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Comparison of PBMCs transcriptional profiles of pigs infected with subtype 1 and 2 PRRSV strains of type 1

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Porcine reproductive and respiratory syndrome virus (PRRSV) is a causative agent of an important infectious disease causing serious economic losses to swine industry. The clinical signs of the PRRS induced respiratory disorders, abortions and variable mortality in piglets. The experimental study was performed to compare the virulence of highly diverse East European strains belonging to subtype 2 (Russian strain ILI and Belarusian strain BOR), as well as Danish strain from classical subtype 1 (DAN). The infection with strain BOR resulted in the most severe clinical picture, while the infection with remaining two strains was milder. To gain insight into transcriptome changes after different PRRSV strains infection, gene expression profiles of peripheral blood mononuclear cells lymphocytes were analysed in piglets infected with three PRRSV strains vs control piglets by microarray analysis. The genes were determined to be differentially expressed if the fold change (FC) was greater than 1.5 in up or down-regulation. Validation of microarray results was performed using RT-qPCR and showed high reliability of FC values determined by both methods. Microarray data were analysed using the Ingenuity Systems Pathway Analysis program to determine most significantly affected immunological pathways and regulators. Surprisingly, despite the differences in clinical picture of infection, ILI and BOR infected groups showed similar patterns of activation score for particular immunological pathways analysed, as well as, comparable upstream regulators activity (IFNG, IFNB1, Ifnar, IFNL1), when compared to DAN group. Therefore further analysis is required to determine genes which may be crucial for the course of PRRSV infection.

Biography

Magdalena Materniak works in Department of Biochemistry of National Veterinary Research Institute in Pulawy, Poland. During her PhD studies she developed the diagnostic tools for the detection of bovine foamy virus infections in cows and determined the prevalence of this virus in dairy cattle in Poland. Afterwards she continued her study in the field of veterinary retrovirology and diagnostics, especially on identification of foamy viruses in livestock and companion animals as well as zoonotic potential of these viruses. She has contributed in several grants carried out in NVRI and papers published in reputed journals.

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