

A Proteomic Review of Factors Related to Neurodegenerative Diseases

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Abstract

The COVID-19 pandemic has killed millions and is a major public health burden worldwide. Previous studies have shown that a large number of his COVID-19 patients and survivors developed neurological symptoms and may be at increased risk for neurodegenerative diseases such as Alzheimer's disease (AD) and Parkinson's disease (PD). I know there is. Our aim is to use bioinformatic analyzes to uncover potential mechanisms that may explain the neurological symptoms and brain degeneration seen in COVID-19 patients, and by intervening early, The aim was to investigate common pathways between COVID-19, AD, and PD. In this study, we used the frontal cortex gene expression dataset to detect common differentially expressed genes (DEGs) in COVID-19, AD, and PD. A total of 52 common DEGs were then probed using functional annotation, protein-protein interaction (PPI) construction, drug candidate identification and regulatory network analysis. We found that synaptic vesicle cycle engagement and synaptic downregulation are common to these three diseases, suggesting that synaptic dysfunction may contribute to the development and progression of COVID-19-induced neurodegenerative disease. Five hub genes and one key module were obtained from the PPI network. Additionally, 5 drugs and 42 transcription factors (TFs) were also identified in the dataset. In summary, the results of our study provide new insights and guidance for follow-up studies on the relationship between COVID-19 and neurodegenerative diseases. The hub genes and potential drugs we identified may offer promising therapeutic strategies to prevent COVID-19 patients from developing these diseases.

Keywords: Bioinformatics; Differentially Expressed genes; Gene ontology; Protein-protein interaction; Hub genes; Drugs

Introduction

With the liberalization of epidemic prevention and control in various countries, more than 600 million people were diagnosed with coronavirus disease (COVID-19) worldwide in 2019. Acute respiratory syndrome). SARS-CoV-2 is known to primarily affect the human respiratory tract and cause typical symptoms such as fever, sore throat, cough, shortness of breath and fatigue. Furthermore, current evidence supports that SARS-CoV-2 can target and invade the central nervous system (CNS) [1]. Neurological symptoms, including both CNS and vegetative/peripheral symptoms, have been observed during and after the acute phase of COVID-19. In particular, recent studies have shown that COVID-19 can cause clinical manifestations of neurodegenerative diseases such as dementia and Parkinsonism, suggesting that his COVID-19 in the future onset of neurodegenerative diseases may contribute to the development of neurodegenerative diseases. Spotlighting potential roles. Some studies have reported an increased risk of these conditions in COVID-19 positive patients. Changes in brain structure in COVID-19 patients also strengthened this hypothesis [2]. In addition, her COVID-19-induced impairment of the frontal cortex, a region critical for cognitive function, is described in complementary studies combining neuroimaging and cognitive screening [3].

Neurodegenerative diseases are characterized by progressive dysfunction and neuronal loss and can affect a person's movement, language, memory, cognition, intelligence, and more. These diseases include Parkinson's disease (PD), Alzheimer's disease (AD), Huntington's disease (HD), multiple sclerosis (MS), amyotrophic lateral sclerosis (ALS), epilepsy, and others [4]. AD and PD are the two most common neurodegenerative diseases in humans, with AD being the leading cause of dementia. Although PD has traditionally been considered a movement disorder, dementia is increasingly accepted as part of the clinical spectrum of PD. A previous study found that mild cognitive impairment (MCI) is one of the most common non-motor symptoms in early-stage PD patients, with 83% of 20-year PD survivors having dementia. There is increasing evidence of a molecular

link between AD and PD. B. Impaired redox homeostasis, misfolded modified proteins, and neuroinflammation. Frontal cortex damage is associated with both AD and PD. Clinical trials have reported that patients with a history of neurodegenerative disease are at increased risk of COVID-19 and at increased risk of COVID-19-related hospitalization and death. Advances in deciphering the common etiology of COVID-19, AD, and PD provide effective strategies for treating neurological symptoms in infected individuals and preventing these patients from developing neurodegenerative disease is useful for the development [5].

