

Investigation of host genes involved in Human Metapneumovirus infection immune response and pathogenesis using *in-silico* analysis

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Background

Human Metapneumovirus infection (hMPV) is one of the major causes of acute respiratory illness, particularly in children, elderly and the immunocompromised. A deeper understanding of how the virus manipulates host cells at the molecular level is crucial for developing better therapeutic strategies. This study aimed to identify differentially expressed genes (DEG's), network and pathway analysis associated with hMPV infection from transcriptomic sequences using in-silico analysis by integrating bioinformatics, molecular biology and systems-level analysis.

Methods

Two transcriptomic datasets from the GEO database were analysed using GEO2R and RStudio to identify DEGs. DEGs were analysed for pathway enrichment using Gene Ontology and KEGG pathway enrichment. Protein-protein interaction (PPI) network and transcription factor were analysed using Cytoscape.

Results

103 DEGs were identified from the hMPV positive group, including 56 that were upregulated and 47 that were downregulated. The top upregulated DEGs included IFIT1, IFIT3 and PAK3 while the top downregulated DEGs include RNVU1-18, RNU1-2 and NEURL1B. Enrichment of key immune pathways, including the NOD-like receptor, JAK-STAT and Toll-like receptor signaling pathways were also identified, together with PPI network such as CDK1, STAT1 and CCNB1. Furthermore, transcription factors including STAT1 and IRF9 were identified.

Conclusion

This study defines a host transcriptional signature of hMPV driven by interferon-mediated antiviral responses and cell cycle dysregulation. Key regulators including STAT1 and IRF9, mediate these

responses and contribute to viral pathogenesis. These signatures have clinical relevance as potential biomarkers for early diagnosis and disease severity stratification, while the identified pathways provide targets for host-directed therapies to improve management of viral respiratory infections.