

IDENTIFICATION OF SCHIZOPHRENIA SUBTYPES FROM COMORBIDITY PROFILES

Sarah E. Bergen¹, Alexander Ploner¹, Kaarina Kowalec^{1,2}, Patrick F. Sullivan^{1,3}

1 Department of Medical Epidemiology and Biostatistics, Karolinska Institutet, Stockholm; 2 College of Pharmacy, University of Manitoba, Winnipeg, Canada; 3 Departments of Genetics and Psychiatry, University of North Carolina, Chapel Hill, USA

Background

The outcomes for schizophrenia patients are variable but often poor, with high rates of comorbidity accounting for most of the substantial reduction in life expectancy. Psychiatric and somatic comorbidities occur in the majority of patients with schizophrenia, and the causes are multifaceted. Since different mechanisms leading to schizophrenia diagnoses are likely to also influence comorbidity patterns, we aimed to identify subtypes of schizophrenia based on the other diagnoses patients experience.

Materials and methods

Data were drawn from the Swedish Schizophrenia Study with 4758 genotyped cases and comprehensive medical and demographic information from the Swedish National Registers. Individual data for 19 commonly comorbid somatic conditions (e.g. type 2 diabetes, cardiovascular disease, epilepsy, etc.) and psychiatric disorders (e.g. major depression, PTSD, anxiety, etc.) was extracted. We used latent class analysis (LCA) to identify groups of participants with similar comorbidity profiles and compared the polygenic risk for schizophrenia and clinical characteristics across clusters.

Results

We identified three clusters: low comorbidity (N=3783), high psychiatric comorbidity (N=582), and high cardiometabolic comorbidity (N=393). Polygenic risk scores did not differ between subgroups. However, sex distributions, total number of antipsychotic medications, clozapine use, hospitalization frequency and duration, all-cause mortality, and suicide rates did differ between the subgroups.

Discussion

The comorbidity profiles of patients with schizophrenia were leveraged to identify three subgroups within this population which have markedly different clinical characteristics, but no difference in overall genomic risk. Additional investigations into the specific genetic risk loci acting within each subgroup are needed to establish whether the observed group differences stem from different constellations in genetic risk for schizophrenia. Improved understanding of the heterogeneity within schizophrenia will facilitate personalized medicine efforts.