

Suppressed transcript diversity and immune response in COVID-19 ICU patients: a longitudinal study

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ABSTRACT (250-300 words)

Background: Understanding the dynamic changes in gene expression during acute respiratory distress syndrome (ARDS) progression in post-acute infection patients is crucial for unraveling the underlying mechanisms, specifically in case of hospital admitted severe COVID-19 patients with ARDS post-acute SARS-CoV-2 infection.

Objective: The study aims to investigate the longitudinal dynamics in both genes and transcripts expression in hospitalized severe COVID-19 patients.

Methods: Blood samples were collected at three different time points, and patients were categorized into severe and mild ARDS based on their oxygenation saturation (SpO₂/FiO₂) kinetics over a 7-day period. RNAseq analysis was performed on peripheral blood mononuclear cells (PBMCs) extracted from the patients. Subsequently, both gene and transcript-level differential expression, along with immune cell and cytokine profiles, were compared over time.

Results: Decline in transcript diversity was observed over time, particularly in patients with higher severity, indicating dysregulated transcriptional landscape. Comparing gene/transcript-level analyses highlighted a rather limited overlap. With disease progression, a transition towards inflammatory state was evident. Strong association was found between antibody response and disease severity, characterized by decreased antibody response and activated B cell population in severe cases. Bayesian network analysis identified various factors associated with disease progression and severity, viz. humoral response, TLR signaling, inflammatory response, interferon response, and effector T cell abundance.

Conclusion: The findings underscore dynamic changes in gene and transcript expression during ARDS progression, their impact on tissue oxygenation, and provide insights into disease pathogenesis.

BIOGRAPHY

I am Priyanka Mehta, a bioinformatician actively pursuing my Ph.D. in Dr. Rajesh Pandey's lab at CSIR-Institute of Genomics and Infectious Diseases, New Delhi, India. My research focuses on elucidating the role of alternative splicing in modulating the severity of infectious diseases. Besides my scientific endeavors, I am deeply passionate about creating captivating data visualizations that can tell compelling stories about complex datasets. With an artist's heart and a curious mind, I envision bridging the gap between science and art to effectively communicate my research findings. My goal is to contribute valuable insights that will advance bioinformatics research and enhance our understanding of infectious diseases.

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