From the developers of Smokescreen: a booster panel for development of addiction polygenic risk scores

Stephen McGee MS¹, Andrew W. Bergen PhD¹,², James W. Baurley PhD¹

¹ BioRealm, LLC; ² Oregon Research Institute

Background: Individuals suffering from addiction-related disorders have been immensely impacted by the COVID-19 pandemic. Given that both addiction and response to SARS-CoV-2 are partially driven by genetic factors, we propose a booster genotyping panel to help foster a better understanding of the genetics of addictions and COVID-19, develop polygenic risk scores (PRS), and help develop treatments for this vulnerable population.

Methods: We are refining our existing Smokescreen database from which the Smokescreen genotyping array was developed to incorporate recent research into addiction (National Library of Medicine) and into COVID-19 comorbidities (COVID-19 Open Research Dataset, CORD-19). We will use molecular identifiers to select up to 0.175M markers to add to the 1.9M available on the Infinium Global Diversity Array (GDA), currently used by the NIH All Of Us Research Program.

Results: Our natural language processing approach of CORD-19 identifies HGNC names and variant identifiers that are weighted based on occurrence. These data will be added to the curated Smokescreen database, and compared to GDA content. A booster for the GDA array will be developed with priorities (existing PRS, novel gene coverage, ethnic coverage, pathway bioinformatics). These addiction and COVID-related markers can be used to prioritize data capture (custom array, querying) and aid in the development of PRS.

Discussion: We envision that applications of this booster will improve our understanding of addiction and the long-term consequences of drug dependence in the time of COVID.