52

Temporal association of new onset alcohol use disorder following SARS-CoV-2 infection from 2020-2022

Veronica Olaker[1], Dr. Pauline Terebuh[1], Dr. David Kaelber[2], Dr. Rong Xu[1], Dr. Pamela Davis[1]
[1]Case Western Reserve University [2]The MetroHealth System

OBJECTIVES/GOALS: During the pandemic, alcohol related deaths increased by 25%. To help understand how we might mitigate this negative outcome, we sought to examine the association of new diagnosis of alcohol use disorder (AUD) with SARS-CoV2 through two years of the pandemic. METHODS/STUDY POPULATION: Using a non-date-shifted TriNetX database, we conducted a retrospective cohort analysis of electronic health records of patients age ≥12 years who had been diagnosed either with COVID-19 (n=1,359,817) or other respiratory infections with no record of COVID-19 (n=2,013,031). Patients were then matched for propensity score risk for AUD, and results were analyzed by three-month intervals from January 2020 through January 2022, in blocks numbered 1-8. Results were expressed as hazard ratios (HR) and 95% confidence intervals (CI) for diagnosis of AUD from two weeks to six months following COVID-19 diagnosis. RESULTS/ANTICIPATED RESULTS: There was significant excess risk compared to control cohorts of AUD following COVID-19 diagnoses made during the first three months of the pandemic (HR (CI)): block 1: 2.41(1.89,3.08); no excess risk was seen for the remainder of 2020 (blocks 2-4) (HR1.01-1.14, NS). The excess risk increased again in 2021 as the delta and omicron variants emerged (HR and 95% CI): block 5 were: 1.26(1.11, 1.43)); block 6: 1.88(1.62-2.18)); block 7: 1.24(1.10,1.41); block 8: 1.12(1.0-1.25). COVID-19 diagnosis was associated with clinically-evident AUD under some pandemic circumstances. DISCUSSION/SIGNIFICANCE: COVID-19 early in the pandemic (block 1) was associated with substantial excess risk for new diagnosis of AUD, with smaller excess risk after COVID-19 during 2021 (blocks 5-7), and no excess risk otherwise. Diagnosis of COVID-19 and pandemic contextual factors are associated with increased risk for AUD.

53

The development of a multi-institutional prospective registry for patients with metastatic invasive lobular carcinoma: identifying new markers of disease progression†

Harriet T Rothschild[1], A Jo Chien[2], Rachel C Jankowitz[3], Mark JM Magbanua[4], Jason A Mouabbi[5], Rebecca A Shatsky[6], Julia Levine[7], Rita A Mukhtar[8]
[1]School of Medicine, University of California, San Francisco [2]Department of Medicine, University of California, San Francisco [3]Department of Medicine, University of Pennsylvania [4]Department of Laboratory Medicine, University of California, San Francisco [5]Department of Breast Medical Oncology, MD Anderson Cancer Center [6]Department of Medicine, University of California, San Diego [7]Lobular Breast Cancer Alliance [8]Department of Surgery, University of California, San Francisco

OBJECTIVES/GOALS: We are launching a multi-center prospective registry for patients with metastatic invasive lobular carcinoma (ILC), the second most common type of breast cancer, to better understand patterns of progression, imaging features of metastatic sites, and if serial cell free DNA measurements can serve as a surrogate marker of disease progression. METHODS/STUDY POPULATION: Patients with biopsy proven metastatic ILC of any receptor subtype will be included in the registry. We will exclude patients with ductal histology only or those with multiple primary malignancies. Patients will be enrolled at four large academic medical centers across the country. Cell free DNA measurements using a tumor informed assay will be obtained every 3 months concurrent with regular clinical imaging. Disease status will be determined by the patient's medical oncologist by taking into account imaging, tumor markers, symptoms, and cell free DNA measurement. At each time point, patients will be surveyed on their quality of life and their medical oncologists will be asked to rate the clinical utility of the cell free DNA value. Patients will be followed indefinitely. RESULTS/ANTICIPATED RESULTS: We will explore whether the use of serial cell free DNA or a combination of blood-based biomarkers and clinical endpoints can reliably identify treatment response and disease progression in patients with metastatic ILC. Many patients with metastatic ILC have unmeasurable disease on imaging and are thereby excluded from clinical trials. The end goal of this registry is to determine if blood-based biomarkers can be used as a proxy for measurable disease in ILC patients and therefore increase clinical trial enrollment for this subgroup of patients. DISCUSSION/SIGNIFICANCE: The creation of this prospective registry will open the door for future studies of blood-based markers that reflect disease stability and progression, which is an unmet need specifically in ILC. Identification of such markers could lead to a novel treatment response endpoint, changing the way patients are enrolled in trials and managed clinically.

