Transcriptome Changes of Hematopoietic Stem and Progenitor Cells in Peripheral Blood of COVID-19 Patients by scRNA-seq

Shao, Zhouqi (School: Whitney M. Young Magnet High School)

The COVID-19 pandemic due to the SARS-CoV-2 virus threatens global public health. The immune response in patients plays a significant role in resisting COVID-19 infection, one part of which are hematopoietic stem and progenitor cells (HSPCs) which can self-renew and differentiate into mature blood cells. Analyzing HSPCs may yield insights into the response mechanism of the immune system. Hence, this project aimed to reveal transcriptome changes of peripheral blood HSPCs after COVID-19 infection. Single cell RNA sequencing data of peripheral blood mononuclear cells (PBMCs) was downloaded and analyzed using R. HSPCs were isolated from the PBMCs, and the frequency of HSPCs were compared between healthy individuals and COVID-19 patients. Cells were then subclustered and enriched pathways were identified. Gene set enrichment analysis was conducted, proliferation of HSPCs by COVID-19 severity was analyzed, and cells were sorted into the cell cycle phases. The results show that there is an increase in the frequency and proliferation signal of HSPCs upon COVID-19 infection. The proportional increase is more profound in patients with more severe symptoms. This shows that the HSPCs are sensitive to COVID-19 infections. More cells were in the S phase of the cell cycle indicating proliferation leads to the higher frequency in COVID-19 patients. Furthermore, one subcluster that had high expression of B-cell related genes was most frequent in critical patients suggesting that the COVID-19 infection reduces B cell numbers or critical patients have greater acquired immunity. This project provides new insights into understanding the immune mechanisms of COVID-19 infection.

Awards Won:
Fourth Award of $500