ANTICIPATED RESULTS: As of 10/18/24, a total of 53 were enrolled, with 52 eligible for the study and were between the ages of 30–75 years. 51 identified as women and 1 identified as nonbinary. 21 (40.4%) identified as Black, 30 (57.7%) identified as White, 2 (3.8%) identified as Hispanic, and 1 (1.9%) identified as mixed race. Of the total enrolled, 25 (48.1%) met criteria to meet with a genetic counselor. Twelve (23.1%) have been scheduled to with meet with a genetic counselor and 2 (3.8%) of this group completed their appointment, but did not pursue genetic testing. 28 (53.8%) completed the survey and reported that they were satisfied with the service. Of the 16 people who screened positive and completed the survey, all 16 (100%) stated that they intended on proceeding with testing. Our study is still ongoing. DISCUSSION/SIGNIFICANCE OF IMPACT: While this model has demonstrated acceptability so far, there are still possible barriers to genetic counseling and testing after the referral has been provided that need to be explored. However, this approach could provide a novel framework for combining risk assessment with screening mammography for all women nationwide.

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Sarcopenia severity in males between the ages of 3 to 20 years old with duchenne muscular dystrophy (DMD) in Puerto Rico

Edwardo Ramos and Jose G Conde
School of Medicine University of Puerto Rico

OBJECTIVES/GOALS: Objectives/Goals (300 characters): Sarcopenia is a progressive skeletal muscle disorder associated with adverse outcomes. There is a gab of having objective measures upon performing interventions in patients with muscular dystrophies. The object of the present study is to describe the severity of sarcopenia in DMD patients in Puerto Rico. METHODS/STUDY POPULATION: Methods/Study Population (700 characters): Forty to 30 patients with DMD who are followed in MDA Care Center in the "Instituto De Rehabilitacion del Caribe." Diagnosis will be confirmed with genetic testing and/or muscle biopsy. Lean muscle mass will be measured with a Whole Body Dexa (WBD) in a Nuclear Medicine Lab. Hand grip, elbow flexor, and knee extensor muscles strength will be measures with an isometric dynamometer. Patients' functionality will done using the North Star Ambulatory Assessment scale and Brook and Vignos scales, which have been validated for patients with DMD and neuromuscular disease respectively. Correlations will be made with lean body mass (independent variable) and muscle strength and functionality (dependent variable). RESULTS/ANTICIPATED RESULTS: Results/Anticipated Results (700 characters): We expect to find severe sarcopenia in patients with DMD in PR and that it will be more severe with older age. There will be a direct correlation between lean muscle mass and muscle strength, and functionality in DMD patients. DISCUSSION/SIGNIFICANCE OF IMPACT: Discussion/Significance of Impact (300 characters): The findings of our study can help us to explore the possibility that Whole Body DEXA can serve as a potential biomarker for future studies since there is a need to develop noninvasive biomarkers that correlate with disease progression and interventions in DMD patients.

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Intestinal CD4:CD8 ratio and systemic inflammatory parameters in suppressed HIV-1 infection

Francesca Cossarini, Pablo Canales-Herrerias, Divya Jha, Alexandra E. Livanos, Michael Tankelevich and Saurabh Mehandru
Icahn School of Medicine at Mount Sinai

