COVID-19 systems biology uncovers new genetic signatures in lung and whole blood

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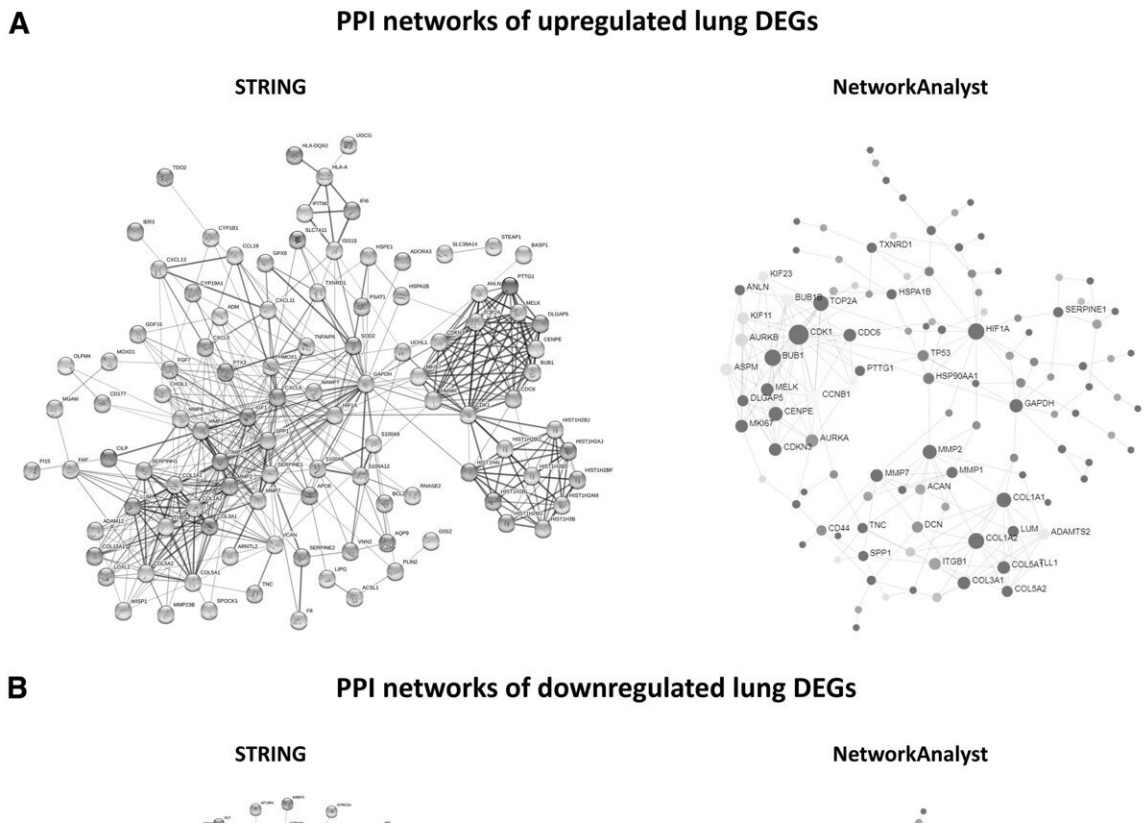

PPI networks and clusters of lung DEGs. (A) PPI networks of upregulated DEGs emerged from the lung datasets, constructed with the platforms STRING (left) and NetworkAnalyst (right). (B) PPI networks of downregulated DEGs emerged from the lung datasets, constructed with the platforms STRING (left) and NetworkAnalyst (right). (C) Neighborhoods of upregulated DEGs clusters from lung datasets, where proteins are densely connected and corresponding pathways. Constructed with Metascape. (D) Neighborhoods of downregulated DEG clusters from lung datasets, where proteins are densely connected and corresponding

pathways. Constructed with Metascape. PPI, protein–protein interaction; STRING, Search Tool for the Retrieval of Interacting Genes/Proteins. Credit: *OMICS: A Journal of Integrative Biology* (2022). DOI: 10.1089/omi.2022.0104

A systems biology approach to examine the effects of SARS-CoV-2 virus in lung and whole blood identified new COVID-19 genetic signatures that could represent potential therapeutic or diagnostic targets. This new study is published in *OMICS: A Journal of Integrative Biology*.

COVID-19 is a systemic disease affecting tissues and organs including and beyond the lung. "The blood is a good indicator of the overall host response as it carries the immune cells throughout the body," state the study authors. "The combined study of the two tissues could unravel the complexity of the host response to SARS-CoV-2."

Corresponding authors Prof. Vangelis Manolopoulos and Nikolas Dovrolis, Ph.D., from the Medical School of the Democritus University of Thrace, and coauthors in Alexandroupolis, Greece, used transcriptomics and analyses of differentially expressed genes in lung samples and whole blood samples from COVID-19 patients and healthy individuals.

They identified 35 differentially expressed genes common between lung and the whole blood, and importantly, two genes, namely CYP1B1 and TNFAIP6, that have not been previously implicated with COVID-19. They also discovered four miRNA potential regulators.

"More than two years into the COVID-19 pandemic, the global struggle with SARS-CoV-2 continues. Our knowledge of the effects of COVID-19 at a whole organism level is still limited. In this context, the study shows the value of a systems biology approach to unpack the

pathophysiology of COVID-19 in multiple tissues. The genetic signatures identified in the study open up new possibilities for COVID-19 drug and diagnostic discovery. I invite new manuscripts on COVID-19 systems biology and multi-omics research for peer-review in the journal," says Vural Özdemir, MD, Ph.D., DABCP, Editor-in-Chief of *OMICS*.

More information: Dimitra Anatolou et al, Unpacking COVID-19 Systems Biology in Lung and Whole Blood with Transcriptomics and miRNA Regulators, *OMICS: A Journal of Integrative Biology* (2022). DOI: 10.1089/omi.2022.0104

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