†The author list and their affiliations have been amended since original publication. A corrigendum detailing these changes has been published at doi: 10.1017/cts.2023.637.

54

The Association of Patient Characteristics on Provider Referrals to a Health-system Based Diabetes Prevention Program in the Bronx, NY.

Cara Stephenson-Hunter, Giovanni Pachecho, Earle Chambers
Albert Einstein College of Medicine

OBJECTIVES/GOALS: The Diabetes Prevention Program (DPP) has been shown to reduce diabetes risk by 58%. Men, particularly men of color, are underrepresented in DPP, while they experience higher diabetes-related morbidity. We examine whether race, ethnicity, and gender disparities in engagement are associated with the risk of referral to DPP in primary care METHODS/STUDY POPULATION: Using electronic health record (EHR) from a large urban health system in the Bronx, NY, with an in-house DPP, we examined patient, visit, referral data for DPP-eligible, adult patients with a primary care visit between July 2015 and December 2017. Eligibility included: hemoglobin A1c between 5.7-6.4%; a body mass index (BMI)≥24 kg/m2 (≥22 if Asian); and having no prior diagnosis of diabetes. A total of 26987 patients were included in this study. We examined patient race, ethnicity, preferred language, visit and prescription history, and health payer, among other characteristics. SPSS was used for univariate and bivariate analyses to examine associations between patient characteristics and referral followed by a logistic regression to examine the multivariate association between predictors and referrals. RESULTS/ANTICIPATED RESULTS: Of all DPP-eligible patients, 49% were Hispanic/Latino, and 39% were non-Hispanic Black. Around one-third (34%) of all eligible patients were men. Among all eligible patients in the sample, only 10% were referred to DPP. There were significant differences in the proportion of eligible patients who were referred versus those who were not referred. Women were referred at more than twice the prevalence

https://doi.org/10.1017/cts.2023.143 Published online by Cambridge University Press

of men (8.26% to 2.41%), with Hispanic women being referred most frequently (3.59%), and non-Hispanic white men being referred least frequently (.07%) Ethnicity, race, sex, age, number of provider visits, and number of chronic conditions all impacted healthcare provider referral rates to DPP. The health system's unique free-of-charge DPP likely influenced the lack of significance of patient health insurance. DISCUSSION/SIGNIFICANCE: Given the implementation of DPP at-scale there is an urgent need to understand the patient and systems-level factors that are associated with referring individuals in the DPP. By detecting characteristics of health systems and patients that warrant special attention, we can improve equitable access to evidence-based diabetes prevention.

56

Using machine learning to predict 30-day readmission and reoperation following resection of supratentorial high-grade gliomas: A national analysis of 9,418 patients.

Abdul Karim Ghaith[1,2], Marc Ghanem[3], Cameron Zamanian[1,2], Antonio A. Bon Nieves[1,2], Archis Bhandarkar[1,2], Karim Nathani[1,2], Mohamad Bydon[1,2], Alfredo Quiones-Hinojosa[4]
[1]Mayo Clinic Neuro-Informatics Laboratory, Mayo Clinic, Rochester, MN, USA [2]Department of Neurological Surgery, Mayo Clinic, Rochester, MN, USA [3]Gilbert and Rose-Marie Chagoury School of Medicine, Lebanese American University [4]Department of Neurological Surgery, Mayo Clinic, Jacksonville, FL, USA

