Partial Phenotyping of an Idiopathic Infantile Hypercalcemia

Mouse Model

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Abstract

Vitamin D is fundamental to mineral homeostasis, and bone development. Disorders in vitamin D metabolism lead to pathologies. For example, loss-of-function mutations in the *CYP24A1* gene were discovered as the first underlying genetic defects in Idiopathic Infantile Hypercalcemia (IIH). Recently, it has been reported that the R396W mutation in the *CYP24A1* gene is detected at high frequency in IIH patients. Our team previously showed that *Cyp24a1*-null mice with a deletion of exons 9-10, unable to produce 24,25(OH)₂D₃, mimicked the disease IIH. The mice also displayed impaired callus formation during the endochondral phase of fracture repair. Based on this earlier work, we hypothesized that a humanized mouse model sporting the site-specific R396W mutation will also exhibit impaired fracture repair.

We commercially contracted out the R396W knock-in embryonic stem (ES) cells and generated R396W-CD1 mouse strain which is a valid mimic of the IIH human condition. We then performed rodded tibial osteotomy on wild-type, heterozygous and homozygous R396W mutated mice. We harvested healing bones at intervals and tested their biomechanical properties.

Despite experimental challenges, torsion tests showed decreased stiffness of the healing calluses in mutant animals. Micro-Computed Tomography (μ CT) scanning, and 3-Point Bending Tests (3PBT) showed significant differences in load at break (strength) in both male and female mutants compared to heterozygous and/or wild-type littermates.

Our results indicate that the humanized preclinical model of IIH, R396W-CD1 strain, has similar phenotypic manifestations to the original *Cyp24a1*-null mice. Furthermore, we suggested that 24,25(OH)₂D₃ has an earlier effect during fracture repair than previously evaluated.

Résumé

La vitamine D est essentielle à l'homéostasie minérale et au développement osseux. Des troubles du métabolisme de la vitamine D entraînent des pathologies. Par exemple, des mutations de perte de fonction dans le gène *CYP24A1* ont été découvertes comme les premiers défauts génétiques sous-jacents dans l'hypercalcémie infantile idiopathique (IIH). Il a été rapporté que la mutation R396W du gène *CYP24A1* est détectée à haute fréquence chez les patients IIH. Notre équipe a précédemment montré que des souris mutantes pour *Cyp24a1* avec une délétion des exons 9-10 présentent un phénotype comparable à IIH. Les souris montrent aussi une formation de cals altérée pendant la phase endochondrale de la réparation des fractures. Sur la base de ces travaux antérieurs, nous avons émis l'hypothèse qu'un modèle de souris humanisé portant la mutation ciblée R396W présentera également une réparation de fracture altérée.

Nous avons généré la souche de souris R396W-CD1 qui est une phénocopie valide de la condition humaine IIH. Nous avons ensuite réalisé une ostéotomie tibiale immobilisée par tige sur des souris sauvages, hétérozygotes et homozygotes R396W. Nous avons prélevé les os en cours de guérison à intervalles réguliers et testé leurs propriétés biomécaniques.

Malgré des défis expérimentaux, les tests de torsion ont montré une diminution de la rigidité des cals cicatrisants chez les animaux mutants. La tomographie assistée par ordinateur (μ CT) et les tests de flexion en 3 points (3PBT) ont montré des différences significatives de charge à la rupture (force) chez les mutants mâles et femelles par rapport aux compagnons de litière hétérozygotes et/ou de type sauvage.

Nos résultats indiquent que le modèle préclinique humanisé de l'IIH, la souche R396W-CD1, présente des manifestations phénotypiques similaires à celles des souris originales

3

Cyp24a1-null. De plus, nous avons suggéré que le 24,25(OH)₂D₃ a un effet plus précoce lors de la réparation des fractures que précédemment évalué.

Table of Contents

Abstract	2
Résumé	3
Table of Contents	5
List of Abbreviations	8
List of Figures	11
Acknowledgements	13
Format of the Thesis	14
Contribution of Authors	15
Chapter I: Introduction, Hypothesis and Aims	16
1. Introduction	16
1.1. The Skeleton and Bone Physiology	17
1.2. Bone Development	18
1.3. Mineralisation	19
1.4. Chondrocyte Differentiation	24
1.5. Bone as an Endocrine Organ	25
1.6. Fracture Repair Stages	29
1.7. Vitamin D	33
1.8. CYP24A1 and 24,25(OH)2D3	39

1.9. l	Idiopathic Infantile Hypercalcemia (IIH)	42
1.10.	Cyp24a1-null Mice	43
Hypothesis		48
Aims		48
Chapter II: N	faterials and Methods	49
2.1. Gener	ration of R396W knock-in strain mutation and feeding	49
2.2. Intram	nedullary Rodded Tibial Osteotomy	50
2.3 Sample	e Collection	51
2.4. Torsic	on Tests (TTs)	52
2.5. Micro	-Computed Tomography	53
2.6. Three	Point Bending Tests (3PBTs)	54
2.7. Statist	ical Analysis	55
Chapter III: I	Results	56
3.1. Torsic	on Testing	56
3.3. Micro	-CT	60
3.2. Three-	-Point-Bending-Testing	62
Chapter IV: I	Discussion	65
Chapter V: C	Conclusions and Future Directions	70
Chapter VI: I	References	72

APPENDIX	83
Copyrights and Permissions	83
Figure 2	83
Figure 7	83
Figure 9	83
Figure 24	83
Research Ethic Board Approval for Mice Studies	83

List of Abbreviations

25OHD : Calcidiol	
3PBT : 3-Point Bending Tests	1, 56
7DHC : 7-Dehydrocholesterol	
ALP : Alkaline Phosphatase	
ACAN : Aggrecan	
BMP : Bone Morphogenic Protein	
BMSCs : Bone Marrow Mesenchymal Stem Cells	14
BV : Bone Volume	
CYP24A1 : Gene encoding CYP24A1 enzyme	passim
CYP27A1 : Mitochondrial vitamin D3-25-hydroxylase	
CYP27B1 : 25-hydroxyvitamin D3-1-α-hydroxylase	
CYP2R1 : Vitamin D3 25-Hydroxylase	
DBP : D-binding Protein	
DHCR : Dehydrocholesterol Reductase	
ECM : Extracellular Matrix	
EGF: Epidermal Growth Factor	
ES : embryonic stem	
Fam57b2 : Family with sequence similarity 57 member B isoform 2	
FEM : Finite Element Modeling	
FGF : Fibroblast Growth Factor	16
FGF23 : Fibroblast Growth Factor	
G : Gauge	

GLP : Glucagon-Like-Peptides	
HR-pQCT : High-Resolution peripheral Quantitative Computed Tomography	
IFN : Interferon	
IGF : Insulin-Like Growth Factor	
IIH : Idiopathic Infantile Hypercalcemia	passim
IL : Interleukin	
KO : knock out	6, 32, 34, 35
LacCer : Lactosylceramide	
LCN : Lipocalin	16
MAPK : Mitogen-Activated Protein Kinase	
MC4R : Melanocortin 4 Receptor	
M-CSF : Macrophage Colony-Stimulating Factor	10
MMP-13 : Matrix Metalloproteinase 13	14
MSC : Mesenchymal Stem Cells	
NC : Nephrocalcinosis	
N.D. : Not Detectable	
NL : Nephrolithiasis	
NOS : Nitric Oxide Synthase	14
OA : Osteoarthritis	14
OCN : Osteocalcin	16
PAX1 : Paired Box 1	
PTH : Parathormon	15
PTHrP : Parathyroid Hormone-related Protein	

PVN : Paraventricular Nucleus	
RANKL : Receptor Activator of NFDB Ligand	10, 27
RUNX2 : Runt- related Transcription Factor 2	
SOX9 : Sex Determining Region related High Mobility Group box Gene 9	11
TT : Torsion Test	
TV : Tissue Volume	
UVA : Ultra Violet A	
UVB : Ultraviolet B	
VDBP : Vitamin D-binding Protein	24
VDDR : Vitamin D-dependent Rickets	
VDR : Vitamin D Receptor	
VDRE : Vitamin D Response Element	
VMH : Ventromedial Hypothalamus	
WNT : Wingless/Integrated	
WTT : Wild-Type	53
μCT : Micro Computed Tomography	passim

List of Figures

Figure 1. Macroscopic bone structure 1	19
Figure 2 Endochondral ossification and cartilage differentiation	23
Figure 3 Generation of hypertrophic chondrocyte2	25
Figure 4 FGF23 is a bone derived protein that affects phosphate metabolism2	26
Figure 5 OCN is a multifunctional hormone generated from the bones	28
Figure 6 Food intake suppressed by osteoblast derived LCN22	29
Figure 7 Phases of normal fracture healing	30
Figure 8 Vitamin D3 (cholecalciferol) and D2 (ergocalciferol)	34
Figure 9 Vitamin D pathway with the key enzymes and metabolites produced	36
Figure 10 The catabolism of 1,25(OH)2D3 by CYP24A1 4	41
Figure 11 R396W mutation protein sequence alignments4	47
Figure 12 Torsional Testing Setup5	52
Figure 13. 3-PBT Setup5	54
Figure 14 Ultimate Torque of male mice5	57
Figure 15 Stiffness of male mice5	58
Figure 16 Ultimate Torque of D14-female mice5	59
Figure 17 Stiffness of D14-female mice	60
Figure 18 Percent bone volume of D10-male mice	61
Figure 19 Percent bone volume of D10-female mice	62
Figure 20 Stiffness and strength of male mice	63
Figure 21 Stiffness and strength of female mice	64
Figure 22 TT- Bone breaks from the weakest point other than callus	68

Figure 24.	Pre- and post-twisting	test 6	58
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Format of the Thesis

The thesis is written and submitted in the traditional format. It contains a total of six chapters and appendix.

