Clinical and Genetic Risk Factors associated with Opioid Use Disorder in Patients with Chronic Pain

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One factor in the recent increase in opioid use disorder (OUD) is the widespread prescription of opioids to treat chronic, non-progressive musculo-skeletal pain. Estimates of OUD in this context range from 1% to 40%. Geisinger is an integrated health system, and has the MyCode Community Health Initiative biorepository of genetic data, with whole exome sequencing (WES) completed on over 90,000 patients as part of the DiscovEHR study. We are evaluating the rate of OUD within the health system, to develop the groundwork for a genetic epidemiology study of OUD within MyCode. We have assessed the rate of OUD using the drug monitoring program at Geisinger. Within this program, patients prescribed opioids for chronic pain agree to a medication use agreement (MUA), requiring random urine drug screens and taking only the opioid dose prescribed by the designated Geisinger physician. Patients who violate this agreement (e.g. claiming lost medication, positive urine test for non-prescribed substances, drug-seeking from other physicians) have the MUA terminated (TMUA), receiving referral for alternative pain management and/or addiction treatment. We predicted that the TMUA group may have more clinical characteristics associated with OUD (e.g. tobacco use, increased rates of psychiatric illness, ER visits) compared to the MUA group. This hypothesis was tested using the anonymized electronic health records (EHR) of Geisinger MUA (n= 17,598) and TMUA patients (n= 1,248). We find the TMUA group is enriched for polysubstance abuse (including alcohol and tobacco use) and demonstrates higher rates of psychiatric diagnoses, including depression and anxiety. We have explored differences in the body location, severity, and the structural nature of pain in the MUA/TMUA groups. In on-going studies, we will explore common and rare variant genetic association analyses in this subset (n=6,247) of patients with available WES and genotyping data.