OBJECTIVES/GOALS: To determine the heterogeneity in CD4:CD8 ratio in a well-characterized cohort of PWH and to investigate the predictors of intestinal CD4:CD8 ratio reconstitution (CD4:CD8>1) and its impact on systemic inflammation. METHODS/STUDY POPULATION: We enrolled 52 PWH on ART and with peripheral HIV-RNA RESULTS/ANTICIPATED RESULTS: PWH had a lower CD4:CD8 ratio both in the peripheral blood [p1. This subset of PWH was more likely female (62% vs. 38%, p = 0.0158), diagnosed with HIV for a longer time [p = 0.0347] have longer duration of most recent viral suppression [p = 0.0365] higher CD4+ T cells at enrollment [p = 0.0262] and higher CD4+ T cell nadir. Multiple logistic regression showed that duration of HIV infection [OR 1.13 (95% C.I. 1.02–1.3)] and CD4 = T cell nadir[OR 1.01 (95% C.I. 1.001–1.016)] were associated with colonic CD4:CD8 >1. Colonic CD4:CD8 ratio partially correlated with the peripheral blood CD4:CD8 ratio (r = 0.274, p = 0.068) and with the pro-inflammatory cytokines IL-20 (r = -0.413, p = 0.036) and SLAMF-1 (r = -0.329, p = 0.074). DISCUSSION/SIGNIFICANCE OF IMPACT: In PWH, CD4:CD8 ratio

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Elucidating the epigenetic regulation of estrogen receptor-positive breast cancer cells by parathyroid hormone-related protein (PTHrP)

Madeline Searcy, Jeremy Kane, Bradley Ludington, Michael Phan and Rachelle Johnson
Vanderbilt University Medical Center

OBJECTIVES/GOALS: We have shown that parathyroid hormone-related protein (PTHrP) is enriched at the LIFR promoter in breast cancer cells and inhibits the expression of dormancy-associated genes including LIFR. The objective of this study is to define where all PTHrP binds DNA and identify pathways that are regulated by PTHrP that promote breast cancer colonization of the bone. METHODS/STUDY POPULATION: In this study, we use human estrogen receptor-positive MCF7 breast cancer cells which we and others have reported lie dormant in the bone. MCF7 cells were engineered to express either PTHrP with an HA-tag (MCF7P), or a vector control (MCF7V). We use Cleavage Under Targets and Release Using Nuclease (CUT&RUN), a method of mapping protein-DNA interactions, to define where PTHrP binds DNA. Here, an HA-specific antibody identifies regions of DNA that are bound to PTHrP in MCF7P cells compared to MCFV cells. Next, we perform DNA sequencing and gene set enrichment analysis (GSEA) on genes identified by CUT&RUN to identify pathways that are regulated by PTHrP. These experiments will determine how PTHrP regulates dormancy and breast cancer colonization in the bone. RESULTS/ANTICIPATED RESULTS: We completed IgG (-control),

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H3K4me3 (+ control), and HA (PTHrP) CUT&RUN on MCF7V and MCF7P cells, and submitted DNA for sequencing. This study will define where PTHrP binds the genome and identify pathways regulated by PTHrP. Previously, through ChIP-qPCR we showed that PTHrP binds the LIFR promoter to repress LIFR expression. Given this result, we expect that PTHrP binds to the promoters of dormancy-associated genes including LIFR in MCF7P cells compared to MCF7V cells. PTHrP may be involved in regulating other processes besides dormancy to induce expansion of breast cancer cells in the bone, so we will use GSEA to identify pathways that are altered in MCF7P cells when PTHrP is over-expressed compared to MCF7V cells. Together, this will define how PTHrP regulates gene expression of bone metastatic breast cancer cells. DISCUSSION/SIGNIFICANCE OF IMPACT: This study will unveil mechanisms of metastatic breast cancer expansion in the bone by defining where PTHrP binds the genome to regulate gene expression. These findings will reveal therapeutic vulnerabilities that will be used to target bone-disseminated tumor cells to prevent lethal recurrence.

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A novel approach to developing and validating a predictive model of functional recovery for adults with stroke in post-acute rehabilitation

Alison Cogan, Dongze Ye, Dingyi Nie, Mary Lawlor and Nicolas Schweighofer
University of Southern California

