Describing Physical Symptoms among Patients with PTSD at an Anxiety Clinic in Puerto Rico

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ABSTRACT IMPACT: Our work will provide valuable information about the associations between physical symptoms and PTSD in patients from a Spanish-speaking, evidence-based clinic. OBJECTIVES/GOALS: In this reserach study, we want to describe physical symptoms of patients with a preliminary PTSD diagnosis. We also want to explain associations between physical symptoms, and the presence, or absence of PTSD, and to evaluate findings in terms of prevention services, referrals, and alternatives for augmenting treatment-adherence. METHODS/STUDY POPULATION: This was a descriptive, secondary database analysis of the Center for the Study of Fear and Anxiety (by its Spanish acronym, CETMA). The database included information of the initial evaluation between 2012 and 2019. We aimed to describe sociodemographic and medical variables, and evaluate associations, in terms of the presence or absence of PTSD. RESULTS/ ANTICIPATED RESULTS: Patients with PTSD were mostly women, single, with a completed bachelor's degree. The majority had at least one neurological, or musculoskeletal condition. Respiratory conditions were the least represented. We found significant associations between musculoskeletal, neurological, and ear/ nose/throat conditions, in terms of PTSD diagnosis. DISCUSSION/SIGNIFICANCE OF FINDINGS: Puerto Rico recently experienced two hurricanes, several earthquakes, and the pandemic. Findings provide data about the interface between mental and physical symptoms of patients with PTSD. We recommend a randomized population study with mental and physical variables, for understanding possible effects of cumulative stress in Puerto Ricans.

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Immune-related adverse events in cancer patients receiving immune checkpoint inhibitors*

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ABSTRACT IMPACT: The existing literature describing immunerelated adverse events (irAE) has predominantly focused on clinical trial populations, which may not be representative of the broader population receiving immune checkpoint inhibitors (ICI), so we sought to perform a comprehensive evaluation of irAE in a realworld population of cancer patients being treated with ICI. OBJECTIVES/GOALS: With a cohort of patients with malignancy treated with ICI, we characterized incidence, severity, timecourse of ir-AE. We sought to inform providers who prescribe ICI to recognize the clinical burden of irAE in an effort to more effectively communicate the benefits and risks of ICI with patients. METHODS/STUDY POPULATION: After obtaining approval from the institutional review board, we used a pharmacy database to identify adult cancer patients treated with an ICI between January 2014 and October 2018. We used electronic medical records to obtain

medical complexity of patients of this population, as defined by the number medical diagnoses, impacts the type of treatment rendered as well as how frequently these patients are seen for dental care (rate of appointments). DISCUSSION/SIGNIFICANCE OF FINDINGS: Over- or under-utilization of dental treatment modalities can impact the oral health status and outcomes for patients with special needs. The differences in types and frequency/ rate of dental treatment rendered for patients of different medical complexity can further impede their oral health and systemic health status and health outcomes.

Genomic epidemiology of SARS-CoV-2 across New Mexico and the Mountain West

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ABSTRACT IMPACT: Genomic data can be used by policy and decision makers to guide, and assess the impact of, public health responses to the COVID-19 pandemic. OBJECTIVES/GOALS: Our objective is to investigate the transmission and population dynamics of SARS-CoV-2 in New Mexico and other Mountain West states using whole genome sequencing. Understanding how the virus is spreading within and between communities is vital for the design of rational, evidence-based control measures. METHODS/STUDY POPULATION: We obtained an aliquot of 500ul - 1 ml of inactivated viral transport media (VTM) from positive SARS-CoV-2 nasopharyngeal swabs as determined by qPCR from the New Mexico Department of Health, TriCore Reference Laboratory, Idaho Bureau of Laboratories, and Wyoming Public Health Laboratory. We extracted viral RNA from the VTM, and sequenced the genomes using the methodology as described by the widely adopted ARTIC amplicon tiling protocol for SARS-CoV-2. Viral genomes were then sequenced on either an Illumina MiSeq or an Oxford Nanopore Technologies (ONT) GridION. We placed these samples within the context of globally representative sequences made available via the GISAID database. Consensus sequences were aligned and added into this global dataset using the Nextstrain augur pipeline. RESULTS/ANTICIPATED RESULTS: We sequenced over 1,000 SARS-CoV-2 genomes thus far from New Mexico (n=861), Wyoming (n=213) and Idaho (n=44). We used this sequence data to infer the transmission dynamics and spread of the virus, both within states and in context of regional and international spread. We inferred at least 128 separate introductions of the virus into New Mexico and at least 29 introductions into Wyoming. The origins of these introductions are diverse, spread across multiple regions in the US and abroad. We also sequenced samples from an individual who had multiple positive tests over time. Our results suggest that this individual was reinfected with a different strain than that of the initial infection. DISCUSSION/SIGNIFICANCE OF FINDINGS: Our data show that New Mexico and other Mountain West states have continually experienced many introductions of the virus that then seed local outbreaks. By understanding the number of introductions over time, we can assess the impact of travel restrictions on transmission. Our data also supports that some individuals can be re-infected.