

in airway resistance than non-CF mice, with heightened response to methacholine. Importantly, this increase in airway obstruction in CF mice was reversible with albuterol treatment, indicating airway smooth muscle dysfunction as a principal driver of lung function abnormalities. Furthermore, TGFbeta induced an increased ASM burden on lung histology in both CF and non-CF mice ( $p < 0.05$ ). IL-6 levels in the BAL of CF mice showed greater increases after TGFbeta treatment compared to non-CF mice ( $p < 0.05$ ). Empty vector control treatment did not cause lung pathology. **DISCUSSION/SIGNIFICANCE OF IMPACT:** Young children with CF have a unique pattern of pulmonary inflammation compared to inflamed non-CF control patients. In CF, TGFbeta pulmonary levels are uniquely associated with IL-6, a driver of ASM dysfunction in other pulmonary diseases. We followed up this clinical observation study by investigating the effect of TGFbeta on pulmonary disease in a mouse model. CF mice demonstrate increased pulmonary IL-6, airway obstruction, and ASM dysfunction after TGFbeta exposure. This study provides evidence that TGFbeta is associated with a distinct cytokine pattern that may promote ASM dysfunction in early CF lung disease. Understanding the mechanism of early CF pathophysiology will be critical in developing targeted therapeutics that can prevent early lung damage.

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### The influence of early life experience on telomere length, health, and behavior of domestic cats

Mikel Maria Delgado<sup>1</sup>, Dr. Melissa Bain and Dr. Tony C.A.T. Buffington

<sup>1</sup>University of California, Davis

**OBJECTIVES/SPECIFIC AIMS:** The primary objective of this research is to determine whether being hand-reared, and deprived of early maternal interaction, will affect telomere length in orphaned kittens. The secondary goal is to examine how early maternal separation impacts the health, growth and behavior of orphaned kittens. **METHODS/STUDY POPULATION:** Kittens were fostered through local rescue groups and shelters. We collected blood samples from 42 orphaned kittens during the first week of their lives. Due to high mortality of this population, we obtained a second blood sample at eight weeks of age from only 30 of these kittens. We collected blood samples from 12 control kittens raised with mothers at during the first and eighth weeks of life. Blood samples are currently being processed with real time quantitative PCR (qPCR) by the Real-time PCR Research and Diagnostics Core Facility at the UC Davis School of Veterinary Medicine (SVM). This includes RNA extraction, cDNA synthesis, Reference Gene Validation, and qPCR analysis. Relative telomere length (RTL) will be calculated by comparing the average telomere abundance across three samples cells with that of a reference gene (single copy number) for each sample. The resulting T/S ratio (telomere to single copy) is proportional to the average telomere length. If T/S = 1, then telomere length in the sample and the reference are the same. **RESULTS/ANTICIPATED RESULTS:** Because telomeres show the fastest rate of shortening early in life, we predict that maternal separation will increase the rate of telomere shortening in kittens. We also predict that the telomeres of orphaned kittens will be shorter at both one week and eight weeks of age, compared to controls. **DISCUSSION/SIGNIFICANCE OF IMPACT:** This study will increase our understanding of early life adversity, a finding that can translate to other mammals. It will inform the practice of fostering neonatal kittens, and illuminate whether these kittens

might be at higher risk than mother-reared kittens for health problems (which could be investigated in future studies). If significant telomere shortening occurs between collection periods, then future studies can take more frequent blood samples to determine what stages of early development are potentially most sensitive. If differences between groups are found, this will establish a protocol for several future research projects, such as testing whether these detrimental effects can be mitigated by environmental enrichment via activation of telomerase. Telomerase is an enzyme that appears to counteract some shortening of telomeres, and is activated by several external factors, including exercise. Thus, a logical follow up study would be developing and testing age-specific and appropriate enrichments that may activate telomerase and reduce telomere loss. Physical contact, whether human, mother, or siblings, is another possible source of telomerase activation in young kittens. Future studies also could quantify the effects of different sources of physical contact on telomere shortening. Finally, a positive finding would establish a need for longitudinal studies of the effects of early weaning on feline health and behavior and whether differences in early-life telomere lengths predict health and longevity of cats.