Chapter 1 comprises of the introduction. Here we give an overview of key features in bone physiology. We cover bone development, mineralisation and chondrocyte differentiation, bone as an endocrine organ, fracture repair stages, vitamin D metabolism, CYP24A1 and 24,25(OH)₂D₃, Idiopathic Infantile Hypercalcemia and *Cyp24a1*-null mice.

Chapter 2 is the materials and methods section. Here we lay out the methodology, experiments and tools utilized in our study.

Chapter 3 is the result section. Here we present all the findings of our study.

Chapter 4 consists of the discussion section. We summarize our work in the context of

previously published literature and provide some limitations of our study.

Chapter 5 concludes the thesis with a description of possible future directions. We present methodologies that can be used to further analyze the implications of our findings.

Chapter 6 catalogues our references.

And **Appendix** includes the copyrights and permissions of the figures that been used in the thesis and finally the research ethic board approval for mice studies.

Contribution of Authors

Dr. Dila Kavame and Dr. René St-Arnaud were responsible for designing the study. The torsion test technique was developed by Dila Kavame under the supervision of Dr. René St-Arnaud. All data generated in this study was obtained by Dila Kavame. Dila Kavame and Dr. René St-Arnaud performed the relevant data analysis. Result interpretation was completed by Dila Kavame and Dr. René St-Arnaud. Funding for this study was obtained by Dr. René St-Arnaud. Initial thesis draft was completed by Dila Kavame. Editing and approval of final version of the thesis was completed by Dr. René St-Arnaud.

Chapter I: Introduction, Hypothesis and Aims

1. Introduction

The human mineral metabolism disorder, Idiopathic Infantile Hypercalcemia (IIH), is characterized by severe hypercalcemia, weight loss, dehydration, muscular hypotonia, lethargy, failure to thrive, vomiting and nephrocalcinosis [1]. The disease origins from the recessive mutations in *CYP24A1*the gene that codes for vitamin D-24-hydroxylase, the cytochrome P450 multi-catalytic enzyme that inactivates 1,25(OH)₂D₃ by converting it into water-soluble calcitroic acid [2]. The mutations in the gene lead to disorder in vitamin-mineral homeostasis causing multi-systemic pathologies.

In this thesis, to better understand the disease, I will focus on the CYP24A1 mutations and its most common seen subgroup, R396W mutations.

A *Cyp24a1* knock out (KO) mouse model was previously generated by our research group, Dr. St-Arnaud's laboratory [3]. In this thesis, I will be providing my research on R396W-mutated mice based on the research schema previously done by Dr. Martineau et al. [4]

In the first chapter, I will provide a brief overview of bone physiology, bone and chondrocyte formation and maturation mechanisms, bone fracture repair, and its relationship to the vitamin D pathway. Also, I will explain vitamin D metabolism and IIH.

Second chapter will include the details of materials and methods that have been used in this research.

Finally, I will be presenting the results, discussing their relevance, and contributing the future directions.

1.1. The Skeleton and Bone Physiology

The adult human skeleton is composed of 206 bones in total which are classified in 3 parts. The appendicular skeleton holds 126 bones, the axial skeleton holds 74 and the last 6 ossicles are associated with auditory stimulus mechanotransduction. As one of the body's solid connective tissues, bone affords structural support, vital organ protection, and is responsible for the maintenance of mineral homeostasis and acid-base balance by holding the sufficient setting for hematopoiesis within the marrow spaces. In addition, it provides the attachment points to support ligaments and tendons to enable locomotion [5] and functions as a reservoir of the growth factors and cytokines [6]. Recent work has suggested that bone is also an endocrine tissue involved in the control of energy metabolism [7].

As a whole, bones are classified into four types: long bone, short bones, flat bones and irregular bones [5].

Bone structures can be broken down into two broad categories: the compact/cortical and the cancellous/trabecular. While both categories are composed of osteons, the composition of these osteons varies between categories. On cortical structures, osteons consist in osteocytes, and trabecular consist in packets, which are thin rods and plates that are aligned towards the areas that support the most stress. Also, while cortical structures are solid and found on the exterior layer of bones and represent 80% of the body's skeletal mass, trabecular structures are comparatively more flexible by virtue of their lower density. They represent 20% of the skeleton [5].

Note that human cortical bones are different from those of mice in several respects. In humans, the osteons are concentric layers of bone matrix involving osteocytes. These interact between each other over small canals designed around a vascular center [5, 8]. By contrast, in mice, cortical bones are composed of circumferential lamellae (thin layers of bone matrix) attached on the periosteal area. Unlike osteons, these are rarely remodelled [8].

1.2. Bone Development

Bone development is different for each of these types, even though they all contain the transformation of mesenchyme to bone tissue. For example, flat bones form by intramembranous bone formation, yet long bones evolve via endochondral ossification and intramembranous formation. Additionally, long bones have diaphysis and epiphyses, meaning a hollow shaft comprised of a cortical bone and composed by trabecular bone preserved by dense cortical bone found above the growth plates, respectively [5].



Figure 1. Macroscopic bone structure

The epiphysis, physis, metaphysis, and diaphysis are the primary areas of long bone. The periosteum, which is also a primary source of stem cells in fracture healing, supplies blood via nutritional arteries. At the physis, endochondral ossification occurs [9]. (2004 Pearson Education, Inc. Publishing as Benjamin Cummings)

1.3. Mineralisation

In bone, osteoblasts are mainly responsible for the secretion of several bone matrix proteins such as osteocalcin, osteonectin, type I collagen, biglycan, and decorin.

The mineralisation in the organic bone matrix starts when calcium restraint in the proteoglycan matrix and phosphate is discharged as a result of alkaline phosphatase activity, shaping hydroxyapatite crystals [10]. As osteoblasts secrete matrix, they could grow to be entrapped inside it and differentiate, turning into osteocytes. These extend long processes to communicate amongst themselves and thus reducing protein production. Acting as a mechanosensory organ, detecting pressure and loading, and communicating these data to other cells to guide bone adaptation are some of osteocytes' fundamental roles. Since osteocytes make up 90-95% of all bone cells, their spatial arrangement supports their function [10].

Osteoclasts, on the other hand, are multinucleated bone-resorbing cells of hematopoietic origin, instead of the mesenchymal origin of osteoblasts. They principally differentiate in the presence of macrophage colony-stimulating factor (M-CSF) and receptor activator of NF κ B ligand (RANKL) [5, 10]. To initiate bone resorption, osteoclasts secrete hydrogen ions into the resorbing compartment to lower the pH of the tissue, optimising the activity of tartrate-resistant acid phosphatase, cathepsin K, matrix metalloproteinase 9 and gelatinase to absorb the organic matrix and mobilize the mineral [11].

1.3.1. Intramembranous Ossification

Skull, mandible, clavicles, and pelvis are the sites where intramembranous bone formation develops. It leads the surface of flat bones to grow and thicken [5]. The process begins by condensing and replicating mesenchymal stem cells (MSC), which are prevalent throughout an extracellular matrix (ECM) lacking collagen. They become osteoprogenitor cells as they become larger and rounder and have more Golgi apparatus and rough endoplasmic reticulum. As the process continues, the cells begin to drift outward, their shape resembles that of osteoblasts, and the runt-related transcription factor 2 (RUNX2) is activated, causing them to commit [12]. Osteoblasts are able to secrete ECM containing type I collagen, forming osteoid, which mineralizes and forms rudimentary bone [13].

Bone spicules, also formed from differentiated osteoblasts, fuse together to construct the bone trabeculae. The woven bone generated by the junction of trabeculae will become filled as ossification progresses [12]. Woven bone is however weaker and immature as the collagen fibrils are secreted in a rather unorganized manner. Thus, the bone must be remodelled to produce a mechanically stronger, lamellar bone where collagen fibrils present alternating orientations [5, 12].

1.3.2. Endochondral Ossification

The presence of cartilaginous tissue distinguishes endochondral ossification from intramembranous ossification. The fetal skeleton is largely made up of cartilage, which will eventually turn into bone through endochondral ossification [14]. This type of ossification occurs in the vertebral column, pelvis, and limbs [12].

The development of a cartilage model that will eventually evolve into bone is the first stage of endochondral ossification. Mesenchymal cells condense to form cartilage, which then differentiate into chondrocytes and secrete ECM components. The activation of transcription factors paired box -1 (PAX1) and SCLERAXIS commits mesenchymal cells to the chondrogenic pathway, and they begin to express transcription factor Sex Determining Region related High Mobility Group box Gene 9 (SOX9) during the condensation stages [15, 16]. The creation of main and secondary ossification centers, which occur when a combination of cells invades the

21

network, will be aided by this cartilage lattice. The primary ossification center is found in the diaphysis, or shaft of the bone, whereas the secondary ossification center is found in the ends, or epiphysis of the bone, at the time of birth [17]. In mice, on the other hand, growth plate remainders stay all through life, although its thickness diminishes after 3 months of life where longitudinal development generally diminishes [8].

To allow longitudinal bone growth in a mechanically secure presence, some bones evolve in this aspect. Cartilage is found within the growth plate and the epiphysis of long bones, and it is organized on morphologically and practically definite areas. The resting chondrocyte zone is found the farthest from the solidification center, amplifying outwards towards the epiphysis. The proliferation comes next, where chondrocytes go through mitosis, smooth, and adjust into stacks. Usually taken after by the zone of hypertrophy, where chondrocytes end up profoundly extended in size and secrete ECM characterized by collagen type II and X, fibronectin and alkaline phosphatase [17]. The ECM gets to be mineralized and hypertrophic chondrocytes in this zone perish as they cannot receive supplements or eliminate squander effectively within the zone of calcification. The cavities cleared out by these apoptotic cells are filled with attacking blood vessels, osteoclasts, osteoprogenitors and bone marrow cells. Osteoclasts resorb the cartilage matrix and osteoprogenitors differentiate into osteoblasts, which secrete ECM that will end up mineralized and renovated within the ossification zone [17].

