative KASH (DNK) and empty

mCherry (MC) plasmids expressing MSCs during 7 days of osteogenesis all shown values were

$p<0.05$. (**B**) FPKM values of osteogenesis genes of Ibsp, Bglap, Alpl, and Phospho1 in MSCs

expressing DNK or MC plasmid during 7-day osteogenesis (**C**) qPCR quantification of same

samples using Alpl primer (Forward: aacccagacacaagcattcc, Reverse: gcctttgaggtttttggtca).

Both undifferentiated controls (UD) and osteogenic media (OS) was shown.

Figure S4. Bone microarchitecture for all four possible genotypes at 8-weeks (n=3/grp): Prx-

Cre(+)/EGFP-KASH2(+), Prx-Cre(+)/EGFP-KASH2(-), Prx-Cre(-)/EGFP-KASH2(+),   Prx-

Cre(-)/EGFP-KASH2(-). There was no significant difference found between genotypes.

Significance determined via ordinary one-way ANOVA.

Figure S5. Breeding scheme for the creation of PDLD mice. Hemizygous Prx-Cre mice were

crossed with floxed KASH2 mice to generate Prrx1-driven LINC disrupted (PDLD) murine model.

LINC disruption mechanism described by Razafsky and Hodzic**.** Genotyping was performed on

tissue biopsies via real-time PCR probing for LacZ and Cre (Transnetyx, Cordova, TN) to

determine experimental animals and controls. Cre(+)/LacZ(+) animals were considered

experimental and all other genotypes were considered controls.

Figure S6. Representative micro-CT images for trabecular and cortical architecture of control

and PDLD animals with and without exercise.

A)

Excitation filter: 535nm
Emission filter: 580nm

B)

Prx-Cre X Ai14 (red reporter)

Ai14

130 µm

130 µm

130 µm

Ai14

130 µm

130 µm

130 µm

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Supplementary Figures

Prrx1-driven LINC complex disruption in vivo reduces osteoid deposition but not bone quality after voluntary wheel running

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Figure S2 eGFP-KASH expressing cells in primary cell culture. A) Representative images of bone marrow aspirated from 12-week female Prx-Cre(+)/Ai14(+)/KASH(+) Number of cells per field expressing the GFP-KASH construct was determined by fluorescent microscopy in the control cells of Prx lineage were determined by tdTomato expression in both the control All counts were done utilizing FIJI. **B)** Graph of each cell percentages to total, error bars represent standard deviation. **C) KASH-GFP expressing cells contribute to the formation of osteogenic nodules.** Images were taken at 10X using a) FITC filter showing eGFP expression b), DAPI filter showing calcein blue fluorescence c) an overlay to qualitatively show that the green KASH-GFP expressing cells were located in the blue Calcein Blue stained nodule region

Figure S3. RNA-seq Analysis of DNK and MC Expressing MSCs During Osteogenesis:
(**A**) Heatmap of FPKM values for mCherry tagged dominant negative KASH (DNK) and empty mCherry (MC) plasmids expressing MSCs during 7 days of osteogenesis all shown values were p<0.05. (**B**) FPKM values of osteogenesis genes of Ibsp, Bglap, Alpl, and Phospho1 in MSCs expressing DNK or MC plasmid during 7-day osteogenesis (**C**) qPCR quantification of same samples using Alpl primer (Forward: aacccagacacaagcattcc, Reverse: gcctttgaggtttttggtca). Both undifferentiated controls (UD) and osteogenic media (OS) was shown.

Figure S4. Bone microarchitecture for all four possible genotypes at 8-weeks (n=3/grp): Prx-Cre(+)/EGFP-KASH2(+), Prx-Cre(+)/EGFP-KASH2(-), Prx-Cre(-)/EGFP-KASH2(+), Prx-Cre(-)/EGFP-KASH2(-). There was no significant difference found between genotypes. Significance determined via ordinary one-way ANOVA.

Tg(CAG-LacZ/EGFP-KASH2)

B6.Cg-Tg(Prrx1-cre)1Cjt/J

Tg(Prrx1 floxCAG-EGFP/KASH2)

Figure S5. Breeding scheme for the creation of PDLD mice. Hemizygous Prx-Cre mice were crossed with floxed KASH2 mice to generate Prrx1-driven LINC disrupted (PDLD) murine model. LINC disruption mechanism described by Razafsky and Hodzic**.** Genotyping was performed on tissue biopsies via real-time PCR probing for LacZ and Cre (Transnetyx, Cordova, TN) to determine experimental animals and controls. Cre(+)/LacZ(+) animals were considered experimental and all other genotypes were considered controls.

Figure S6. Representative micro-CT images for trabecular and cortical architecture of control and PDLD animals with and without exercise.