SARS-CoV-2 infection Severity and Mortality is modulated by Repeat-mediated regulation of Alternative Splicing

Priyanka Mehta[1,2,#], Partha Chattopadhyay[1,2,#], Varsha Ravi[1], Rajesh Pandey[1,2,*]

[1]*Division of Immunology and Infectious Disease Biology, INtegrative GENomics of HOst-PathogEn (INGEN-HOPE) laboratory, CSIR-Institute of Genomics and Integrative Biology (CSIR-IGIB), Mall Road, Delhi-110007, India.*
[2]*Academy of Scientific and Innovative Research (AcSIR), Ghaziabad-201002, India.*

Corresponding author: *Dr. Rajesh Pandey (rajeshp@igib.in), Division of Immunology and Infectious Disease Biology, INtegrative GENomics of HOst-PathogEn (INGEN-HOPE) laboratory, CSIR-Institute of Genomics and Integrative Biology (CSIR-IGIB), Mall Road, Delhi-110007, India.*

ABSTRACT

Background: Like single-stranded RNA viruses, SARS-CoV-2 hijacks the host transcriptional machinery for its own replication. Numerous traditional differential gene expression-based investigations have examined the diverse clinical symptoms caused by SARS-CoV-2. The virus, on the other hand, also affects the host splicing machinery, causing host transcriptional dysregulation which can lead to diverse clinical outcomes.
Objective: Hence, in this study, we performed transcriptome sequencing of 125 hospital admitted COVID-19 patients to understand the transcriptomic differences between the severity sub-phenotypes (Mild, Moderate, Severe and Mortality).
Methods: Nasopharyngeal swabs were collected from COVID-19 patients, and RNA was extracted and performed whole transcriptome RNA sequencing (RNAseq). Subsequently, RNAseq analysis was conducted to explore transcript-level differential expression, examine differential isoform usage, and investigate splicing patterns within the pool of differentially expressed transcripts (DTE).
Results: Our DTE analysis showed evidence of diminished transcript length and diversity as well as altered promoter site usage in differentially expressed protein coding transcripts in COVID-19 mortality patients. We also looked at the possible mechanisms driving the alternate splicing and discovered a compelling differential enrichment of repeats in the promoter region and specific enrichment of SINE (Alu) near the splicing sites of differentially expressed transcripts. These genomics-based findings suggested a repeat-mediated plausible regulation of alternative splicing as potential modulation of COVID-19 disease severity.
Conclusion: In this study, we have emphasized the significance of transcript-level expression analysis and the role of alternative splicing in shaping COVID-19 disease severity sub-phenotypes and its potential mechanism.

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.

- Mobile Number*: +91 8420727949
- Category*: (Oral presentation/ Poster presentation): Oral presentation
- Linked In: https://www.linkedin.com/in/priyankamehta1811/
- WhatsApp No: (for conference updates) :+91 8420727949
- Research Interest*: Infectious Diseases, Dengue, SARS-CoV-2, Genomics
- Fax No: NA