Finally, growth happens in the presence of cartilage in the bone tissue. That can be in two ways, interstitial, and appositional growth. Interstitial growth, also called longitudinal, exists when chondrocytes segregate and remain excreting the matrix. Oppositional growth, on the other

22

hand, is the increase in the diameter or thickness by addition of ECM by chondroblasts and osteoblasts [12].



Figure 2 Endochondral ossification and cartilage differentiation

At the physis, chondrocytes undergo proliferation, hypertrophy, and death during endochondral ossification. The mineralized matrix that remains is infiltrated by blood vessels. Osteogenesis is aided by growth factors such as growth hormone, thyroid hormone, and FGF23. To govern and regulate chondrocyte proliferation and hypertrophy, Indian hedgehog and PTHrP form a feedback loop. This procedure is necessary for fracture healing as detailed in this thesis. Figure adapted from White et al. (2001) [18], with permission.

1.4. Chondrocyte Differentiation

Articular cartilage is a solid connective tissue that is devoid of nerves, blood vessels, or lymphatic vessels. In joint movement, it acts as a load bearing, buffering, and protective structure [19, 20]. Chondrocytes are the only cell type in the articular cartilage tissue and release growth factors and enzymes that govern ECM formation. They continue to embed themselves in the ECM, forming cartilage [21]. Collagen type II and aggrecan (ACAN), two main ECM components, are classic chondrocytic phenotype markers. The ECM network oversees absorbing articular cartilage mechanical stress, increasing chondrocytes adhesion, and controlling intracellular signal transduction [20].

Chondrocytes develop from bone marrow mesenchymal stem cells (BMSCs) in the bone marrow. To begin with, aggregated BMSCs can differentiate into chondroprogenitor cells the differentiate into chondrocytes, which then undergo a series of differentiation events to become hypertrophic chondrocytes. After apoptosis and endochondral ossification, chondrocytes are gradually replaced by osteoblasts as the cartilage matrix becomes partially calcified. Although chondrocyte hypertrophy and apoptosis are natural processes of endochondral ossification, when cartilage is damaged, they will hasten the progression of osteoarthritis (OA) [22]. Furthermore, chondrocytes cultured in vitro have a highly susceptible growth and differentiation regulation mechanism, which can readily lead to cell ageing and differentiation. Differentiation of chondrocytes is followed by changes in fibrous phenotype, decreased collagen II expression, and increased collagen I, matrix metalloproteinase 13 (MMP-13), and nitric oxide synthase (NOS) production [20, 23, 24].



Figure 3 Generation of hypertrophic chondrocyte

MSCs evolve to chondrocytes, which go through a series of transformations. Sox9 enhances MSC proliferation and differentiation into chondrocytes, whereas Runx2 stimulates chondrocytes ends in hypertrophy. BMPs regulate the expression of Sox9 and Runx2 and alter various stages of chondrocyte development.

The ability to regenerate and repair cartilage is severely limited. It is nearly impossible for cartilage to self-heal once it has been damaged, and it may even deteriorate. Cartilage repair is not efficient but involves chondrocyte proliferation and ECM synthesis [25]. The proliferation, metabolism, and differentiation of chondrocytes is a sophisticated process. Several cytokines and cellular signals cooperate to maintain cartilage homeostasis and regulate chondrocyte function [20, 26].

1.5. Bone as an Endocrine Organ

Bone has traditionally been thought of as a structural organ that develops as a result of the activity of specialized cells such as chondrocytes and osteoblasts. Osteoblasts produce bone matrix and eventually get encased in it to become osteocytes, cells that operate as gravity force sensors and mediators within the remodelling unit [27, 28]. In addition to being a structure for mobility, calcium homeostasis and haematological function are all dependent on bone. The role of the skeleton as an endocrine organ has recently been highlighted by breakthroughs in bone biology [29].

There are numerous bone cell hormones identified previously. Such as sclerostin, an osteocyte-released bone-specific protein that might have a function as a paracrine inhibitor of osteoblast differentiation [30]. Furthermore, it was previously recognised that osteocytes produce and secrete fibroblast growth factor-23 (FGF-23) into the circulation, a key regulator of vitamin D-1-alpha-hydroxylase, PTH and serum phosphate homeostasis [31] (fig. 4).



Figure 4 FGF23 is a bone derived protein that affects phosphate metabolism

Through its binding to a complex of FGFR1 and the co-receptor Klotho in the kidney, FGF23, inhibits phosphate resorption and reduces the synthesis of 1,25(OH)2D3. in the parathyroid, FGF23 decreases PTH production and secretion in a Klotho-dependent manner. 1,25(OH)2D3 and PTH both influence FGF23 synthesis and secretion in osteoblasts and osteocytes. PTH, can inhibit phosphate resorption and 1,25(OH)2D3 synthesis in the kidney [32]. (Copyright 2018, Yujihao Han et al.)

In addition to its role in mineral metabolism, bone could function as a mediator to metabolic homeostasis by its specific protein, osteocalcin (OCN). It is a bone-derived hormone that affects the biological processes of various organs, including liver, bone, adipose, brain testes, muscle and, pancreas [32-34] (Fig. 5). Furthermore, new research shows that osteoblast-derived lipocalin-2 (LCN2) modulates glucose tolerance, insulin sensitivity, and insulin secretion to maintain glucose homeostasis by binding protein to the melanocortin 4 receptor (MC4R) in the hypothalamus and inhibiting food intake [32, 35] (Fig. 6).



Figure 5 OCN is a multifunctional hormone generated from the bones

OCN is C-carboxylated (GlaOCN) and secreted into the extracellular matrix (ECM) of bone by osteoblasts. GlaOCN is decarboxylated into undercarboxylated active osteocalcin (GluOCN), which enters the blood to act as a hormone, due to the acidic pH (4.5) in the resorption lacunae generated by osteoclasts. Enhancement of glucose uptake in muscle, insulin generation in the pancreas, insulin sensitivity in the liver and adipose tissue, elevation of adiponectin expression in adipose tissue, and promotion of b-cell proliferation in the pancreas are all regulated by GluOCN. Furthermore, OCN increases cognitive function of the brain by increasing neurotransmitter synthesis and facilitating hippocampal growth by stimulating testosterone synthesis in Leydig cells, which improvise male fertility. OCN acts in the testis, pancreas, and muscle via binding to the GPRC6A receptor, although OCN receptors in the brain, adipose tissue, and liver are still unknown [32]. Copyright 2018, Yujihao Han et al.



Figure 6 Food intake suppressed by osteoblast derived LCN2

LCN2 produced by osteoblasts and crosses the blood-brain barrier to reach the hypothalamus, where it binds to the MC4R receptor in the paraventricular nucleus (PVN]) and ventromedial hypothalamus (VMH) and triggers MC4R-dependent anorexigenic signalling. LCN2 is also involved in the regulation of glucose tolerance, insulin sensitivity, and insulin secretion [32]. Copyright 2018, Yujihao Han et al.

Bone is also having a role as a target organ of several endocrine glands and tissues such as glucagon-like-peptides-1 (GLP1), PTH, adipokines and immune cell-produced cytokines.

1.6. Fracture Repair Stages

Bone fracture healing is a complex process that requires the tightly ordered cooperation of cells, growth factors, and extracellular matrices [14]. Bone fracture healing is categorized as

primary or secondary, due to underlying healing mechanisms relying on rigidity of the fracture construct. Primary healing occurs when bone fragment are in direct contact with one another and highly stable with minimal strain [14]. Haversian remodelling aids fracture healing by relying on osteoclasts and osteoblasts to directly rebuild the bone fragments. Secondary healing is more common and is characterized by four steps: 1) the initial inflammatory phase, 2) soft callus formation, 3) hard callus formation, and 4) remodeling [36].



Figure 7 Phases of normal fracture healing

Secondary fracture healing is depicted as a step-by-step process that restores the bone's natural strength and shape without leaving a scar. The presence of hematoma from broken blood arteries

generates a clot during the inflammatory phase, which attracts immune cells and, mesenchymal progenitor cells via inflammatory signalling. The bone gap is bridged by a soft callus, which is mostly formed of cartilage. The process of endochondral ossification leads to the production of new bone. Remodelling by osteoclasts and osteoblasts restores the normal shape of the bone. Figure adapted from Einhorn et al.(2014) [37], with permission.

The early inflammatory phase of secondary fracture healing is crucial to the entire healing process [38]. When the inflammatory cascade is triggered, endothelial, neuronal, and mesenchymal stem/progenitor/precursor cells are brought into the site of injury, leading to formation of a vascularized and innervated fibrous granulation tissue [36]. As macrophages, neutrophils, lymphocytes, and platelets arrive at the injury site and release cytokines, inflammation begins, peaking at 24 hours. Initially haematoma occurs when blood vessels in the bone and surroundings soft tissue are disrupted, triggering an inflammatory response. Transforming growth factor beta (TGF- β), Insulin-like growth factor (IGF) and FGFs released by macrophages recruit mesenchymal cells to the injury site [38, 39]. Immune cells drawn to the injury site generate growth factors and cytokines such as TNF- α , interleukin -1 beta (IL-1 β), IL-6, and monocyte chemoattractant protein-1 (MCP-1), which attract mesenchymal stem cells from periosteum, bone marrow, and the systemic circulation [40, 41]. The proliferation in MSCs starts within 3 days post-fracture and differentiates into chondrocytes following nearly 21 days. The hematoma and inflammatory reaction support chondrogenic and osteogenic differentiation, which ultimately leads to soft callus formation.

The soft callus is made up of cartilage and granulation tissue, and it serves as a biologic scaffold for the formation of new bone. Chondrogenic maturation remains to enable bone

31

formation. The steps are proliferation, hypertrophy, apoptosis, followed by vascular invasion. On the scaffold of destroyed chondrocytes, osteoblasts form primary bone that turns into a hard callus. And finally, the remodelling phase, the last phase of fracture healing process, takes longer duration according to the other phases. This phase also includes the remodelling of the woven bone and formation of the lamellar bone. The remodelling of the medullary canal and endosteal callus to allow for reconstitution of the bone marrow also appears in this phase. The optimum bone renewal includes its original strength, histology, and physiology. The duration and the healing status depend on the age, the injury site, comorbidity, sex, and other health condition [36].

