

Vulnerability and resilience for mental illness following viral infections in the NESDA deep-phenotyped longitudinal cohort

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Infectious diseases significantly elevate the risk of developing mental illness (MI), with an estimated 30% of the population exhibiting vulnerability for post-infection MI. Despite previous research efforts, underlying pathophysiological mechanisms driving this relation remain unidentified. It is hypothesized that infections can trigger neurobiological changes in the central nervous system, leading to psychiatric symptomatology. To understand these mechanisms, fine-grained clinical and biological data are required, which are immensely difficult to obtain.

In this state-of-the-art study, we will investigate the impact of SARS-CoV-2 seroconversion on the relapse risk of MI and its underlying mechanisms. Our investigation uses a unique, large-scale, longitudinal deep-phenotyped database including biomarkers, genome-wide association study (GWAS), neuroimaging, and psychosocial data. We have collected blood samples and clinical data before and after the COVID-19 pandemic in individuals vulnerable for depressive and anxiety disorders. We hypothesize that infections increase the risk of MI relapse in vulnerable individuals.

MI imposes a major personal, societal, and economic burden worldwide. However, clinical guidelines for identifying, managing or preventing infection-related mental health complications are lacking. By advancing our understanding of the pathophysiology of post-infection MI, our research can facilitate the development of novel personalized therapeutic and preventive strategies.