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### The Power of Phenotypic Extremes in Detecting Novel Genetic Modifiers of Hemophilia

Ohad Shimshon Bentur<sup>1</sup> and Barry S. Collier, MD<sup>1</sup>

<sup>1</sup>Rockefeller University

**OBJECTIVES/SPECIFIC AIMS:** 1. To identify novel genetic modifiers that result in a mild bleeding phenotype in patients with FVIII <1%. 2. To examine the feasibility of a practice model that incorporates the principles and methods for both obtaining consent for NGS and returning individual research results from the sources described above. **METHODS/STUDY POPULATION:** 1. We plan a 3-step approach for identifying novel genetic modifiers of hemophilia: a. Obtain samples from individuals with an extremely mild bleeding phenotype: The study will be narrowed to patients with confirmed FVIII <1%, a null mutation in the gene for FVIII, and a mild bleeding phenotype according to a detailed bleeding history. b. Identify variants that modify phenotype: Whole exome sequencing will be performed, followed by a focused analysis of genes known or suspected to be involved in thrombosis and hemostasis and prediction of variant impact using algorithms that account for conservation and deleteriousness of all variants. c. Verify the impact of novel variants in independent samples: In silico (analyze genetic databases for suspected variants), in vivo (assess bleeding in animal models of hemophilia after introducing presumed modifier variants). 2. We will employ a model for obtaining informed consent and communicating individual genetic research results and results with potential clinical impact to research participants: a. The informed consent process will be performed after potential participants read a pamphlet entitled "Genetic Research at The Rockefeller University Hospital and Center for Clinical and Translational Science." The pamphlet includes 16 questions that the potential participants are urged to ask the investigator, including, "What will you look for in my genetic information?", "Will I receive results from this study?". Potential participants will also be informed of the meaning of clinically actionable variants, either pathogenic variants related to phenotype or secondary ("incidental") findings (i.e. variants unrelated to phenotype, the knowledge of which could lead to actions that may improve health). Participants who do not want to receive

information about potentially actionable variants will be excluded from the study to avoid a situation where the investigator has clinically important information that cannot be shared with the participant. b. Genetic testing will be performed in a CLIA-certified lab to allow investigators to share the results with the study participants. c. Results will be reported to study participants according to a standard operating procedure (SOP) that classifies the report of variants according to the relation to phenotype and the pathogenic potential. d. Participant satisfaction with the informed consent process and the return of results will be assessed by a questionnaire for obtaining participants' perceptions of their research experience, based on a standard set of validated research participation experiences measures (Kost RG et al, *J Clin Transl Sci.* 2018;2:31). **RESULTS/ANTICIPATED RESULTS:** Samples from individuals with severe null mutation hemophilia and a mild bleeding phenotype will be enriched in genetic modifier variants. After completing participation, participants will express satisfaction with the informed consent process and the results of the return of genetic information. **DISCUSSION/SIGNIFICANCE OF IMPACT:** Genetic risk assessment to predict bleeding risk has the potential to provide hemophilia patients with tailored therapy, allowing for very early initiation of treatment (prophylactic thrice weekly IV administration of FVIII) in patients with a high bleeding risk and deferring this costly and burdensome treatment in patients who are expected to be mild bleeders. Genetic modifier variants of hemophilia may be found to predict thrombosis in non-hemophiliac patients and profoundly impact the treatment of venous thrombosis. A structured process for obtaining consent for NGS and return of genetic results to study participants can protect them from uncertain genetic information. Moreover, this process will prevent a situation in which investigators have knowledge about clinically actionable variants but they are not allowed to report them to the participants or do not have a process for doing so. Sharing individual research results and results with clinical significance with participants of studies that involve whole exome sequencing can promote transparency and engagement of participants throughout the research enterprise.