Beside the factors mentioned earlier, signaling pathways have a particular role during the fracture repair. They include MAPK (mitogen-activated protein kinase), WNT/ β -catenin, Notch, BMP (bone morphogenic protein) and PDGF (platelet derived growth factor) [36]. The MAPK pathway has a crosstalk role in other pathways and transduces the epidermal growth factor (EGF), FGF and IGF signals in bone healing [36]. It can be also triggered by some inflammatory markers such as TNF α and NF- κ B [39, 42]. In osteoblasts, this pathway has been demonstrated to have opposing effects on osteoblast differentiation and osteoblast marker gene expression [43]. Canonical WNT signaling is activated during bone healing and enhances osteoblastogenesis. This stimulates MSC differentiation into osteoblasts is Notch signaling. The inhibition of this pathway could cause non-union via reducing the MSCs derivation from bone-marrow [45, 46]. BMP signaling is important to activate endochondral bone formation, thus, osteogenesis advancement [47]. Through differentiation of MSCs of bone marrow origin into osteoblasts and through the chemotaxis attraction of macrophages, PDGF

32

signalling has a role in bone repair [48]. While the IGF pathway leads the osteoblast differentiation, matrix deposition and expression of type I collagen, the FGF pathway has a role in angiogenesis, wound healing and intramembranous and endochondral signaling in osteoprogenitor cells [49-51].

1.7. Vitamin D

The discovery of vitamin D is linked to the search for a remedy for a disease called rickets. The search for the cure to this endemic disease during the beginning of the 19th century, firstly led the use of the cod fish oil and finally ended by the discovery of Vitamin D in 1820s. The use of vitamin D as a nutritional supplement succeeded to lower the incidence of the two seriously damaging bone diseases, rickets and osteomalacia.

Vitamin D is an essential molecule in bone metabolism and has numerous roles in many cellular and immunological processes. It can be either synthesized in the body or consumed through the diet.

1.7.1. Vitamin D forms and sources

In humans, the synthesis of vitamin D in the skin via exposure to the sun's ultraviolet B (UVB) light is the most generous source of their vitamin D [52]. In addition to the endogenous production in the skin, there are also plant (vitamin D_2 or ergocalciferol), or animal vitamin D (vitamin D_3 or cholecalciferol) forms. The main differences between these two forms rely on the presence of a double bond between C-22/C-23 and a methyl group bound to C-24 (fig. 8). Even though some of the hydroxylating enzymes could use vitamin D_2 as a substrate, both metabolites don't follow the same metabolic pathways [2].

Some of the best natural sources of vitamin D_3 are fatty fish, such as fresh wild salmon (can produce nearly 600-1000IU of vitamin D_3 per 100 gram serving) and fish oils, such as cod liver oil (400-1000 IU of vitamin D_3 per 1 tablespoon) [52]. Among plants, sun-dried mushrooms are a rich source of vitamin D_2 (1600 IU of vitamin D_2 per 100 gr of sun dried shiitake mushrooms) [52].



Figure 8 Vitamin D3 (cholecalciferol) and D2 (ergocalciferol)

Different than cholecalciferol, ergocalciferol (vitamin D2) has a double bond at C-22 and a methyl group at C-24.

Due to limited food sources of vitamin D and their lack in diets, several countries routinely fortify certain food sources with vitamin D such as fluid milk products, margarines, plant milk products etc. [53].

1.7.2. Vitamin D metabolism

Vitamin D can be synthesized upon exposure of ultraviolet B (UVB) photons in both animals and plants, through UVB photoisomerization of provitamins. In plants and fungi, synthesis happens in basically a similar way upon exposure to UVB, although provitamin D_2 or ergosterol (and not 7DHC) is the forerunner of vitamin D combination in plants and organisms, and the subsequent nutrient D_2 is ergocalciferol [52].

In mammals, vitamin D is synthesized from provitamin D₃ (7-dehydrocholesterol (7DHC)) which is found in large quantities in the skin of many vertebrate animals, including humans [52]. Exposure to sunlight triggers the high-energy UVB photons to penetrate the epidermal and dermal cells of the skin and are absorbed by 7DHC and this reaction results in creation of previtamin D₃ (from the precursor 7DHC) [54]. From this thermodynamically unstable form (previtamin D₃) a rearrangement occurs with cleavage at the B ring to produce a more stable form, vitamin D₃ (cholecalciferol). Vitamin D₃ infuses into the dermal capillary bed by the vitamin D-binding protein (VDBP) and makes its way to the circulation [55].

To form the physiologically active hormone, $1,25(OH)_2D_3$, vitamin D must undergo two hydroxylation steps after entering the circulation. An endocrine mechanism or a more recently suggested autocrine pathway can cause these effects [56].

In the well-known endocrine pathway, circulating vitamin D₃, cholecalciferol, from all sources is transported to the liver. It is hydroxylated in liver hepatocytes by the high affinity CYP2R1 enzyme (vitamin D₃ 25-hydroxylase) or by the lower affinity CYP27A1 enzyme at the 25^{th} carbon to form 25-hydroxyvitamin D₃ (called calcifediol or $25(OH)D_3$). In the circulation, calcifediol is bound by D-binding protein (DBP), an α -globulin that increases its solubility. The production of $25(OH)D_3$ in the liver is not highly regulated. Cholecalciferol found in the circulation can readily be converted into $25(OH)D_3$ in a concentration-dependent manner, which can be used to measure vitamin D status in clinic. DBP-25(OH)D₃ is transported throughout the

35

body, where it is hydroxylated at the 1- α position by the CYP27B1 enzyme (25-hydroxyvitamin D₃ 1-alpha-hydroxylase) in the kidney proximal tubules to create calcitriol or 1,25(OH)₂D₃. The action of this enzyme is strictly regulated by the body's calcium and phosphorus requirements [2].



Nature Reviews | Cancer

Figure 9 Vitamin D pathway with the key enzymes and metabolites produced

Figure adapted from Deeb et al. (1969) [41], with permission.

In the presence of biologically sufficient amounts of $1,25(OH)_2D_3$ in the circulation, previtamin D₃ and vitamin D₃ are transformed by solar UVA or UVB to a variety of inert byproducts, therefore excessive sunlight exposure cannot lead to overproduction of the biologically
active $1,25(OH)_2D_3$, which is toxic at high concentrations [57]. The normal concentration is within the 20 to 65 ng/mL range [2].

1.7.3. Vitamin D and VDR signaling

The most active form of vitamin D is 1,25(OH)₂D₃ and it works by diffusing through the cell membrane an attaching to the vitamin D receptor (VDR), a ligand-activated transcription factor that belongs to the nuclear receptor family. VDR and the retinoid-X receptor (RXR) form a heterodimer and bind the vitamin D-responsive regions of target genes. The parathyroid gland, pancreas, macrophages, skin keratinocytes, mammary glands, reproductive organs, tubular epithelial cells of the kidney, osteoblasts, and osteoclast precursors are all reported to express VDR [2].

Mutations on the vitamin D metabolic pathway enzymes cause different hereditary pathologies. 7-Dehydroholesterol reductase (DHCR7) enzyme polymorphisms, for example, are linked with low 25OHD levels, and inactivating mutations manifest with high vitamin D [58]. CYP2R1, which is the major vitamin D 25-hydroxylase, inactivating mutations develop a rickets form called vitamin D-dependent rickets, type 1B (VDDR1B) [59]. VDDR1B manifests in the affected individuals with low 25OHD but normal 1,25(OH)₂D₃ levels. It is also associated with hypocalcaemia, hypophosphatemia, and infantile onset. The disease responds to 25OHD (calcidiol) treatment and does not require treatment as adults. Mutations in the CYP27B1 enzyme are characterized by another form of rickets, pseudo vitamin D deficiency rickets or vitamin D-hydroxylation deficient rickets (VDDR1A) [60]. The affected individuals have similar clinical symptoms as VDRR1B patients but have lower 1,25(OH)₂D₃ and normal 25OHD levels. VDRR1A responds to calcitriol. CYP24A1 enzyme mutations result in a form of idiopathic infantile hypercalcemia (IIH) [1, 61]. It is characterized with hypercalcemia in children and kidney stone history and elevated $1,25(OH)_2D_3$ levels in adulthood. The discoveries of the mutations and association with the adult life changed the approach to the IIH disease. It is no longer idiopathic, and also not only seen in childhood [61]. The disease and mutations on CYP24A1 will be mentioned in detail later in this thesis.

1.7.4. Role in Calcium Homeostasis

The production of 1,25(OH)₂D₃ by CYP27B1 is regulated by the parathyroid hormone (PTH) in response to circulating calcium and phosphate levels. Low levels of those ions trigger the PTH release which stimulates 1,25(OH)₂D₃ production. 1,25(OH)₂D₃ in turn stimulates calcium and phosphorus absorption in the small intestine. It promotes calcium reabsorption in the kidney's distal convoluted tubules. PTH stimulates RANKL expression by osteoblasts, which accelerates osteoclastogenesis and bone resorption, mobilising calcium from bone [62]. Although 25(OH)D₃ is not the natural ligand of the VDR, it can compete with normal amounts of circulating 1,25(OH)₂D₃ and cause effects generally attributed to it when it is circulating at high quantities (1000 ng/mL or above), such as in vitamin D toxicosis [55].

PTH expression is inhibited by 1,25(OH)₂D₃ in the parathyroid gland to prevent CYP27B1 stimulation [55]. In a negative feedback loop, 1,25(OH)₂D₃ also promotes fibroblast growth factor 23 (FGF23) secretion, which stimulates phosphate excretion from the body while decreasing CYP27B1 activity. Osteocalcin and osteopontin, which are involved in bone remodelling, are transcriptionally activated in osteoblasts, while involucrin and carbonic anhydrase are active in keratinocytes and macrophages, respectively [62].

