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Nuclear protein profile changes in response to infections of human metapneumovirus vaccine candidates

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Human metapneumovirus (hMPV) is a leading cause of lower respiratory infection in pediatric populations globally. This study examined the proteomic profile changes of A549 cells by hMPV and its two attenuated mutants with deleted PDZ domain binding motif(s) of M2-2 protein. These motifs are involved in the interruption of antiviral signaling, namely the interaction between the TRAF-MAVS. The aim of this study is to provide insight on the overall and novel impact of M2-2 motifs on cellular responses via an unbiased comparison. Tandem-Mass-Tagging (TMT) stable isotope labeling and high-resolution mass spectrometry were used for quantitative proteomic analysis. Quantitative proteomics and Venn analyses revealed there were 1248 common proteins detected in all infected samples of both technical sets. Hierachical clustering of the differentiated proteome displayed distinct proteomic signatures controlled by the motif(s). Bioinformatics and experimental analysis confirmed the differentiated proteomes, revealed novel cellular biological events, and implicated key pathways controlled by hMPV M2-2 motif(s), providing further insight into evaluating M2-2 mutants as potent vaccine candidates.

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