To investigate the molecular mechanisms of COVID-19-associated neurodegenerative symptoms, we used two datasets to estimate transcriptome changes in the frontal cortex of patients with COVID-19, AD, and PD. Gene ontology and pathway enrichment, protein-protein interaction (PPI) and key module extraction, hub gene and potential drug identification, transcription factor (TF) regulatory network construction based on shared DEGs under COVID Further analyzes were carried out including -19. 19, AD and PD. A set of workflows for our study is presented [6].

Results

Identification of DEGs

To identify common genetic interrelationships between COVID-19, AD, and PD, we first accessed frontal cortex transcriptomic data for each disease in the GEO database [7]. Before the differential analysis

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procedure, perform normalization and removal of stacking effects to standardize the expression matrix and show the results of the treatment in a density plot. After standardization, normality tests and PCA plots for each dataset show that the sources of the samples are reliable. We then performed differential gene expression analysis by controlling for age and gender that differed significantly between patients and healthy controls. Finally, 1344 genes were identified as DEGs for COVID-19. This includes 927 upregulated and 417 downregulated genes. Similarly, the AD dataset yielded 2655 degrees (651 upregulated, 2004 downregulated) and the PD dataset yielded 2589 degrees (882 upregulated, 1707 downregulated) [8]. Results are displayed in a volcano plot. After excluding genes with opposite expression trends in COVID-19, AD, and PD using intercomparison analysis, 9 common upregulated genes and 43 common downregulated genes were identified. We identified 52 common DEGs containing genes.

Identification of potential therapeutics

In addition, we screened drug targets for common DEGs to identify potential therapeutic targets. Here, we identified 6 drug targets and 18 related drugs based on DrugBank. Among them, five drugs were considered potentially therapeutic, including ibutilide, azelidipine, dotaridine, copper, and arteminol [9]. It is a class III antiarrhythmic drug used and can be considered an alternative to cardioversion. Azelidipine is a dihydropyridine calcium channel blocker. It has a gradual onset of action, with a slight increase in heart rate leading to a long-lasting decrease in blood pressure. It is currently being investigated for treatment after ischemic stroke. Dotarizine is a calcium channel blocker used for the treatment and prevention of migraine headaches. Copper is an essential element in the body and is incorporated as a cofactor for many oxidase enzymes. The exact mechanism of copper deficiency effects is obscure due to the different enzymes that use the ion as a cofactor. Arteminol, an artemisinin derivative, is an antimalarial drug used to treat uncomplicated *Plasmodium falciparum* infections [10].

Discussion

In this study, we used three frontal cortex datasets from COVID-19, AD, and PD patients in the GEO database to clarify the underlying mechanisms and potential neurodegenerative diseases caused by SARS-CoV-2 infection. I found a therapeutic strategy. Through cross-over analysis, we identified 52 common DEGs, most of which were downregulated, suggesting that COVID-19, AD, and PD may cause suppression of general cellular function in the frontal cortex of patients. It suggests that there is a

We then performed pathway-based analysis to identify common biological pathways in COVID-19, AD, and PD. Pathway analysis revealed that these shared DEGs were significantly enriched in synaptic vesicle cycle pathways. Synaptic vesicles undergo a complex transport cycle that can be broken down into a series of steps.

Formation of synaptic vesicles; docking of synaptic vesicles in the active region of the presynaptic membrane. Fusion of synaptic vesicles with presynaptic membranes. Release of neurotransmitters by exocytosis. Independent GO analysis of normal up-regulated and down-regulated DEGs showed that all top terms mainly associated with synaptic vesicle cycling were down-regulated. In addition, GSEA of the three datasets also showed that synapses, synaptic components and synaptic function were downregulated in these three diseases. Our results suggest that synaptic loss and damage and synaptic dysfunction may be responsible for neurodegenerative disease-related symptoms in COVID-19 patients or survivors.