CYP24A1, the gene that encodes 1,25-dihydroxyvitamin-D₃ 24-hydroxylase, is responsible for hydroxylating 1,25(OH)₂D₃ and its precursor 25(OH)D₃ at the 24th carbon, resulting in 1,24,25-trihydroxyvitamin D₃ (1,24,25(OH)₃D₃) and 24,25-dihydroxyvitamin D₃ (also known as secalciferol or 24,25(OH)₂D₃). Until recently, 24,25(OH)₂D₃ was a metabolite largely believed to be inactive. The carbons located in the side chain, specifically C-23, C-24, C-26, are more prone to being hydroxylated. These metabolites can be metabolized further to produce calcitroic acid, which is water-soluble and eliminated from the body [55].

1.8. CYP24A1 and 24,25(OH)2D3

The stereospecific hydroxylation of the 24th carbon of $1,25(OH)_2D_3$ and $25(OH)D_3$ is carried out by CYP24A1, a heme-containing cytochrome P450 enzyme located in the inner membrane of mitochondria of humans and other species. It is thought to be a catabolic enzyme since $1,25(OH)_2D_3$ induces its expression to regulate its breakdown and prevent hypervitaminosis D [55]. In vitro studies of the activation of *Cyp24a1* by $1,25(OH)_2D_3$ revealed that the promoter of this gene has two VDREs 100bp apart in the non-coding section, a tandem structure unique to this promoter [63]. Recent research has revealed a more complicated control of *Cyp24a1* expression in vivo [64, 65].

Because 25(OH)D₃ is more common in the body and has a lower Michaelis constant (*K*m) than 1,25(OH)₂D₃, the primary metabolite generated is 24,25(OH)₂D₃. Furthermore, 1,24,25(OH)₃D₃ is unstable in the circulation and has a greater affinity to CYP24A1, causing it to bind to the enzyme and be rapidly destroyed. In the plasma, 24,25(OH)₂D₃ circulates at a concentration of 2-5ng/mL, which is 10-fold lower than circulating 25(OH)D₃ [55].

CYP24A1 initiates a reaction process in which its substrates are hydroxylated and then oxidised at carbon 24, followed by hydroxylation of the 23rd carbon and cleavage of the side chain to produce the ultimate degradation product, calcitroic acid. Calcitroic acid is water soluble, which means it can be excreted (figure 10). CYP24A1 is classified as a multi-catalytic enzyme since it can execute multiple steps in the degradation of 24,25(OH)2D3. Although human CYP24A1 is primarily a C24-oxidation enzyme, it can also express C23-hydroxylation activity, which results in lactone and carboxylic acid as end products. Point residue variations in the enzyme's substrate binding and catalytic core determine this differential in activity [66].

Cyp24a1 expression is induced by 1,25(OH)₂D₃ in all target tissues. This activates the 24-oxydation pathway, which results in catabolic inactivation of 1,25(OH)₂D₃, allowing vitamin D homeostasis to be maintained. PTH and 1,25(OH)D₃ concentration are the major regulators of CYP24A1 activity in the kidney [2, 67]. PTH treatments prevents the 1,25(OH)₂D₃ -mediated rises in renal *Cyp24a1* mRNA expression, whereas 1,25(OH)₂D₃ administration increases renal *Cyp24a1* mRNA expression [68, 69]. Because intestine cells lack a PTH receptor, *Cyp24a1* is predominantly controlled by 1,25(OH)₂D₃ in the gut. The injection of 1,25(OH)₂D₃ stimulates intestine *Cyp24a1* expression, causing it to catabolize, and this response is more severe than one seen in the kidney [70]. *Cyp24a1* expression declines in differentiated mature cells, limiting 1,25(OH)₂D₃ but expression declines in differentiated mature cells, limiting 1,25(OH)₂D₃ breakdown as osteoblasts mature. In macrophages, interferon-gamma (IFN γ) stimulates the production of 1,25(OH)₂D₃ to regulate itself.



Figure 10 The catabolism of 1,25(OH)2D3 by CYP24A1

First branch shows the forming of calcitroic acid by oxidization at C-24 and hydroxylation at C-23. Second branch shows the lactone and carboxylic acid pathway hydroxylation C-23. [1]

The *CYP24A1* gene is present on chromosome 20 in humans and the mutation in the gene causes a disease called Idiopathic Infantile Hypercalcemia (IIH) which occurs mostly in infants. Dehydration, failure to thrive, weight loss, fever, and vomiting are the common symptoms. Also, it manifests with high vitamin D levels, hypercalcemia, low PTH, nephrocalcinosis, and hypercalciuria [1]. We mention more about this disease in the following sections.

1.9. Idiopathic Infantile Hypercalcemia (IIH)

Idiopathic infantile hypercalcemia (IIH) was first reported by Lightwood in the 1950's in the United Kingdom. An elevation of the number of IIH cases was observed following introduction of an increased prophylactic dose of vitamin D in infant formula and milk products [71, 72]. The infants were found to have high levels of serum and urinary excretion of calcium, and physiologic levels of serum phosphate and magnesium and occasionally low serum alkaline phosphatase (ALP). Halving the vitamin D dose lowered the observed incidence. Lightwood afterwards hypothesized fluctuation in infants' sensitivity to vitamin D due to unaffected cases during the treatment.

The general manifestations of this rare disease are high serum calcium and high urinary calcium loses, failure to thrive, vomiting, constipation, polyuria with dehydration and Ca deposits in the kidney, with a susceptibility to renal complications such as nephrolithiasis (NL) or nephrocalcinosis (NC). Affected infants may also manifest muscular hypotonia and lethargy, which leads to growth impairment, delays in mental and mobility development [73]. Affected adults could also manifest some extra-renal pathologies, such as Ca deposits in the joints and in the cornea, a low bone mineral density with osteoporosis, mainly based on enhanced osteoclastic activity [74, 75]. The genetic cause of IIH remained unknown until Schlingmann and coworkers identified it in 2011. They found inactivating mutations in *CYP24A1* that appeared to drive the disease evolution [1]. They furthermore characterized a disease subgroup that presented idiopathic renal Pi depletion in addition to the other typical IIH traits, without carrying *CYP24A1* mutations. In these patients, the pathology was caused by *SLC34A1* genetic variants. In this new study, the clinical and biochemical pathologies remained following the cessation of vitamin D

prophylaxis while a sudden response to Pi registration emerged, contradictorily to the *CYP24A1* mutated patients [76]. These findings, which confirm the significance of *SLC34A1* as a substitute genetic cause of IIH, highlight the disease's molecular heterogeneity and provide another avenue for increasing the number of individuals for whom a specific molecular diagnosis can be made.

1.10. Cyp24a1-null Mice

Using embryonic stem cell technology, the St-Arnaud lab created a knockout (KO) mouse model for CYP24A1 by replacing the heme-binding domain of *Cyp24a1* on exons 9 and 10 with a PGK-neo (phosphoglycerate kinase promoter driving the neomycin phosphotransferase II gene) selection cassette. The heterozygous offspring are phenotypically normal, and the mutation is passed down with the usual Mendelian ratio. However, at roughly 3 weeks of age, half of the mutant progeny dies. The function of macrophages was studied to rule out an inadequate response to infection as the cause of severe neonatal mortality. By examining the stunted progeny, it was discovered that the lethality was caused by hypercalcemia caused by high levels of 1,25(OH)₂D₃ which could not be cleared from the circulation. In the late stages of pregnancy, pregnant knockout mice have very high levels of 1,25(OH)₂D₃ which cannot be regulated by CYP24A1-mediated catabolism [3, 77]. In addition, continued administration of extrinsic 1,25(OH)₂D₃ resulted in cortical tubular dilation, necrotic debris, and renal calcification observed in these mice, with excess of 1,25(OH)₂D₃ that caused fatal calcium imbalance [3].

However, the surviving half of the breed is thought to have survived by regulating vitamin D in a different way. They were showing normal calcium and phosphate levels when they were fed standard rodent chow. The clearance of 1,25(OH)₂D₃ remained poor in these mice, as seen by the absence of 24-hydroxylated metabolites as well as 1,25(OH)₂D-26,23-lactone,

implying that vitamin D is regulated through inhibiting 1,25(OH)₂D₃ synthesis rather than catabolism [3, 78]. The surviving pups had lower baseline circulating levels of 1,25(OH)₂D₃ than their WT counterparts, implying that they are downregulating 1,25(OH)₂D₃ production, allowing them to survive without major mineral homeostasis impairment [78].

When mice are bred from *Cyp24a1*-null mothers, the pups manifested high levels of 1,25(OH)₂D₃. They also had osteoid accumulation and impaired bone mineralisation. Furthermore, the 24,25(OH)₂D₃ administration during pregnancy to rescue the phenotype showed no improvement in bone abnormalities. The phenotype was rescued when crossed to VDR-ablated mice by preventing activity of the higher 1,25(OH)₂D₃ levels during development [3].

On the other hand, albuminuria, hyperlipidemia, reduced circulating $25(OH)D_3$ and $24,25(OH)_2D_3$, low bone mineral density, and normal circulating $1,25(OH)_2D_3$ are observed after 8 weeks-of-age in transgenic rats where CYP24A1 is constitutively expressed. Also, the majority of the phenotype is thought to be caused by a change in renal function, although the cause is unknown. These findings suggest that $1,25(OH)_2D_3$ may have a role in vitamin D metabolism regulation [79, 80].