OBJECTIVES/GOALS: High-grade gliomas (HGG) are among the rarest, most aggressive tumors in neurosurgical practice. We aimed to identify the clinical predictors for 30-day readmission and reoperation following HGGs surgery using the NSQIP database and seek to create web-based applications predicting each outcome. METHODS/STUDY POPULATION: We conducted a retrospective, multicenter cohort analysis of patients who underwent resection of supratentorial HGG between January 1, 2016, and December 31, 2020, using the NSQIP database. Demographics and comorbidities were extracted. The primary outcomes were 30-day unplanned readmission and reoperation. A stratified 80:20 split of the available data was carried out. Supervised machine learning algorithms were trained to predict 30-day outcomes. RESULTS/ANTICIPATED RESULTS: A total of 9,418 patients were included in our cohort. The rate of unplanned readmission within 30 days of surgery was 14.9%.Weight, chronic steroid use, pre-operative BUN, and WBC count were associated with a higher risk of readmission. The rate of early unplanned reoperation was 5.47%. Increased weight, higher operative time, and a longer period between hospital admission and the operation were linked to increased risk of early reoperation. Our Random Forest algorithm showed the highest predictive performance for early readmission (AUC = 0.967), while the XG Boost algorithm showed the highest predictive performance for early reoperation (AUC = 0.985).Web-based tools for both outcomes were deployed: https://glioma-readmission.herokuapp.com/, https://glioma-reoperation.herokuapp.com/. DISCUSSION/SIGNIFICANCE: A high fraction of documented early unplanned readmission and reoperation were considered preventable and related to surgery. Machine learning allows better prediction of resected HGG's prognosis based on findings from baseline methods leading to more personalized patient care.

57

Utility of Digital Phenotyping in Big Data to Answer Clinical Questions: Puberty as a Transdisciplinary Science Case Example

David J. Schnabel, Jr., Lorah D. Dorn
Pennsylvania State University

OBJECTIVES/GOALS: A disease-agnostic translational science framework for data mining is proposed for use across disciplines to: Answer clinical questions, justify future clinical research recruitment, and explore under-represented populations. As a case example, male puberty demonstrates utility of the framework. METHODS/STUDY POPULATION: As a case example using the generalizable framework, the following interdisciplinary question was asked: Does early pubertal timing increase the risk of developing type II diabetes (T2d) in boys? A digital phenotype of males < 18 years old was created in the TriNetX Diamond Network utilizing Boolean operator data queries. TriNetX contains patient electronic health record information (ICD-10 diagnoses, anthropometric measures). A case control analysis leveraging patient counts from various digital phenotypes allowed for outcome (T2d) comparison of boys diagnosed with precocious puberty (E30.1, ICD code for early pubertal timing) to those without, while controlling for body mass index (BMI). RESULTS/ANTICIPATED RESULTS: Subjects (N=12,996,132) displayed the following digital phenotype: Male, < 18 years old, without ever having a BMI documented >85th percentile. Boys diagnosed with precocious puberty (E30.1) were 6.89 times more likely to develop T2d when aged 14-18 years old than those without (OR 6.89, 95%CI: 5.17-9.19, p. DISCUSSION/SIGNIFICANCE: Boys are under-represented in the early pubertal timing literature, justifying future human subjects research on male puberty. This case example demonstrates a broader disease-agnostic framework which can be adapted across disciplines. Opportunities may include public health digital phenotyping.

58

Utilizing VA Data to Define Long COVID and Identify Patients at Risk

Peter L. Elkin[1,2,4,5], Skyler Resendez[1,2], H. Sebastian Ruiz[1], Wilmon McCray[1,2], Steven H. Brown[3], Jonathan Nebeker[3], Diane Montella[3]
[1]Department of Biomedical Informatics, Jacobs School of Medicine and Biomedical Sciences, University at Buffalo [2]Department of Veterans Affairs, VA Western New York Healthcare System and VA Research Service 3Office of Health Informatics, Department of Veterans Affairs 4Department of Internal Medicine, Jacobs School of Medicine and Biomedical Sciences, University at Buffalo 5Faculty of Engineering, University of Southern Denmark

OBJECTIVES/GOALS: To determine the signs, symptoms, and diagnoses that are significantly upregulated in cases of long COVID while identifying risk factors and demographics that increase one's likelihood of developing long COVID. METHODS/STUDY POPULATION: This is a retrospective, big data science study. Data from Veterans Affairs (VA) medical centers across the United States between the start of 2020 and the end of 2022 were utilized. Our cohort consists of 316,782 individuals with positive COVID-19 tests recorded in the VA EHR with a history of ICD10-CM diagnosis codes in the record for case-control

https://doi.org/10.1017/cts.2023.143 Published online by Cambridge University Press