Consistent with our results, several studies have shown that SARS-CoV-2 infection can cause synaptic disruption based on high-throughput His sequencing and systematic bioinformatic analysis. Andreas et al. found that synaptic signaling in upper excitatory neurons associated with cognitive function was preferentially affected in COVID-19 patients. This is being profiled in COVID-19 patients by detecting large mononuclear transcriptomes from control frontal cortex and choroid plexus samples. We also confirmed that neurons infected with SARS-CoV-2 undergo degeneration, including shortening of neurite length and loss of synapses.

Conclusions

Previous studies have found that COVID-19 survivors are at increased risk of neurodegenerative disease, with degeneration in brain regions associated with cognitive function in mild cases. SARS-CoV-2 infection has also been shown to adversely affect outcomes in patients with neurodegenerative diseases. In the future, with the increase of infectious diseases, it is imperative to prevent or treat these neurological symptoms. Our study examined the relationship between these three diseases in the context of transcriptome analysis of AD, PD and COVID-19 using bioinformatic analysis. We can identify five major hub genes from DEGs common to these three diseases and validate them with other transcriptomic data. Most importantly, we found that synaptic vesicle cycling is a common pathway in COVID-19, AD, and PD. Further analysis suggested that SARS-CoV-2 infection could lead to synaptic dysfunction and extensive synaptic downregulation in the patient's cortex, thereby inducing or exacerbating neurodegenerative disease. The study contributes to a better understanding of the association between SARS-CoV-2 and neurodegenerative diseases, and identifies potential therapeutic targets and related drugs that may represent promising therapeutic strategies for further clinical investigation.

Our study also had some limitations. First, this study was based on bioinformatics and transcriptome analysis. Differences in microarray platforms, tissue sampling, RNA extraction methods, and statistical methods can lead to potential bias in results. Furthermore, our study was limited by the amount of available transcriptome expression data derived from the frontal cortex. Therefore, the size of the dataset used in this study should be increased to obtain more convincing results. It would be better to include larger cohorts of COVID-19, AD, and PD patients, and future cell or animal experiments could also be performed to provide compelling evidence for our findings. You can, so be careful with the results above.

References

1. Romeo DM, Guzzetta A, Scoto M, Cioni M, Patusi P, et al. (2008) Early neurologic assessment in preterm-infants: integration of traditional neurologic examination and observation of general movements. *Eur J Paediatr Neurol* 12: 183-189.
2. Zafeiriou DI (2004) Primitive reflexes and postural reactions in the neurodevelopmental examination. *Pediatr Neurol* 31: 1-8.
3. Sheppard JJ, Mysak ED (1984) Ontogeny of infantile oral reflexes and emerging chewing. *Child Dev* 55: 831-843.
4. Allen MC, Capute AJ (1986) The evolution of primitive reflexes in extremely premature infants. *Pediatr Res* 20: 1284-1289.
5. Capute AJ, Palmer FB, Shapiro BK, Ross A, Accardo PJ, et al. (1984) Primitive reflex profile: a quantitation of primitive reflexes in infancy. *Dev Med Child Neurol* 26: 375-383.
6. Futagi Y, Toribe Y, Suzuki Y (2012) The grasp reflex and moro reflex in infants: hierarchy of primitive reflex responses. *Int J Pediatr* 2012: 191562.

7. Campbell SK, Hedeker D (2001) Validity of the test of infant motor performance for discriminating among infants with varying risk for poor motor outcome. *J Pediatr* 139: 546-551.
8. Harel S (2000) Pediatric neurology in Israel. *J Child Neurol* 10: 688-689.
9. Gu J, Gong E, Zhang B, Wu B, Shi X, et al. (2005) Multiple organ infection and the pathogenesis of SARS. *J Exp Med* 202: 415-424.
10. Nagata N, Iwata-Yoshikawa N, Taguchi F (2010) Studies of severe acute respiratory syndrome coronavirus pathology in human cases and animal models. *Vet Pathol* 247: 881-892.