There is also evidence that 24,25(OH)₂D₃ has an effect on chondrocytes during growth and fracture repair and itis probably affecting via a different mechanism than binding to the VDR receptor. Seo et al. (1997) found that circulating levels of 24,25(OH)₂D₃ and CYP24A1 enzymatic activity increased in chicks by day 10 post-fracture and returned to basal levels by day 15, indicating that this metabolite and CYP24A1 enzymatic activity may be significant when damaged bones heal. They first found tritium-labeled 1,25(OH)₂D₃ and 24,25(OH)₂D₃ accumulation in growth plate cartilage [81]. However, no alteration of the growth plate cells

could be found in *Cyp24a1*-KO mice's growth plate chondrocytes [3]. They also discovered that tritium-labeled $24,25(OH)_2D_3$ binds specifically to membrane portions of cells in chicks fracture callus [81]. When bones heal, however, $24,25(OH)_2D_3$ and $1,25(OH)_2D_3$ combination injected into the callus formation has a greater effect in bone renewal than $1,25(OH)_2D_3$ solely [82].

Additional to those findings, it has been showed that the supplementation of the 24,25(OH)₂D₃ with the other D₃ metabolites during bone fracture repair had an improving effect on healing. They hypothesized that 24,25(OH)₂D₃ is required at a certain stage of chondrocyte development in the callus formation in chicks [83]. And also, it demonstrated that local injection of 24,25(OH)₂D₃ had an effect in rescuing rachitic cartilage and promoting fracture healing [84]. The callus membrane contained the putative binding protein/receptor with high and specific affinity to 24,25(OH)₂D₃, suggesting that 24,25(OH)₂D₃ might be acting via signal transduction response different from the regular steroid nuclear receptor [81].

The effect of 24,25(OH)₂D₃ on fracture repair was studied using *Cyp24a1*-null mice developed in the St-Arnaud's lab [3]. Their study showed that there is a significant delay on callus formation and healing in *Cyp24a1*-null mice compared to control littermates. Following the stabilized, transverse mid-diaphyseal fractures, at day 14 post-osteotomy, bone volume, force required to break the bone, and percentage of mineralized tissue were all reduced, and this could not be restored with 1,25(OH)₂D₃. However, the same group showed the improved histological appearance, biomechanical properties, and static histomorphometric index (BV/TV) when they were given daily injections of 24,25(OH)₂D₃ [4]. They also identified and cloned *Family with sequence similarity 57, member B2 (Fam57b2)*. It encodes a protein that interacts with 24R,25(OH)₂D₃ in a saturable and stereo-specific way.

The *Fam57b* gene produces 3 isoforms through differential promoter usage [49]. Martineau et al. identified that cartilage and skin have the highest levels of expression of the second isoform, Fam57b2. Furthermore, the FAM57B gene was shown to have higher expression in patients with normal fractures compared to those with non-union fractures, indicating that it could play a role in fracture repair. Martineau et al. generated a mouse strain in which the Fam57b gene can be specifically inactivated in selected tissues. They bred Fam57b-floxed mice with Col2-Cre-transgenic mice to achieve chondrocyte-specific gene inactivation. Moreover, they identified the genetic pathway involving 24R,25(OH)₂D₃- induced, FAM57B2-dependent lactosylceramide (LacCer) production to rescue endochondral ossification during fracture repair using Cyp24a1 KO mice [4]. LacCer are a class of glycosphyingolipids and the most abundant of the diosylceramides. In mammals, it acts as a metabolic branch point to produce many kinds of complex glycosphingolipids. It is thought to also control various aspects of cellular function [85]. Additionally LacCer-dependent signal transduction pathways have been identified [85]. Cell proliferation [86], adhesion [87, 88], apoptosis [89], and angiogenesis [90] have all been demonstrated to be influenced by these pathways. The St-Arnaud laboratory recently identified LacCer effect during bone healing [4].

Even though the *Cyp24a1*-null strain's feature and mimicking capacity of IIH disease were known, the locations of the mutations were unknown. Recently, 43 missense and deletion mutations of *CYP24A1* were described [91]. A small set of mutations in the *CYP24A1* gene comprising p. E143del, p.R396W, and p.L409S is detected in high frequency in the majority of patients. To find out whether a humanized mouse IIH model would also exhibit impaired fracture repair as *Cyp24a1*-KO strain, we generated the R396W mutated strain.

Initially the R396W knock-in embryonic stem cells were obtained from Cyagen and confirmed targeted clone was injected into C56Bl6/N blastocytes to develop the strain on this homogenous background.



Figure 11 R396W mutation protein sequence alignments

The electrogram shows R396W missense mutation. Arginine (R) amino acid turns into Tryptophan (W) in position 396.

The R396W mutated on C56Bl6/N background showed higher 25(OH)D₃/24,25(OH)₂D₃ relativity (38.8) compared to WT littermates (6.7) as also seen in *Cyp24a1*-null mice. The strain showed a very low survival rate due to having lethally high concentrations of calcium. Also, the autopsy of non-surviving pups was showing nephrolithiasis. Finally, our laboratory crossed the R396W- C56Bl6/N strain with outbred CD1 mice. Eventually, the final generation, R396W-C56Bl6/N backgrounded littermates.

Hypothesis

Based on our earlier work with the *Cyp24a1*-deficient model of IIH, we hypothesize that the humanized model sporting the R396W mutation will also exhibit impaired fracture repair. We will test this hypothesis through the following specific aims:

Aims

- Characterizing the fracture repair phenotype in the IIH mouse model.
- Determining the onset of the activity of $24,25(OH)_2D_3$ during fracture healing in IIH by setting new timepoints different than previous research.
- Outlining the biomechanical properties of the IIH mouse model.

Chapter II: Materials and Methods

2.1. Generation of R396W knock-in strain mutation and feeding

All animal procedures were reviewed and approved by the McGill Institutional Animal Care and Use Committee and followed the guidelines of the Canadian Council on Animal Care. Mice were kept in an environmentally controlled barrier animal facility with a 12-h light, 12-h dark cycle, and were fed mouse chow and water ad libitum.

The R396W knock-in ES cells were generated by Cyagen under contract. A confirmed targeted clone was injected into C57Bl6/N blastocysts to develop the strain on this homogeneous background. The R396W/R396W genotyped mice showed very low survival rate. More than 80% of the newborns did not survive past post-natal day 15. Homozygous mutants showed elevated doses of calcium levels and nephrolithiasis.

To improve survival, we crossed the strain with outbred CD1 mice. The R396W-CD1 pups all survived, and the strain is a valid mimic of the IIH human condition.

Eventually, we designed the study as 1) Generation of the mutant mice, 2) Performing the surgeries on their left tibias on the age of 3-months, 3) Harvesting the left tibias on day 10, day 14, and day 28 4) Testing the bones with TT on D14 and 28 or 3PBT and μ CT scanning on D10. We finally tested 127 mice in total in order of 37, 49, and 41 mice in three different genotypes (Wild type [WT], heterozygous [+/R396W], homozygous mutant [R396W/R396W]), respectively. During surgeries, the right tibiae were protected and not included to the testing data.

2.2. Intramedullary Rodded Tibial Osteotomy

The surgical procedures were done as described in "Standard Procedure for Rodded Immobilized Fracture Surgery in the Mouse" of McGill University.

The intramedullary rodded immobilized open fracture surgery was performed on the left tibia at 2 and 3-months of age. The analyses of the fractured bones were performed on post-surgery days 10, 14 and 28 (D10, D14, D28).

Initially, the mice were weighted to determine the appropriate dosage of analgesic and to help monitor animal recovery. Then, the mice were injected subcutaneously with 1mg/kg body weight Buprenorphine (slow-release form, Chiron Computing Pharmacy, Inc.) thirty minutes prior to anesthesia. Mice were then anesthetised using oxygen and isoflurane gas and kept under anesthesia during the entire procedure. Following the anesthesia, a small amount of Natural Tear ointment was applied to each eye to prevent corneal drying during surgery. Subcutaneously 0.9% saline (0.2-0.5 ml/10g body weight) and Carprofen (Pfizer, NY, USA) (5ml/g body weight) were administered. The left leg was shaved from top of the leg to the foot to remove all fur surrounding the tibia and then washed with 70% alcohol and 2% chlorhexidine solutions, respectively. A 3mm vertical incision in the skin over the kneecap was made and the patellar ligament was exposed where a vertical medial parapatellar incision (approximately 1-1.5 mm in length) was made on the tibial plateau. A 26 G needle was vertically inserted through the incision into the tibial canal until the tip of the needle has reached the hollow canal, and through the needle, the internal wire guide of a 25 G BD spinal needle (Quincke 25 G 3" spinal needle, BD #450170, Franklin Lakes, USA) inserted into the canal and the 25 G needle was then removed while keeping the internal wire core guide in the tibial canal. The protruded part of the

wire core was cut, and a small 90° bend was made at its proximal part to avert puncture of the patellar ligament. The incision on the patellar ligament was then sutured. A mid-tibial shaft osteotomy was made using a bone scissor (Fine Science Tools #14082-09, Vancouver, Canada) by protecting the muscles around. Prior to closing the surgical site, 2-3 drops of Lidocaine 2% / Bupivacaine 0.5% (Wyeth, Ontario, Canada and Abbott Laboratories Ltd., Quebec, Canada, respectively) mixture were dropped to the site and incision then sutured with a single 6-0 vicryl suture (Johnson & Johnson, Skillman, USA) using horizontal mattress sutures as needed. Following the surgery, the mice were replaced into their clean cages on a heated pad and allowed to move around freely. The mice were then given subcutaneous injections of 5 ml/g body weight Carprofen at 24 hours and 48 hours post-surgery. The animals were closely monitored and any mice showing signs of severe pain, impaired mobility, bleeding, or swelling were euthanized.

All procedures were done under aseptic conditions in the procedure room of the animal facility at the Shriners Hospital for Children – Canada, Montreal, Quebec, Canada.

2.3 Sample Collection

The mice were sacrificed using isoflurane and CO₂ at D10, D14, and D28 post-surgery. The tibiae and calluses were dissected at the level of the knee and ankle. The intramedullary nail was carefully taken off. Tibiae and calluses were then harvested in PBS and directly transferred to test by μ CT or kept in -20°C for further analyses via Torsion Test or 3-Point-Bending Test as planned.

