

# A novel zebrafish mutant to elucidate the consequences of Wnt16 cysteine deletion Emily G. Ramirez<sup>1,2,3</sup> and Ronald Y. Kwon<sup>2,3,4</sup>



<sup>1</sup>Washington NASA Space Grant Consortium; <sup>2</sup>Department of Orthopaedics and Sports Medicine; <sup>3</sup>Institute for Stem Cell and Regenerative Medicine; <sup>4</sup>Department of Mechanical Engineering, University of Washington, Seattle, Washington, USA

## INTRODUCTION

- Osteoporosis is a common disease characterized by bone fragility that impacts over 200 million people worldwide<sup>5</sup>
- The WNT family of proteins has been implicated in numerous developmental and disease pathways<sup>4</sup>
- Mutations involving one of the 24 cysteines conserved across the WNT family often have functional consequences<sup>4</sup>
- WNT16 has been linked to genetic risk for osteoporosis<sup>4</sup>
- The impact of cysteine 10 (c10) alteration in any WNT remains unknown<sup>4</sup>
- Zebrafish are an ideal model for skeletal research<sup>3</sup>

## METHODS

#### **STEP 1: Creating somatic mutants using CRISPR-Cas9**

- Cas9:gRNA injected into embryos at the 1- or 2-cell stage
- Mutations created at the *wnt16* locus at the c10 position



\*Figure 1: Workflow for creating somatic mutants (breeding, injecting, and rearing).

### **STEP 2: Creating germline mutants**

- Somatic mutants outcrossed with WT fish (F0)
- Heterozygous offspring of F0 selected and inbred (F1)
- Homozygous offspring of F1 used for experiments (F2)



\*Figure 2: Creating germline mutants via outcrossing, selecting, and inbreeding.

### **STEP 3: Confirming c10 deletion**

- Sanger sequencing used to determine mutant genomic sequence
- Genomic sequence translated to protein sequence
- Consequences on protein sequence determined through sequence alignment



\*Figure 3: 9 base pair deletion that resulted in the deletion of cysteine (C), histidine (H), and glycine (G). \*Figures 1, 2, and 3 created with BioRender.com









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\*Figure 4 adapted from Cosman, F., de Beur, S. J., LeBoff, M. S., Lewiecki, E. M., Tanner, B., Randall, S., & Lindsay, R. (2014), Clinician's Guide to Prevention and Treatment of Osteoporosis, Osteoporosis International, 25(10), 2359–2381 https://doi.org/10.1007/s00198-014-2794-2.

## HYPOTHESIS & AIM

• **Hypothesis**: loss of c10 in Wnt16 will result in altered bone mass indicative of elevated osteoporosis risk.

• Aim: generate zebrafish mutants where c10 is deleted in Wnt16.

#### **OSTEOPOROSIS: "POROUS BONE"**

Figure 5: Prevalent fracture locations in osteoporotic individuals Adapted from Hurley, D. L., & Khosla, S. (1997). Update on Primary Osteoporosis. Mayo Clinic Proceedings, 72(10), 943–949. https://doi.org/10.4065/72.10.943 and United States., United States., 8 Milwaukee Academy of Medicine. (1918). Manual of surgical anatomy: Authorized by the Secretary of War and under the supervision of the Surgeon General and Council of National Defense. Washington

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## **RESULTS + DISCUSSION**

#### **RESULTS**

- 3 amino acid deletion discovered at Cys214, corresponding to c10 (p.Cys214 Gly216del)
- Previously characterized *Xenopus* Wnt8 crystal structure indicates c10 contributes to the integrity of WNT tertiary structures via a disulfide bond formed between c10 and c11<sup>4</sup>
- c10 and c11 exist in the hairpin 2 "Thumb" region, which directly interacts with Frizzled receptors<sup>4</sup>



<sup>4</sup>Figure 6: (A) Xwnt8 tertiary structure with subdomains shown. (B) Schematic of the 24 conserved cysteines of Wnt3a with known disulfide bonds modeled from the crystal structure of Xwnt8.

#### DISCUSSION

- We hypothesize that Wnt16 will have altered secretion/ activity in our novel mutant as a result of the c10 deletion
- Our novel animal model will help us understand the function of c10 in Wnt16
- Drug treatments for osteoporosis are only effective for half of all patients<sup>5</sup> (no known therapies for osteosarcopenia<sup>2</sup>)
- This research will allow us to assist in developing new therapies that may alleviate a global health burden

## NEXT STEPS

- Quantitatively evaluate bone phenotypic characteristics in wnt16<sup>w1012</sup> mutants (using calcein staining and microcomputed tomography imaging)
- Compare *wnt16<sup>w1012</sup>* mutants to *wnt16* knockouts previously characterized by our lab:

#### We predict that *wnt16<sup>w1012</sup>* mutants will phenocopy *wnt16* knockouts, suggesting that c10 plays an essential role in WNT16 secretion and/or activity.