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### The role of CypD/mPTP during osteogenic differentiation - a potential target to prevent bone loss

Rubens Sautchuk Jr.<sup>1</sup>, Brianna H. Shares<sup>1</sup> and Roman A. Elisev<sup>1</sup>  
<sup>1</sup>University of Rochester Medical Center

**OBJECTIVES/SPECIFIC AIMS:** The study aims to further investigate how cyclophilin D (CypD), the key mPTP opening regulator, affects BMSCs fate and to determine potential regulatory mechanisms involved in CypD regulation during osteogenesis. **METHODS/STUDY POPULATION:** We evaluated CypD mRNA expression in mouse BMSCs and in osteogenic-like (OL) cells during the course of OB differentiation. CypD protein level was also probed. Moreover, BMSCs had their mPTP activity recorded during osteoinduction. We further analyzed the effect of CypD genetic deletion on osteogenesis in vitro and in vivo. For our in vivo model, we performed the ectopic bone formation assay to assess differences in ossicle formation when CypD KO BMSCs were transplanted compared to wild type littermate BMSCs. In our in vitro model, we transfected OL cells with either CypD gain of function or CypD loss of function vector and measured their osteogenic differentiation potential. Additionally, we treated BMSCs with CypD inhibitor and compare to non-treated BMSCs for mineralization level. To determine potential regulatory mechanisms involved in CypD regulation, we analyzed the CypD gene (Ppif) promoter for potential

transcription factor (TF) binding sites and found multiple Smad-binding elements within this promoter. Smads (Smad1, 5, 8) are TFs downstream from Bone Morphogenic Protein (BMP) signaling pathway that transmit cell differentiation signaling, and exert either activating or inhibitory effects on a variety of genes. We also transfect OL cells with Smad1 vector and analyzed for CypD mRNA levels. **RESULTS/ANTICIPATED RESULTS:** - Our data showed that CypD mRNA levels decreased in both primary cells and OL cells at day 7 and day 14 in osteogenic media. - Osteogenic induction also decreased mPTP activity. - In vivo ectopic bone formation assay showed increased ossicle fo **DISCUSSION/SIGNIFICANCE OF IMPACT:** Our data suggest that downregulation of CypD increases OB differentiation due to improved OxPhos activity led by mPTP closure. Our results corroborate reports of CypD downregulation and mPTP closure during neuronal differentiation in developing rat brains as well as in cardiomyocyte differentiation in developing mouse hearts. Our studies also suggest a yet unknown mechanism linking differentiation signaling with mitochondrial function - BMP/Smad mediated downregulation of CypD transcription. As initially mentioned, in a previous study, our lab showed that CypD KO mice present higher mitochondrial function and osteogenicity in aged BMSCs and less osteoporosis burden. Taken together, these results suggest that CypD can be a potential target to prevent bone loss in aging.

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### The role of myostatin in diabetic bone disease

Evangelia Kalaitzoglou<sup>1</sup>, Callie Knuckles and John Fowlkes  
<sup>1</sup>University of Kentucky Center for Clinical and Translational Science

**OBJECTIVES/SPECIFIC AIMS:** Our primary objective is to determine the mechanism of action of myostatin on osteoblasts by measuring markers of osteoblast differentiation. With these experiments we will evaluate the effects of myostatin on an osteoblastic cell line (MC3T3 cells) and primary murine osteoblasts during baseline and hyperglycemic conditions and assess whether these effects are altered in the presence of a hyperglycemic environment. **METHODS/STUDY POPULATION:** Primary osteoblasts from calvaria of WT mice will be isolated and cultured per previously published protocol. MC3T3 cells (murine pre-osteoblast cell line) and primary osteoblasts will be plated in 6-well plates until they reach confluency. They will subsequently be stimulated with or without myostatin at various concentrations under control and hyperglycemic conditions. Additional experiments will assess myostatin stimulation during cell differentiation/maturation in the presence of osteogenic induction medium. Subsequently, cells will be lysed and processed for gene analysis with qPCR. Genes of interest (e.g., myostatin, RUNX2, osteocalcin etc.) will be assessed. Additionally, cells will be collected and processed for protein quantification with western blot to assess myostatin-related pathways, such as Smad2/3 and MAPK signaling. **RESULTS/ANTICIPATED RESULTS:** We have demonstrated that the receptor for myostatin (Activin receptor 2b, AcvR2b) is present in MC3T3 cells and we have evidence of Smad2 phosphorylation in MC3T3 cells as a result of myostatin stimulation, confirming that myostatin can exert intracellular signaling events in bone cells (Fig 1). We anticipate to observe negative effects of myostatin on differentiation of primary osteoblasts and MC3T3 cells. Specifically, we anticipate suppression of Runt-related transcription factor 2 (RUNX-2), a transcription factor known as the "master regulator" of osteogenic gene expression and programming, as a result of