2.4. Torsion Tests (TTs)

Torsion testing (twisting testing) was done to measure the biomechanical properties of the tibiae. The tibiae samples tested were D14 and D28 post-surgery. Initially, a small piece of tape covering the bottom of each disposable M6 fixture was used to hold the resin. The bone was embedded inside the M6 nuts with fast curing orthodontic acrylic resin mix (Ortho-Jet Liquid & Powder, Lang, USA) to rigidly constrain both ends. The bones were wrapped with 1X PBSsoaked gauze to maintain the hydration while the resin was hardening, usually overnight. The samples were inserted into holders attached to the micromechanical testing system (MACH-1 MA303-ART01-D v1 Lab Module, Biomomentum, Canada) as the proximal-end of the tibia was fixed and the distal-end was rotated.



Figure 12 Torsional Testing Setup

The testing set with zero load and started from the theta position on the axis stage. Move relatives set as -360° amplitude and 0.5 deg/s velocity.

The biomechanical properties such as ultimate torque and torsional stiffness were acquired. Torsional stiffness (G) of the tibiae were measured from the slope of the linear portion of the curve and expressed in N-mm/deg (G dMt/d θ t), and the torsional elasticity was measured as ultimate failure (Wt) [torque], named integral, and expressed in N-mm.deg (Wt= $\int_{\theta_0}^{\theta_0}M_t.d\theta$). in total 76 samples were tested (25 WT, 25 +/R396W, and 26 R396W/R396W).

2.5. Micro-Computed Tomography

The Micro-Computed Tomography (µCT imaging were done to obtain the mineralized callus volume (percentage of bone volume to tissue volume [BV/TV]). To scan the tibias, mouse calluses and tibiae were harvested, on post operational day 10, discarded from soft tissue and stored in 1X PBS at -20°C until the analysis date. Right before the analysis, samples were dissolved, wrapped with 1X PBS-soaked gauze, and replaced to 0.6 ml tubes for imaging. The scanning of the tibias done by the desktop microtomographic imaging system (SkyScan 1272, Bruker AXS, Antwerp, Belgium).

The reconstruction was performed using 60kV, 166µA, 5-µm resolution, and a 0.5° rotation with 0.5-mm aluminum filter. The scanned samples were then moved to perform the 3-point bending tests (3PBTs) at the same day. The raw images were captured using NRecon software (Bruker). The trabecular volumes of interest (VOI) were defined and used to measure BV/TV. Trabecular regions set to cover all cancellous bone in metaphysis, within 2-mm-region slices. The manual contouring approach on a slice-by-slice basis was used for the callus

formational region of tibia. Tissue volume was set as a 20-mm³ rectangular prism. And the analysing done using DataViewer and CTAn (both Bruker, Antwerp, Belgium). In total 44 samples were scanned (12 WT, 17 +/ R396W, and 15 R396W/ R396W)

2.6. Three Point Bending Tests (3PBTs)

3-Point bending testing is another biomechanical test that was used. The test was performed on tibiae isolated and then, scanned by μ CT, using the Instron model 5943 singlecolumn table frame machine. Bones were maintained in 1X PBS solution to maintain the hydration until testing. A downward bending load-sensing cell was applied on the widest part of the callus at 0.05 mm/s flow with a supporting distance 3 mm on each side of the callus which were held in place by holders spaced 6 millimetres apart. Raw output used for comparison is stiffness (N/mm) and strength (N). In total 45 samples were tested (12 WT, 19 +/ R396W, and 14 R396W/ R396W).



Figure 13. 3-PBT Setup

2.7. Statistical Analysis

The statistical analyses were done with GraphPad Prism (GraphPad Software). Statistical analyses were performed using a 2-tailed *t* test or 1-way ANOVA, followed by Bartlett's or, Bonferroni's post hoc test. The statistical significance threshold was set at a *P* value of less than 0.05.

Chapter III: Results

We used two separate methods to assess the biomechanical properties of the repair callus from mutant animals and littermate controls: torsion testing and the 3-point bending assay.

3.1. Torsion Testing

In a first set of experiments, torsion testing was performed. For this test, male and female mice from the three genotypes (Wild type [WT], heterozygous [+/R396W], homozygous mutant [R396W/R396W]) were analyzed. Mice were sacrificed and tibias were harvested at post-surgery D14 for female mice and D14 and D28 for male mice.

The results for male mice are presented first. A total of 25 male mice were analyzed at D14 (8 WT, 7 +/R396W, 10 R396W/R396W) and a total of 14 male mice (4 WT, 3 +/R396W, 7 R396W/R396W) were analyzed at D28.

We measured the ultimate torque parameter to assess the torsional elasticity of the callus tissue. At day 14 post-surgery, we did not see any significant differences among genotypes for this parameter (Figure 14, left). However, both heterozygous and homozygous male mice showed increase in ultimate torque at D28 post-surgery, and the difference were significant for the +/R396W genotype (Figure 14, right).



Figure 14 Ultimate Torque of male mice

The elasticity of the calluses was assessed by torsion test and calculated from the ultimate torque. (Left) Male mice on D14, did not show statistical significance. P>0.05, by one-way ANOVA followed by Bonferroni's post-test. (**Right**) Male mice on D28, showed significance between WT and +/R396W. *P 0.045, by one-way ANOVA followed by Bonferroni's post-test.

We next assessed the differences in the stiffness (slope) of the callus tissue among the different genotypes. At day 14 post-surgery, the WT data was too low to detect, and both heterozygous and homozygous mice showed an increase in callus stiffness as compared to WT male mice. The stiffness showed lowering trend compared to heterozygous littermates, but the difference was statistically non-significant. (Figure 15, left). However, when we analyzed the calluses at D28 post-surgery we noticed a significant decrease in stiffness for homozygous mutant mice as compared to their wild-type and heterozygous littermates (Figure 15, right).



Figure 15 Stiffness of male mice

The stiffness of the calluses was assessed by torsion test and calculated from the slope. (Left) Male mice on D14, WT data was too low to detect (N.D. for Not Detectable). The difference between +/R396W and R396W/R396W was non-significant. P 0.072, by 2 -tailed t test. (Right) Male mice on D28, showed significance between mutant and both control genotypes. Median P 0.0139, *P 0,0250, **P 0.0415 by one-way ANOVA followed by Bonferroni's post-test.

For the female sex, 34 mice been used in total as 12 WT, 13 +/R396W and, 9 R396W/R396W. The bones were harvested at D14. The ultimate torque data were not statistically different between the genotypes (Figure 16). And the stiffness showed significant decrease towards mutant genotype and the difference were significant between heterozygous and mutant littermates (Figure 17).



Figure 16 Ultimate Torque of D14-female mice

The elasticity of the calluses was assessed by torsion test and calculated from the ultimate torque. Female mice on D14, did not show significant differences. P>0.05, by one-way ANOVA followed by Bonferroni's post-test.



Figure 17 Stiffness of D14-female mice

The stiffness of the calluses was assessed by torsion test and calculated from the slope. Female mice on D14, showed statistical significance between +/R396W and R396W/ R396W. *P 0.0478, by one-way ANOVA followed by Bonferroni's post-test.

3.3. Micro-CT

We then analyzed the structural morphology of the callus tissue using micro-computed tomography imaging. We assessed the mineralized callus volume by calculating the percentage of bone volume to tissue volume (BV/TV) among the different genotypes. Males and females were sacrificed, and tibias were harvested on day 10 post-surgery.

A total of 34 male mice have been analyzed (10 WT, 10 +/R396W and, 14 R396W/R396W). The μ CT analysis of calluses did not show a significance in mineralization between male littermates (Figure 18).



Figure 18 Percent bone volume of D10-male mice

The mineralized callus volume was assessed by μ CT scanning and calculated as BV/TV. Male mice on D10 did not show significant differences between littermates. P>0.05, by one-way ANOVA followed by Bonferroni's post-test.

Similarly, a total of 24 female mice was analyzed (7 WT, 10 +/R396W and, 7 R396W/R396W). We measured significant differences in mineralized tissue among the genotypes (Figure 19).



Figure 19 Percent bone volume of D10-female mice

The mineralized callus volume was assessed by μ CT scanning and calculated as BV/TV. Female mice on D10 showed a significant difference between the +/R396W and R396W/R396W littermates. *P 0.0383, by one-way ANOVA followed by Bonferroni's post-test.

3.2. Three-Point-Bending-Testing

To study the biomechanical properties of the callus tissue, the three-point bending test was performed following the μ CT scanning. Females were sacrificed and tibias were harvested at post-surgical D10. Stiffness (N/mm) and strength (N) were measured.

For the male sex, 34 mice were used in total as 10 WT, 10 +/R396W and, 14 R396W/R396W. At D10 post-surgery, the analysis of the callus did not reveal any significant differences in stiffness among the different genotypes (Figure 20, left). We then analyzed the changes in the load at break parameter to assess the strength of the callus tissue. Interestingly, the analysis of heterozygous and homozygous calluses showed a significant decrease in load at break as compared to wild-type callus tissues (Figure 20, right).



Figure 20 Stiffness and strength of male mice

The stiffness and strength of callus volume were assessed by 3PBTs and calculated from slope and load at break, respectively. (Left) The stiffness of male mice on D10 did not show differences between the littermates. P >0.05, by one-way ANOVA followed by Bonferroni's post-test. (**Right**) The strength of repair calluses from male mice on D10 showed a significant decrease as compared to wild-type callus tissues. *, P<0.05; **, P<0.01, by one-way ANOVA followed by Bonferroni's post-test.

A total of 24 female mice have been analyzed (7 WT, 10 +/R396W, and 7 R396W/R396W). The stiffness data were not significantly different between groups (Figure 21, left). As observed for the males, the strength data were significantly different compared to the wild-type genotype (Figure 21, right).



