

# First assignment

## Bioinformatics and system biology approach to identify the influences of COVID-19 on cardiovascular and hypertensive comorbidities

### INTRODUCTION

Recent studies have tracked down that some prior conditions significantly increment the danger of extreme side effects and mortality in COVID-19 patients. These contain pulmonary diseases, cardiovascular diseases, kidney disease, type 2 diabetes, and hypertension. While COVID-19 essentially influences the respiratory system in the beginning stages of the disease, while it additionally influences the cardiovascular system of patients, extraordinarily increasing the risk of fatality. Numerous examinations revealed raised death rates in patients with SARS-CoV-2 infections and increased levels of markers of chronic heart failure. Also discovered hypertension as comorbidity is related with an increased danger of extreme disease with SARS-CoV-2 disease. discovered 32% of COVID-19 patients with another medical issue. studies are needed to identify the interactions between these diseases and COVID-19. Further, the treatments under the examination for COVID-19 may affect cardiovascular disease, hypertension, or other critical comorbidities by impacting the pathways that intercede their interaction with COVID-19.

Angiotensin-Converting Enzyme 2 (ACE2) is known to play an important role in facilitating SARS-CoV-2 cell entry, and this gene is accounted for many human tissues including the intestine, testis, kidneys, heart, and lungs. ACE usually converts Angiotensin I in the renin-angiotensin-aldosterone system (RAAS) of human physiology to Angiotensin II that impact human blood pressure. ACE2 interacts with SARS-CoV2 that may cause vascular dysfunction. ACE inhibitors is used as treatments for hypertension and cardiovascular disease by modulating the RAAS pathway. These drugs inhibit the RAAS and interrupt the performance of ACE and increase the level of ACE2 receptors. In any case, recent investigations found that increased ACE2 levels can be gainful in COVID-19, This serves to show the possible significance of interaction among cardiovascular diseases and hypertension with COVID-19.

In this paper, we considered the interaction of COVID-19 with chronic heart failure (CHF) and idiopathic portal hypertension (IPH), pulmonary arterial hypertension (PAH), and preeclampsia.

**CHF** is a condition that reduces cardiac output and blood oxygenation insufficiency. **IPH** is a condition of blood pressure in the portal vein and its branches. **PAH** is a case of increased blood pressure within the lungs. **Preeclampsia** is a pregnancy complication that is characterized by hypertensive conditions.

We have found significant cell signaling pathways and gene networks that are commonly associated with these diseases and SARS-CoV-2 infection on human blood cells. The identified pathways and networks are associated with other diseases that may lead to improved therapeutic way for life-threatening SARS-CoV-2 infections.

### ABSTRACT

Severe acute respiratory syndrome corona virus 2 (SARS-CoV-2) infected persons that have hypertension or cardiovascular comorbidities have an elevated risk of serious (COVID-19) disease and a high rates of mortality but how COVID-19 and cardiovascular diseases interact are obscure. We looked to identify a new mechanism of interaction by recognizing genes with expression in SARS-CoV-2 infection that is relevant to the pathogenesis of cardiovascular disease and hypertension. Some research shows the SARS-CoV-2 uses the angiotensin-converting enzyme-2 as a receptor to infect human susceptible cells. ACE2 usually converts Angiotensin I in the renin-angiotensin-aldosterone system to Angiotensin II, which affects blood pressure levels. We use bioinformatics to identify genetic links using MRNA data peripheral blood cells from COVID-19 patients and compared them with blood samples from patients with either chronic heart failure disease or hypertensive diseases. Differentially expressed genes (DEGs) popular to COVID-19 and chronic heart failure, and common to COVID-19 and hypertension, COVID-19 does not share a large number of differentially expressed genes with the conditions under consideration. However, those that were recognized included genes playing roles in T cell functions, such as receptor pathways, cytokines, chemokines, cell stress, type 2 diabetes, and gastric cancer. The result of this study may help in recognizing significant targets of treatment that can combat the progressing pandemic due to SARS-CoV-2 infection.

### RELATED WORK

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