UTHealth
The University of Texas Health Science Center at Houston
School of Biomedical Informatics

CPH Seminar in Precision Medicine

"Post GWAS Schizophrenia Study: What we do now?"

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Genetic study of schizophrenia have made significant progress, genome wide association studies have identified more than risk 100 loci. In the post GWAS era, what should we do now? In this seminar, I plan to outline a few projects we are doing and discuss my thoughts for future direction. The topics covered include 1). Use family design to discover functional variants. Family history is one of the most reliable predictors of schizophrenia, however, GWAS with case control design did not provide useful information as what genetic risks constitute family history. We conducted whole genome sequencing for families with two affected individuals and one unaffected sibling to investigate those risk genes in these families. 2). Explore cellular model for functional study of GWAS identified variants. The immune system has been implicated in schizophrenia but there is no cellular model to test variants in the immune system. We adopted a method to develop a microglia model for functional study of genetic variants. 3). Apply GWAS findings for objective diagnosis, subtype classification and disease prediction. Like other psychiatric disorders, the diagnosis of schizophrenia is somewhat subjective and has substantial misdiagnoses. We explored shared genetic liability among multiple comorbid traits to facility objective diagnosis and subtype classification. Although these projects are not completely mature and progress to a different level, the hope is that these discussions inspire new ideas and directions for schizophrenia study.

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