Figure 21 Stiffness and strength of female mice

The stiffness and strength of callus volume were assessed by 3PBTs and calculated from slope and load at break, respectively. (**Left**) The stiffness of female mice on D10 did not show differences between the littermates. P >0.05, by one-way ANOVA followed by Bonferroni's post-test. (**Right**) The strength of female mice on D10 showed a significant decrease in heterozygous and homozygous mutant genotypes (+/R396W and R396W/ R396W) compared to wild-type callus tissues Median P 0.0037, *P 0.0152, **P 0.0045, by one-way ANOVA followed by Bonferroni's post-test.

Taken together, the biomechanical analysis of the callus tissue of the different genotypes suggests a decrease in the mechanical strength towards the mutant (R396W/R396W) callus tissue as compared to wild-type calluses.

Chapter IV: Discussion

IIH is a rare genetic condition for which the genetic etiology remained unknown until 2011 when Schlingmann and coworkers identified the inactivation of CYP24A1 as a molecular basis [1]. The clinical manifestation of the disease is characterized by severe hypercalcemia, hypercalciuria, decreased PTH, nephrolithiasis, nephrocalcinosis with a predisposition to renal complications as well as dehydration, vomiting, and constipation [1]. In addition to *CYP24A1* mutations, the Schlingmann group identified *SLC34A1* genetic variants as the cause of IIH forms with some clinical differences [76]. These results suggest that a complete diagnostic of patients presenting with IIH symptoms should include genetic testing together with assessment of the 25(OH)D₃-to-24,25(OH)₂D₃ ratio [76, 92].

Biallelic mutations causing complete loss-of-function of the CYP24A1 activity have been demonstrated previously. As a result, hypervitaminosis D occurs and that leads to increased intestinal absorption of calcium and symptomatic hypercalcemia.

Even though it was hypothesized that *CYP24A1* mutations were leading to IIH condition, the locations of the mutations were unknown. Recently, 43 missense and deletion mutations of *CYP24A1* were described [91]. A small set of mutations in the *CYP24A1* gene comprising p.E143del, p.R396W, and p.L409S is detected in high frequency in the majority of patients. Our team previously showed that *Cyp24a1*-null mice with a deletion of exons 9-10 replaced by a PGKneo selection cassette, mimicked the disease IIH [4]. It also displayed impaired callus formation during the endochondral phase of fracture repair. They also observed that treatment with 24,25(OH)₂D₃ was able to rescue callus size and stiffness, but 1,25(OH)₂D₃ treatment was ineffective to correct the impaired bone fracture healing. Based on previous findings, we hypothesized that a humanized model of IIH in genetically modified mice harboring a knock-in R396W mutation will exhibit impaired fracture repair. We predicted that this mutation would cause a slower healing rate and weaker bone biomechanical properties on the mutant R396W/R396W genotype compared to WT by affecting production of the 24,25(OH)₂D₃ metabolite. To test our hypothesis, we designed the proper research model. We initially obtained the R396W knock-in ES cells from Cyagen under contract and finally generated the R396W-CD1 mice strain. This strain is a phenocopy of the IIH human condition (unpublished data from the St-Arnaud laboratory). We then performed a bone fracture healing study design based on experiments previously done by the St-Arnaud laboratory to assess whether the strain has impaired fracture repair. We performed the rodded tibial osteotomy on 12-weeks-of-age mice and harvested the healing tibial bones at D10, D14, and D28.

In the current study, in addition to the previous biomechanical endpoints, we added a new technique to obtain material properties of the callus tissue post-surgery, i.e. torsion testing.

A torsion test ideally examines bone behavior under shear stress, which is also important in vivo. The callus diameter has a significant impact on the strength when calculating biomechanical properties under torsion, with the cross-sectional moment of inertia corresponding to the fourth magnitude of the radius diameter. As a result, even slight changes in callus size have a significant impact on the bone's ability to bear torsional pressures [93]. Based on these parameters, one would expect the torsion breaking strength of the larger calluses to be significantly higher.

Our findings did not entirely agree with these notions and torsional testing generated some discordant results. For example, the callus elasticity (integral) from the homozygous mutant animals was higher than their WT littermates at D28 post-surgery in male mice. Also, the

stiffness levels were higher in heterozygous and mutant male animals than WT mice at D14 postsurgery.

The cause of these disparities appears technical. Stiffness of male WT calluses was not detectable at D14 (Figure 15, left panel). When results from heterozygous animals were compared to homozygous mutants, the lower stiffness measured in mutants showed lowering trend even though the difference was not significant.

Torsion stresses the entire bone between the fixation points equally, causing the weakest component of the bone to break first. Newly generated calluses continue into previously unfractured bone sections with biomechanical qualities that are very similar to native bone. It was not possible to isolate the calluses and assess their torsion strength with this test since some calluses were stronger than non-fractured regions of the bone (Figure 22). Also, when we looked through the literature, we found out that another research group was faced with a similar problem (Figure 23) [94]. In the research design of Bosemark et al., they performed the torsion testing following the rodded femoral osteotomy on rat's femur. They harvested the rats' femurs on post-operational week 6 and implemented biomechanical testing such as 3-PBT and TT. They were successful to measure the properties of the callus formation on 3-PBT but, during TT (twisting) some of their samples were breaking from points other than callus area [94].



Figure 22 TT- Bone breaks from the weakest point other than callus

During TT, numerous tibias broke from the weakest point regardless of their sex and genotype. Thus, the data were obtained from the bone sections other than the callus formation. Meaning that, biomechanical properties of callus were not being tested.



Figure 23. Pre- and post-twisting test.

The figure shows the rat femurs on post-surgery week 6. The intramedullary rod can be seen on pre-twisting images (**A and C**). As it shows the breaking line is on callus formation in post-3PBT image (**B**), but it is in below callus, towards to distal end in post-twisting (**D**). Figure adapted from Bosemark (2014) [94], with permission.

So even though we estimated that torsion testing would be preferable, we found that there are technical limitations to analyzing the samples as seen in our and Bosemark and coworkers research [94]. This issue might be overcome by changing the bone harvesting days to an earlier time point than 14 days. So, the callus might be the weakest point in the sample.

We then prepared another cohort to test the biomechanical properties of our R396W-CD1 strain with more conventional assays, μ CT scanning and 3PBTs. After performing the same intramedullary rodded fracture surgery, we followed the same procedure as previously done in our lab [4] except we changed the timeline from post-operational D14 to D10 to additionally determine the onset of the activity of 24,25(OH)₂D₃ during fracture healing in IIH.

Our µCT scanning results showed similar outcomes as Martineau et al. obtained [4]. R396W-CD1 mouse strain showed significantly lower sizes of mineralized callus volume (BV/TV) in female mice compared to heterozygous littermates, and it showed a lowering trend in male sex towards the mutant genotype.

3PBTs results were also having similarities with previous findings [4]. The stiffness did not show significance in both sexes although they were having a lowering rate towards the mutant strain. The strength data (load at break), on the other hand, showed a significant decrease in R396W-mutated mice in both sexes.

Chapter V: Conclusions and Future Directions

Our study aimed to characterize fracture repair in a humanized IIH mouse model and outline the biomechanical properties of the IIH mouse model.

As R396W mutations are among the most common types of mutations associated with *CYP24A1* polymorphisms, we expected to see impaired fracture repair as seen in Martineau et.al research [4]. Our data supported our hypothesis that the mutant littermates would exhibit impaired fracture repair compared to WT littermates. These outcomes show that the humanized preclinical model of IIH has similar phenotypic manifestations to the original *Cyp24a1*-null mice which sported a deletion of exons 9-10, insertion of a selection cassette in the opposite transcriptional orientation and did not express the *Cyp24a1* transcript [3].

Previously, it has been shown that optimal bone fracture repair requires 24,25(OH)₂D₃ and its effector molecule FAM57B2 [4]. In our study, by changing the analysis timepoints from D14 to D10, we observed similar outcomes at the level of biomechanical properties. This suggests that 24,25(OH)₂D₃ has an earlier role during fracture repair. This has an important impact on bone health and the healing rate in both healthy and ill individuals, as the literature points to high rates of immobility and fatality in adults with long bone fractures. Also, it is known that IIH patients have imbalanced vitamin-mineral homeostasis and lower bone mass compared to unaffected individuals [74]. Taken together, our results raise the question as to whether 24,25(OH)₂D₃ supplementation as part of treatment would help achieve complete fracture healing or not. Our mouse model is promising to be used in such research in the future.

During our research, even though we estimated that torsion testing would be preferable, we found that there are technical limitations to analyzing the samples. It showed that using torsion testing for fracture healing research should be considered carefully. Setting an earlier

timepoint might help to overcome the issues. Also, performing histological analysis in addition to the methods that we have used would help to further characterize the phenotype of R396W mice.

Another limitation of our work is the lack of histological scanning. We suggest applying histological scanning to the future researches.

Based on our work and previous findings in this regard, it has been shown that 24,25(OH)₂D₃ has a significant role during fracture repair. However, it is still unknown whether the effect of 24,25(OH)₂D₃ on bone regeneration is dependent exclusively on chondrocytes or involves some other cell type. To answer this question, a chondrocyte-specific mouse model is being generated to further investigate this issue.

Furthermore, in patients with IIH, it should be possible to study fracture repair in a prospective way following the fracture, by taking high-resolution peripheral quantitative computed tomography (HR-pQCT) images at intervals to find evidence of reduced callus size. Finite element modeling (FEM) could predict that the biomechanical parameters of affected bones are weaker. This would support the use of 24,25(OH)₂D₃ as therapy for treating fractures.

As every human being is unique, so are their diseases. Mapping the subtypes of genetic diseases could help the development of personalized medicine approaches as new treatments. Identifying the subtypes and applying specific treatments may have a big impact on enhancing the life quality of patients and minimizing the healthcare expenses.

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McGill University

Institution name Expected presentation Apr 2022 date Portions figure 2

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