

DOWNLOAD PDF 115 50

# Differential Gene Expression and Transcriptomics Reveal High M-Gene Expression in JN.1 and KP.1/2 Omicron Sub-Variants of SARS-CoV-2: Implications for Developing More Sensitive Diagnostic Tests

CELLULAR EFFECT COVID-19 EVOLUTION GENE EXPRESSION GENETIC VARIABILITY SARS CORONAVIRUS VIRUS CLASSIFICATION

Aktarul Islam Siddique, Neelanjana Sarmah, Nargis Bali K, Norman Nausch, Biswajyoti Borkakoty

## Abstract

SARS-CoV-2, a positive-strand RNA virus, utilizes both genomic replication and subgenomic mRNA transcription. Whole genome sequencing (WGS) from clinical samples can estimate viral gene expression levels. We conducted WGS on 529 SARS-CoV-2 positive clinical samples from Assam and northeastern India to track viral emergence and assess gene expression patterns. Our results reveal differential expression across structural, non-structural, and accessory genes, with notable upregulation of the M gene, especially in the Omicron variant, followed by E and ORF6. The mean Transcript Per Million (TPM) expression levels of the M gene were significantly higher in Omicron variants (175611±46921), peaking in the KP.1/KP.2 sublineage (220493±34917), compared to the Delta variant (129717±33773). The relative fold change of M gene expression between Delta and Omicron 2024 subvariants showed a 1.6-fold change. Variant-wise gene expression analysis suggests a correlation between gene expression and viral mutation, impacting replication and transmission. As anticipated, the expression levels of genes surge with the increase in the virus mutation. The Chi-square trend for average substitution count vs. average TPM of the M gene was highly significant (72.78, p<0.0001). The M gene's high expression and low mutation rate make it an ideal target for designing a real-time RT-PCR kit assay. These findings highlight the need for continuous surveillance and understanding of viral gene expression dynamics for effective COVID-19 management. Further studies are necessary to elucidate the significance of these observations in viral pathogenesis and transmission dynamics.

Peer review status: ACCEPTED

31 Jul 2024 Submitted to *Journal of Medical Virology*  
05 Nov 2024 Editorial Decision: Accept

Cite as: Aktarul Islam Siddique, Neelanjana Sarmah, Nargis Bali K, et al. Differential Gene Expression and Transcriptomics Reveal High M-Gene Expression in JN.1 and KP.1/2 Omicron Sub-Variants of SARS-CoV-2: Implications for Developing More Sensitive Diagnostic Tests. *Authorea*. August 28, 2024.  
DOI: 10.22541/au.172481225.50240383/v1

This is a preprint and has not been peer reviewed. Data may be preliminary.

TPM\_manuscript\_JMV 31-07-2024-B.docx

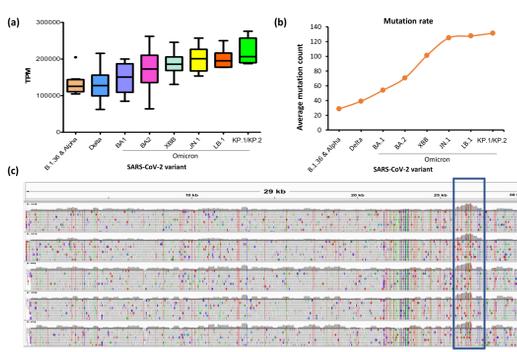
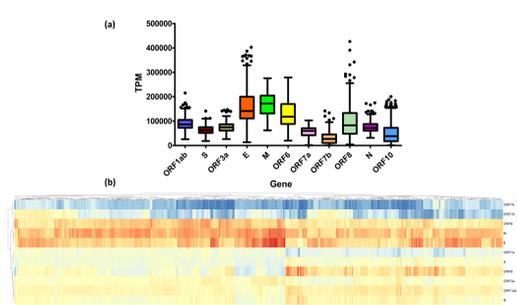
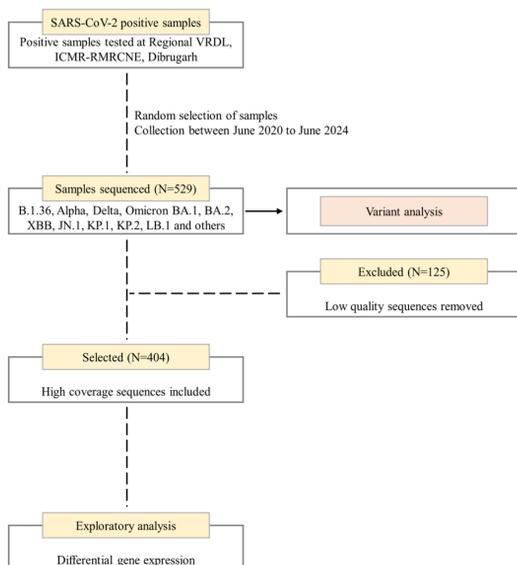
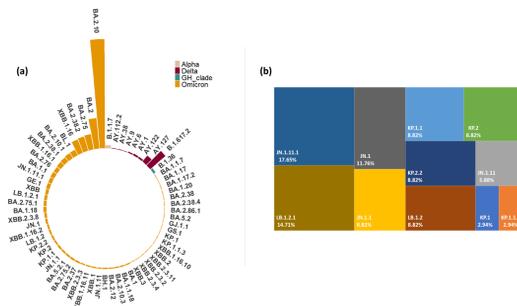
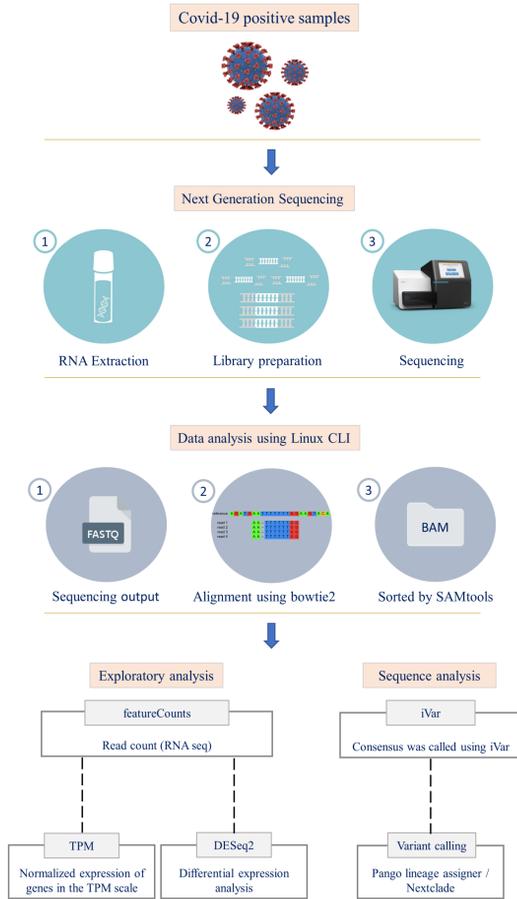


Table 1.docx