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Identifying Predictive Variables of High-Intensity Binge Drinking Through the Use of a Machine Learning Algorithm

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OBJECTIVES/GOALS: To test if a machine learning algorithm could predict a person's capacity to binge drink and explore what measures might be important for identifying individuals at risk for high-intensity binge drinking behaviors. METHODS/STUDY POPULATION: The sample included 1177 (474 female) non-treatment-seeking drinkers (age: 18-91 years), that were assigned to a group based on their heaviest drinking day reported in a 90-Day Alcohol Timeline Followback questionnaire. The groups were Non-Bingers (female: 12 drinks, male:>15 drinks). The sample was divided into a training sample (N = 884) and a testing sample (N = 293). A machine learning algorithm called random forest was then used to generate a predictive model based on measures of substance use, personality traits, and trauma. The model was applied to the testing sample to determine accuracy. RESULTS/ANTICIPATED RESULTS: The first model correctly assigned 190 out of 293 subjects, giving it a total error rate of 0.35, with lowest rates for non-binge (0.19) and high-intensity (0.18), while medium-intensity had the highest error rate (0.86). The most important variables for the accuracy of the model included: total score on the Alcohol Use Disorder Identification Test, first five sub-score of the Self-Reported Effects of Alcohol, Compulsive Drinking subscale, and presence of a current psychiatric diagnosis. As a follow-up analysis, we built and tested another random forest model without the use of drinking dependence measures. This model had a total error rate of 0.39, and introduced other important variables such as smoking behaviors, perceived stress, IQ, and number of negative life events. DISCUSSION/SIGNIFICANCE OF IMPACT: Our study showed that it was possible for a machine learning algorithm to predict binge drinking intensity better than chance. Drinking patterns were the most robust predictors, and stress, IQ, and psychiatric diagnoses were also useful in predicting binge drinking intensity.

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Identifying Symptom Pattern Trajectories among Heart Failure Patients in a Palliative Care Trial: A Work In Progress

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OBJECTIVES/GOALS: This work-in-progress aims to: 1) identify and differentiate symptom pattern trajectories in a sample of older adult heart failure (HF) patients over 24 weeks, and 2) examine associations between sociodemographic/clinical/physiological characteristics, dyadic health, and symptom trajectories. METHODS/STUDY POPULATION: ENABLE CHF-PC, a palliative care RCT (NCT02505425), was conducted at a Southeastern US medical center. Between 2016-2018, 415 older adult HF patients and 159 family

caregivers were randomized to receive a psychoeducational intervention or usual care. Baseline sociodemographic information (age, gender, rurality, etc.) were collected. Outcome variables of interest include symptoms (Kansas City Cardiomyopathy Questionnaire (KCCQ), Functional Assessment of Chronic Illness Therapy-Palliative 14, Hospital Anxiety and Depression Scale (HADS)) and dyadic health (PROMIS-SF Global Health). We have calculated baseline descriptive statistics. Future work includes latent growth mixture modeling to identify distinct symptom trajectories and univariate associations with patient level factors. RESULTS/ANTICIPATED RESULTS: Of 415 patient participants, mean age was 64, 53% were male; 55% were African American; 26% were rural dwellers; 46% had +15.8) and low anxiety (6.7+3.6) and depressive symptoms (5.7+4.3) on the HADS. Of 159 family caregivers participants, the mean age was 57.9, 85.4% were female, 51.9% were African-American, and 65.2% were the patient's spouse/partner. DISCUSSION/SIGNIFICANCE OF IMPACT: Limited data describes HF symptom pattern trajectories. How co-occurring symptoms affect quality of life or are affected by personal or situational factors are not well-understood. This study will help to identify factors and symptom phenotypes that may serve as targets for future interventions.

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Identifying the needs of family caregivers of people with dementia to improve service delivery: Bridging a research-practice gap*

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OBJECTIVES/GOALS: The goal of this mixed methods project is to develop a comprehensive framework of the personal and care-related needs of informal caregivers of people with dementia. This model can be used to enhance targeted delivery of evidence-based services to caregivers in need. METHODS/STUDY POPULATION: To create a model of the personal and care-related needs of family caregivers of people with dementia, we conducted semi-structured indepth interviews with current caregivers (N = 12) and conducted a content analysis of materials related to government reports and evidence-based interventions (N = 28) and existing measures of dementia caregiver needs (N = 54). Content analysis is a systematic qualitative methodology that is used to distill complex source material into content-related categories and is well-suited for both interview data and document data (Elo & Kyngäs, 2008). We identified themes related to caregiver needs through examination of materials within and across source categories. RESULTS/ ANTICIPATED RESULTS: We propose a framework of five inter-related need categories: Environmental needs (e.g., transportation, health-care access, financial resources, time), psychological needs (e.g., emotional wellbeing, identity/autonomy, perceived preparedness), social needs (e.g., social support, family dynamics), health-related needs (e.g., health behaviors, sleep), and needs related to the care and functioning of the person with dementia. We also consider how needs and background characteristics transact to influence which services may be of greatest use. In the future, we plan to test this model empirically with a nationally representative sample of caregivers. DISCUSSION/SIGNIFICANCE OF IMPACT: Evidencebased services exist to meet the needs of dementia caregivers. A dearth of models clearly defining caregiver needs limits empirically-based plans for dissemination of services. We have identified

a framework of the needs of family caregivers from which to create targeted dissemination plans.

