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I am a human geneticist with a passion for developing computational and statistical methods to analyze large-scale genomic studies. My prior scientific training includes my Ph.D. work with advisors Drs. Alison Goate and Carlos Cruchaga, in which I performed deep sequencing in candidate Alzheimer's disease (AD) genes, analyzed AD-related endophenotypes and performed *in vitro* cell-based experiments to identify and functionally characterize novel genetic variants affecting AD risk. As a postdoctoral associate in the lab of Richard Lifton, I developed novel statistical models and bioinformatics pipelines to reveal the significant contribution of rare transmitted and *de novo* mutations on congenital heart disease risk. I also led genomic analyses and methodology development in several genetic studies of complex diseases for the Yale Center for Mendelian Genomics. More recently, I shifted my focus to reveal genetic etiologies of neurodevelopmental disorders. After working with multi-site genomics consortia, we identified novel genes and biological pathways contributing to congenital hydrocephalus, idiopathic cerebral palsy, and Vein of Galen malformation. I was then recruited back to Washington University School of Medicine as faculty in 2020. My lab is currently focused on the development and application of human genetics, bioinformatics, and functional genomics to a better understanding of complex genetic models driving neurodevelopmental disorders and COVID-19.

ABSTRACT

Individuals with COVID-19 have had a wide range of symptoms reported – ranging from mild symptoms to severe illness. Previous studies have shown that both host and viral genetics work together to influence the course of viral infections. Still, the mechanism and consequences of this interaction during COVID-19 infection remains unknown. It remains unclear why some people infected with COVID-19 are asymptomatic, whereas others require hospitalization. While comorbidities like asthma are known to influence the severity of symptoms during COVID-19 infection, medical comorbidities alone are insufficient to explain the spectrum of severity among COVID-19 patients. Therefore, several laboratories at Washington University (WashU) School of Medicine, including the Jin Lab, are working closely to understand the relative contribution of the host and viral genomes to the pathogenesis of COVID-19. We are utilizing an integrative genomics approach to study the genetic architecture and gene regulation network of SARS-CoV-2 and developing tools to support navigation, visualization, and interpretation of the viral omics data. In this webinar, Dr. Jin will give an overview of what we know about genetic susceptibility to COVID-19 and what our WashU Informatics team is working on to advance our understanding of the virus. Finally, Dr. Jin will share his firsthand experiences and observations from kicking off his lab in April 2020.