

## Developing topics

## Alzheimer's Association International Cohort Study of Chronic Neuropsychiatric Sequeale of SARS-CoV-2 (CNS-SARS-CoV-2)

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#### Abstract

**Background:** The pandemic of SARS-CoV-2 is focusing all energies on the impact on survival of affected individuals, treatment and prevention, but increasingly attention is focusing on its enduring consequences. We established a global consortium to study a longitudinal representative cohort of individuals, to characterize neurological and neuropsychiatric sequelae from direct viral, immune-, vascular- or accelerated neurodegenerative injury to the central nervous system (CNS).

**Method:** We propose to characterize the neurobehavioral phenomenology associated with SARS-CoV-2 in a large, multinational, longitudinal cohort of post COVID-19 infection patients following three sampling strategies: 1) Opportunity sample of patients discharged after hospital admission for COVID-19 related symptoms. 2) A stratified random sample from COVID-19 testing registries (including asymptomatic and negative participants). 3) Ascertaining COVID-19 exposure (antibody) status in ongoing longitudinal, community-based cohort studies that are already collecting biosamples, cognitive, behavioral and neuroimaging data. We will obtain core data within 6 months of discharge or testing. Core characterization will include interviews with the Schedules of Clinical Assessment in Neuropsychiatry (SCAN), neurological exams, emotional reactivity scales and a neurocognitive assessment. Wherever feasible, we will also collect neuroimaging, biosamples and genetic data. Longitudinal follow up will be conducted at 9 and 18 months of the initial evaluation. An mHealth *keeping-in-touch* process will be set up to minimize attrition rates. The population cohorts provide a large, unbiased, normative and validation sample, albeit with more heterogeneous outcome ascertainment. They also permit examination of pre- and post-COVID trends in symptoms and biomarkers. Since some ethnic groups, as well as in individuals with blood type A, are at higher risk of COVID-19 infection and death, a role of genetics in determining susceptibility to infection and poor outcomes seems well supported. We will collect genome-wide genotypes from our cohort individuals to address the role of ancestry and genetic variation on susceptibility to neuropsychiatric sequelae. High rates of mutation in COVID-19 strongly suggest that viral infectivity, including neurotropism, may not be uniform across countries affected by the pandemic.

**Results:** Pending.

**Conclusion:** Our consortium is in a unique position to address the interaction between genetics (including ancestral DNA), and viral strain variation on CNS sequelae of SARS-CoV-2.