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Immune control of plasma cell disorders – in-depth analysis of Sox2 immunity in MGUS

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OBJECTIVES/GOALS: We aim to identify and characterize anti-Sox2-specific CD8+ T cell responses in stable MUGS patients expressing HLA class I alleles-A*02:01 and /or -B*07:02. METHODS/STUDY POPULATION: Cross sectional study of patients with stable MGUS defined as stable serum paraprotein for \geq 12 months from the MM Research Clinic at the Abramson Cancer Institute. Sox2 T cell reactivity will be assessed by IFN-y ELISPOT assays. Rested PBMC will be pulsed with candidate Sox2-derived peptides predicted to display high affinity to HLA class I alleles and known to be processed and presented as determined by "targeted MS/MS" (mass spectrometry). The presence of anti-Sox2specific CD8+ T cells will be confirmed in peptide/HLA multimer assays using flow cytometry. Anti-Sox2-specific CD8+ T cells will be characterized for HLA restriction and TCR $\alpha\beta$ composition. RESULTS/ANTICIPATED RESULTS: Our work is still in progress. From Aug to Dec 2019, 22 MGUS subjects have been analyzed, 11 of which were found to have the HLA of interest. Positive Sox-2 reactivity by ELISpot was found in 3 subjects. DISCUSSION/ SIGNIFICANCE OF IMPACT: Anti-Sox2 immune responses may maintain MGUS in a clinical indolent state by eliminating Sox2expressing clonogenic MM cells. A detailed characterization of anti-Sox2 T cells followed by in-vivo assessment of their antimyeloma activity could provide the foundation for a Sox2 based immunotherapy approach in MM.

Immune markers in tumor immune microenvironment of neuroblastoma correlate with risk groups

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OBJECTIVES/GOALS: Neuroblastoma (NB) is the most common extra-cranial solid tumor with outcomes varying from spontaneous regression to metastatic with high mortality rates. The tumor immune microenvironment (TIME) may play a significant role in this disease. In this study we analyze the TIME comparing high-risk (HR) and low-risk (LR) NBs using multiplex platforms. METHODS/ STUDY POPULATION: Two tissue microarrays (TMAs) with 2mm cores were created from 41 patients treated at Columbia University Irving Medical Center. Five micron TMA slides were stained for Digital Spatial Profiling (DSP, nanoString) and multiplex immunofluorescence (mIF). For DSP, a 24-patient subset including 11 HR, 8 LR and 4 intermediate risk patients was analyzed for 34 proteins. Protein expression among risk groups was compared using Mann-Whitney t-test. For mIF, TMA FFPE slides were stained for DAPI, CD3, CD8, CD68, HLA-DR, PDL1 and Chromogranin A.

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Whole TMA cores were captured as 9 -20X multispectral images (MSIs) stitched into a 3x3 MSI using Vectra (Akoya). MSIs were processed with inForm and qualitative analysis performed comparing HR and LR tumors. RESULTS/ANTICIPATED RESULTS: With DSP, we find significantly more HLA-DR in HR compared to LR tumors (p = 0.016). When controlling for immune cells with CD45 we find HLA-DR/CD45 to be higher in HR than LR tumors (p = 0.026). We found increased PD1 and PDL1 expression in all groups without significant difference between LR and HR (p = 0.778and p = 0.310, respectively). Preliminary analysis of mIF on 9 patients (4 HR and 5 LR) finds HR tumors appear to have more immune cells than LR tumors, specifically more CD3+CD8- T cells while total CD8+ cells may be similar. There may be less macrophages in the HR compared to LR tumors. Completion of image processing and quantitative analysis of mIF data is underway. DISCUSSION/SIGNIFICANCE OF IMPACT: Increased expression of immune markers in NB TIME correlates with higher risk, which is unlike many other tumors. We compared TIME in HR and LR NB using multiplex platforms, DSP and mIF. We find that HLA-DR is more expressed in HR NB while PD1 and PDL1 expression is consistently high and not different between risk groups. Further analysis is underway. CONFLICT OF INTEREST DESCRIPTION: Robyn D. Gartrell-Corrado received grant support from nanoString for Digital Spatial Profiling and received honoraria and travel support from Northwest Biotherapeutics and PerkinElmer, respectively.

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Immunoglobulin administration and hypogammaglobulinemia during pediatric acute leukemia therapy

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OBJECTIVES/GOALS: Intravenous immunoglobulin (IVIG) is used for infection prevention in pediatric B-cell acute lymphoblastic leukemia (B-ALL), but evidence for this is lacking. We describe the prevalence of hypogammaglobulinemia in pediatric B-ALL, predictors of IVIG use and its efficacy for infection prevention. METHODS/STUDY POPULATION: We will conduct a retrospective review of children age 1-21 years with B-ALL treated at Aflac Cancer and Blood Disorders Center from 2010 to 2017. The cohort was identified through the cancer registry. Demographics, disease factors, laboratory values, medications and infection outcomes were linked between the electronic medical record and an institutional database. Outcomes of interest include emergency department (ED) visits, hospitalization days, and episodes of infection. Descriptive statistics will be performed. Outcomes will be compared between IVIG recipients and non-recipients. Univariate and multivariate logistic regression models will assess predictors of IVIG administration. RESULTS/ANTICIPATED RESULTS: We identified 443 patients with B-ALL during the study period who met inclusion criteria. Exclusion criteria included receipt of IVIG or hematopoietic stem cell transplant prior to diagnosis. The average age at diagnosis is 6.5 years (standard deviation 4.8 years); 52.6% are male; 61.6% are white; 61.0% are standard risk per National Cancer Institute criteria. Among eligible patients, 137 (31.1%) received IVIG. We hypothesize that IVIG initiation is associated with hypogammaglobulinemia and history of severe infection. We also anticipate that frequency of emergency department visits, hospitalization days, and episodes of infection will decrease after IVIG