OBJECTIVES/GOALS: To use patient-level Center for Medicare and Medicaid Services (CMS) mandated quality metrics for inpatient rehabilitation facilities (IRFs) to develop and validate predictive models of functional recovery and interactions of baseline characteristics with therapy time. METHODS/STUDY POPULATION: Retrospective cohort study of a national US sample of ~40,000 adults with a primary diagnosis of stroke admitted to IRFs in 2023. Records will be randomly allocated to equal training and validation samples. We will use a random forest approach to generate predictive models for self-care and mobility functional outcomes using patient baseline and demographic data from a CMS-mandated assessment for IRFs (Section GG). We will also examine how predictive variables modulate the effects of occupational, physical, and speech-language therapy minutes. The random forest is a machine-learning approach that trains multiple models and combines their predictions to improve their overall performance. RESULTS/ANTICIPATED RESULTS: Predictive models developed from the training sample will be applied to the validation sample to confirm their capacity to support new observations. Preliminary results will be reported, including the F1 score and area under the curve (AUC), with 95% confidence intervals. A unique feature of this study is the large sample, which contrasts with prior research in stroke rehabilitation using machine learning approaches. This study will produce powerful models that will inform the design of a clinical decision-support tool for application into clinical practice in a future study. DISCUSSION/SIGNIFICANCE OF IMPACT: By using CMS-mandated quality metrics that are collected as part of standard clinical practice in IRFs, results will support clinical interpretation and application of metrics and inform the development of a clinician-facing intervention to support personalized rehabilitation approaches.

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Comparison of profile and utility measures of health-related quality of life in pediatric Hodgkin lymphoma

Brian Felter, Angie Mae Rodday and Susan K. Parsons
Tufts University, Clinical & Translational Science Graduate Program

OBJECTIVES/GOALS: Our aim is to compare scores collected from a health utilities measure (Health Utility Index, HUI) to those collected from a profile measure (Child Health Ratings Inventories, CHRIs- Global) among youth with newly diagnosed, high-risk classic Hodgkin lymphoma. METHODS/STUDY POPULATION: We will analyze existing data collected during the Children's Oncology Group AHOD 1331 trial, which was a phase 3 clinical trial comparing the efficacy of adding brentuximab vedotin to standard-of-care treatment with multiagent chemotherapy in children and adolescents with high-risk Hodgkin lymphoma. The study also had a prespecified patient-reported outcomes (PRO) secondary aim, which involved recruiting a subset of the initial 309 patients aged 11 years or older enrolled in the trial for serial PRO measures taken over the trial period. Health-related quality of life (HRQoL) was assessed by CHRIs, HUI version 2, and HUI version 3 assessments at six planned points throughout treatment. RESULTS/ANTICIPATED RESULTS: The first step of our analysis will be to ascertain agreement in scoring for parent–child dyads for the HUI2, HUI3, and CHRIs scores by comparing mean scores via two-sample t-testing. Bland–Altman plots will be constructed to compare agreement between the scores for HUI2/3 and the CHRIs. Similarly, Spearman's correlation coefficients will be calculated for CHRIs with HUI2/3 for both parents and children. We hypothesize the CHRIs and HUI scores should roughly correlate with one another, but there may be divergence of correlation because the HUI has greater emphasis on functionality (e.g., sensation, mobility), and the CHRIs further emphasize social and emotional well-being in addition to physical health. DISCUSSION/SIGNIFICANCE OF IMPACT: The composite score of the HUI 2/3 has allowed for direct comparison with other global HRQoL measures, providing greater clarity of its performance in different patient populations and clinical settings. The current study will improve understanding of the HUI 2/3 performance in a pediatric cancer population over time.

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Evaluating prediction models for conversion of clinically isolated syndrome to multiple sclerosis: A systematic review*

Mei-An Nolan[1], Danielle Howard[2] and James Beck[3]
[1]Tufts University; [2]Tufts School of Medicine and [3]New York University School of Medicine

OBJECTIVES/GOALS: Accurately stratifying patients with clinically isolated syndrome by risk of developing multiple sclerosis is of great clinical importance. Though numerous prediction models attempt to achieve this goal, no systematic review exists to independently evaluate these models. We aim to systematically identify and assess the risk of bias in all such models. METHODS/STUDY POPULATION: Studies developing or validating prediction models

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