Biomarker identification in plasma samples from patients with post-Covid Condition (PCC) by shotgun proteomic techniques

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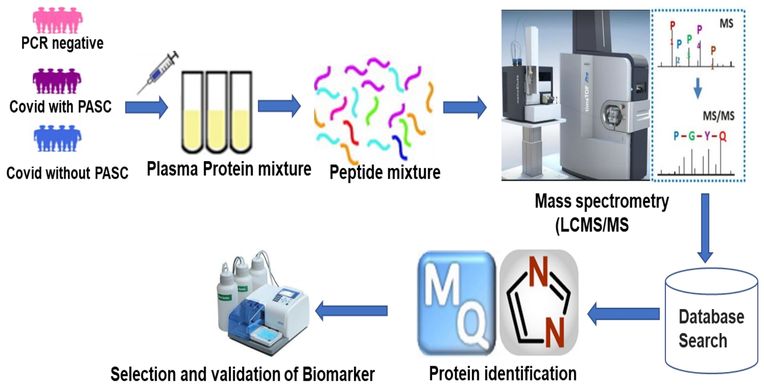
BACKGROUND

Most Covid-19 infections are asymptomatic and relatively mild, with recovery typically occurring within 2–3 weeks. A significant proportion of patients across the spectrum manifest long-lasting symptoms referred to as post-covid condition (PCC) that include extreme chronic fatigue, breathlessness, dyspnea, and cognitive problems. The physiological and pathological basis for PASC is not known. It is unclear whether vaccination completely mitigates or limits the development of PCC. ***The aim of this study is to identify plasma markers that characterize recovered individuals with PCC.***

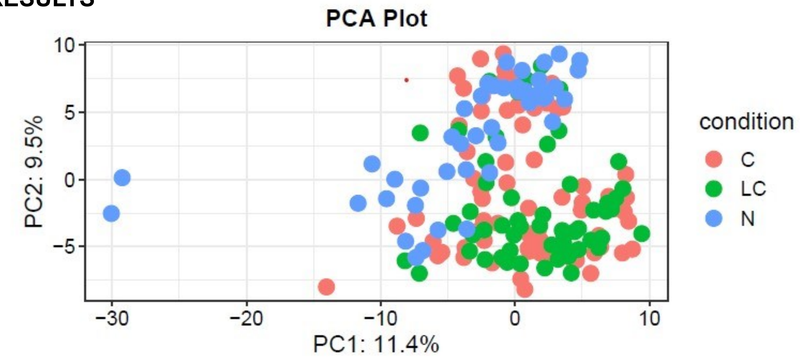
METHODS

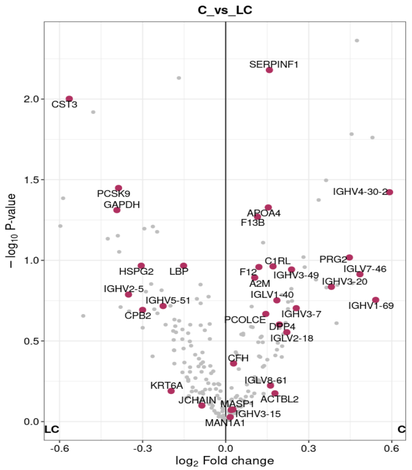
Plasma samples (3-month post-Covid-19 diagnosis) were obtained from the Banque Quebecoise de la Covid-19 (BQC-19) in collaboration with Dr. Alain Piché. We analyzed the plasma protein profiles of 150 plasma samples which were categorized into 52 PASC patients (LC), 62 Covid patients (C), and 35 PCR-negative healthy volunteers (N) by DIA quantitative proteomics. In brief, plasma proteins were denatured, alkylated, digested, and peptides purified. For DIA-based LC-MS/MS analysis, peptides were passed through a TimsTOF Pro ion mobility mass spectrometer equipped with a Captive Spray nano electrospray source. The raw files were analyzed using proteomics data platform DIA-NN.

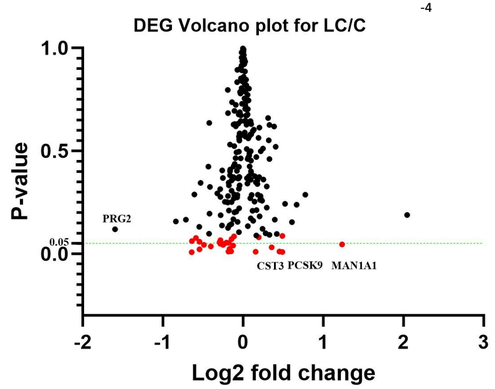
STUDY DESIGN



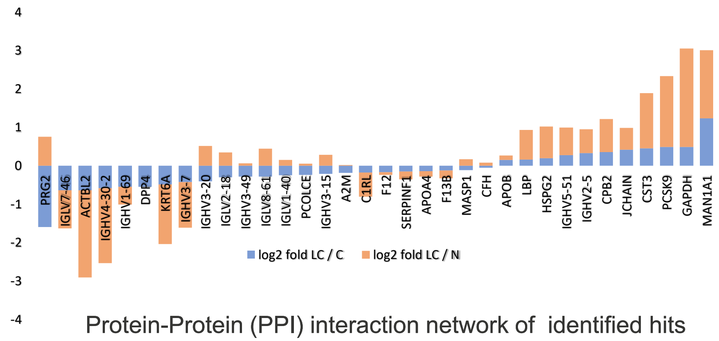
RESULTS



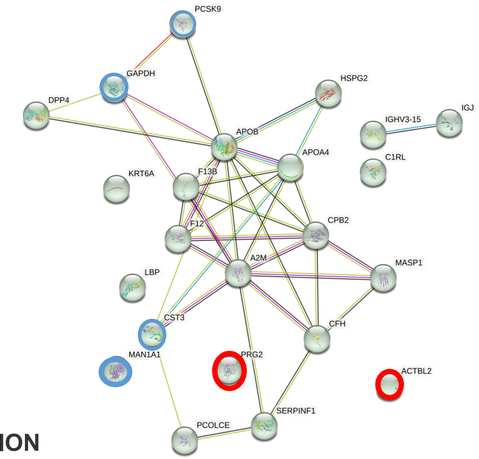




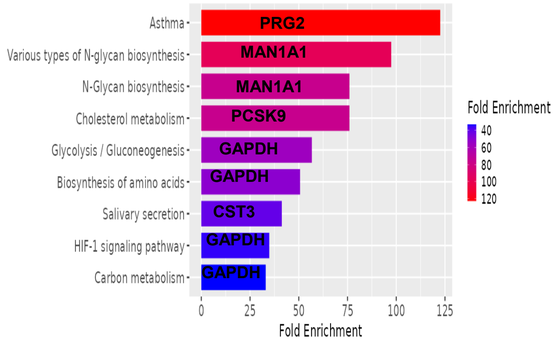
Differentially expressed proteins analysis among Covid, Long-Covid and uninfected individuals



Protein-Protein (PPI) interaction network of identified hits



KEEG pathway enrichment analysis



CONCLUSION

Plasma protein alterations are well-known indicators of pathophysiological changes caused by a variety of diseases, including viral infections. Using the DIA-NN neural network and bioinformatics analysis, we identified 34 differentially expressed proteins (DEP) among the three groups. We observe that some of these were significantly upregulated and downregulated in the Long Covid patients compared to Covid and uninfected individuals.

The most promising identified DEP and their related pathways will be examined in a largecohort using ELISA and other suitable methods. The completion of this project may enable us to find novel specific PASC biomarkers from plasma samples.