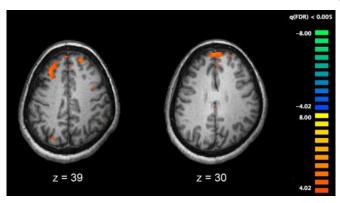


Study uses polygenic risk scores to determine schizophrenia risk in patients with chromosome deletion syndrome

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Functional magnetic resonance imaging (fMRI) and other brain imaging technologies allow for the study of differences in brain activity in people diagnosed with schizophrenia. The image shows two levels of the brain, with areas that were more active in healthy controls than in schizophrenia patients shown in orange, during an fMRI study of working memory. Credit: Kim J, Matthews NL, Park S./PLoS One.

A new study involving researchers from Children's Hospital of Philadelphia (CHOP) has uncovered genetic clues that may help identify which patients with chromosome 22q11.2 deletion syndrome (22q11.2DS) might develop schizophrenia. The findings, published in *Nature Medicine*, highlight the potential of polygenic scores, which account for the effects of numerous common genetic variants across the genome, to determine whether a patient is at high or low risk of developing the psychiatric condition.

22q11.2DS results from a missing segment of approximately 45 genes on one copy of chromosome 22 and is the most common genetic cause of <u>schizophrenia</u>, occurring in nearly 30% of patients with the deletion. However, not all patients with the condition go on to develop schizophrenia,

which prompted the researchers to explore the potential contributions of other genetic variants across the genome.

Using genetic data from the International 22q11.2
Brain and Behavior Consortium (IBBC), a large NIHfunded consortium led by CHOP and the Perelman
School of Medicine at the University of
Pennsylvania, the researchers analyzed 965
patients with 22q11DS and evaluated genetic
associations using polygenic risk scores for
schizophrenia and cognitive ability. The research
team found polygenic risk scores were key in
assessing the probability of a given patient
developing schizophrenia or cognitive decline.

"This work is an important next step in better understanding the causes of behavioral health differences associated with the chromosome 22q11.2 deletion," said co-author Donna McDonald-McGinn, MS, LCGC, Director of the 22g and You Center and, Associate Director of Clinical Genetics, Chief of the Section of Genetic Counseling at CHOP, Clinical Professor of Pediatrics at UPenn and Co-Principle Investigator of the IBBC. "Although the funding for the IBBC ended in 2017, this important work continues through another NIHfunded program entitled the Genes to Mental Health Network (G2MH), where we have expanded our target populations to include other chromosomal deletions and duplications that have associated behavioral phenotypes, including the 22q11.2 deletion and duplication syndromes and the 16p11.2 deletion and duplication syndromes, among others."

More information: undefined undefined et al. Using common genetic variation to examine phenotypic expression and risk prediction in 22q11.2 deletion syndrome, *Nature Medicine* (2020). DOI: 10.1038/s41591-020-1103-1



Provided by Children's Hospital of Philadelphia

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