

The transcriptional characteristics of NADC34-like PRRSV in porcine alveolar macrophages

ABSTRACT

The widespread and endemic circulation of porcine reproductive and respiratory syndrome virus (PRRSV) cause persistent financial losses to the swine industry worldwide. In 2017, NADC34-like PRRSV-2 emerged in northeastern China and spread rapidly. The dynamics analysis of immune perturbations associated with novel PRRSV lineage is still incomplete. This study performed a time-course transcriptome sequencing of NADC34-like PRRSV strain YC-2020-infected porcine alveolar macrophages (PAMs) and compared them with JXA1-infected PAMs. The results illustrated dramatic changes in the host's differentially expressed genes (DEGs) presented at different timepoints after PRRSV infection, and the expression profile of YC-2020 group is distinct from that of JXA1 group. Functional enrichment analysis showed that the expression of many inflammatory cytokines was up-regulated following YC-2020 infection but at a significantly lower magnitude than JXA1 group, in line with the trends for most interferon-stimulated genes (ISGs) and their regulators. Meanwhile, numerous components of histocompatibility complex (MHC) class II and phagosome presented a stronger transcription suppression after the YC-2020 infection. All results imply that YC-2020 may induce milder inflammatory responses, weaker antiviral processes, and more severe disturbance of antigen processing and presentation compared with HP-PRRSV. Additionally, LAPTM4A, GLMP, and LITAF, which were selected from weighted gene co-expression network analysis (WGCNA), could significantly inhibit PRRSV proliferation. This study provides fundamental data for understanding the biological characteristics of NADC34-like PRRSV and new insights into PRRSV evolution and prevention.