infarction, stroke and stent thrombosis over 6 months. Dataset is divided into training (60%) and testing (40%) sets, respectively. Two different supervised ML approaches (i.e. multiclass classification and regression algorithms) are applied to the study dataset using Python v3.5 and WEKA, and tested by receiver operating curve (ROC) analysis. A case-control association analysis between MACEs at 6 months and genotypes is performed by using chi-squared test. RESULTS/ANTICIPATED RESULTS: Average age of participants was 68 years-old, 55% males, with high prevalence of risk factors (i.e., overweight: 28.4 kg/m2; hypertension: 83.8%; hypercholesterolemia: 71.9% and diabetes: 54.8%). MACEs rate is 13.8%, with 33.5% resistant to clopidogrel. Logistic regression, KNN and gradient boosting showed the best performance, as suggested by ROC analysis and AUC CV scores of 0.6-0.7. A significant association between MACE occurrence and â‰¥3 risk alleles was found (OR=8.17; p=0.041). We anticipate that these genetic variants (CYP2C19*2, rs12777823, PON1-rs662, ABCB1-rs2032582, PEAR1-rs12041331) will uniquely contribute to clopidogrel resistance and MACEs in Caribbean Hispanics. DISCUSSION/SIGNIFICANCE: Our findings help address in part the long-standing problem of excluding minorities from research, which entails a gap of knowledge about clopidogrel pharmacogenomics in Puerto Ricans. This study provides a possible ML model that integrates clinical and pharmacogenomics for MACE risk estimation.

332

Association of sphingolipid de novo synthesis with airway response to magnesium

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OBJECTIVES/GOALS: MgSO4 is a frequently used to treat asthma exacerbations. Its role in the management of pediatric asthma remains controversial. Our objective is to demonstrate that the response of the small (peripheral) airways depends on airway de novo sphingolipid synthesis, clinically and experimentally. The small airways are the main site of asthma pathology. METHODS/STUDY POPULATION: We investigated airway reactivity in response to MgSO4 in murine small airways and children 1. Precision-cut lung slices (PCLS): Using heterozygous knockouts mice of one of the Sptlc2 subunit of the serine palmitoyl-CoA transferase (SPT) which results in reduced tissue sphingolipid levels compared to wild-type control littermates (Sptlc2+/+). We compared small airway dilation to MgSO4 in Sptlc2+/- and Sptlc2+/+ mice. This was assessed by directly visualization of small airway contractility in PCLS from Sptlc2+/- mice using video phase-contrast microscopy 2. Clinical response to MgSO4 in children by using a respiratory score before and after the treatment. The response to MgSO4 was the correlated to asthma-associated 17q21 specific single nucleotide polymorphisms (SNPs) from DNA isolated from buccal swabs RESULTS/ANTICIPATED RESULTS: Sphingolipid-mediated activity alters magnesium response in small airways. We assessed whether downregulation of SPT could lead to alterations in MgSO4-induced small airway dilation and in MgSO4 responsiveness in mouse tracheal rings and found that the magnesium-induced relaxation of airways pre-contracted with methacholine was impaired in Sptlc+/- mice

compared to the control group (p=<0.05) Clinical response to MgSO4 in children with status asthmaticus. A respiratory score was assessed in a cohort of 5 to 21-year-old who received IV MgSO4. An increase of 3 or more points was considered positive. Only 32% of the patients showed a favorable improvement to the medication, showing variability of response between individuals. The correlation of sphingolipid-deficient SNPs and MgSO4 responsiveness is ongoing DISCUSSION/SIGNIFICANCE: This suggest that decreased SPT activity in the respiratory track alters the response of the airways to magnesium. Connecting decreased de novo SL synthesis to alterations in cellular magnesium homeostasis provides a mechanistic link to differential airway reactivity to MgSO4 in pediatric asthma management.

334

Web-based Methods for Family Health History Collection

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OBJECTIVES/GOALS: Family health history is widely recognized as an important step of genetic counseling; however, <50% of adults collect family health history due to implementation gaps such as suboptimal collection tools. Our objective is to create KIT, an interactive chatbot to administer a family history survey in comparison to a form-based data collection tool. METHODS/STUDY POPULATION: Both family health history collection tools were designed by adapting the NIH All of Us Research Family History Survey. The study population consists of 1000 individuals recruited from the crowdsourcing platforms, subreddits r/Health, r/SampleSize, and r/GeneticCounseling and Amazon Mechanical Turk. Eligible participants must be U.S. adults who know at least two first-degree relatives with at least one condition. Study participants are randomized to interact with either tool and complete a survey that measures the usability, engagement, accuracy, and impact of the two data collection strategies. We will use an independent t-test to compare differences in our outcome variables between the two family health history collection tools with demographic variables as covariates. RESULTS/ANTICIPATED RESULTS: The hypothesis of this study is that KIT will be more usable, more engaging, with similar accuracy in comparison to form-based tools, which are currently being used for family healthy history collection at low rates. The primary outcome of this study is usability, which will be measured based on standardized surveys. Secondary metrics of this study include engagement, accuracy, and impact. Engagement metrics include time to completion and number of resource link clicks. To assess accuracy and impact, we have included survey questions about the quality of the final summary report provided by both tools. Additionally, we ask users to rank areas for design feature improvement and feature importance; these features were determined by shared-decision-making concepts. DISCUSSION/SIGNIFICANCE: This study provides recommendations for design features important for the usability, engagement, and impact of future family health history collection tools. With a more usable and engaging tool, we can maximize rates of collection and support both patients and genetic counselors by ensuring features align with shared-decision-making frameworks.