IVIS2023

KRUGER PARK | SOUTH AFRICA

13TH INTERNATIONAL VETERINARY IMMUNOLOGY SYMPOSIUM

17-21 NOVEMBER 2023

PROGRAMME & ABSTRACTS

www.ivis2023.org

074 - Transcriptomic profiling shows the induction of humoral and cellular response-related genes in pigs following vaccination with an Influenza A nanovaccine

Adriana MG Ibelli[1,2], Lana T Fernandes[1], Vanessa Haach[3], Danielle Gava[1], Ana Paula Bastos[1,2], Cintia H Okino[4], Jane O Peixoto[1,2], Francisco N Fonseca[5], Marcos AZ Mores[1], Maurício E Cantão[1], Rejane Schaefer[1], Mônica C Ledur[1,6]

[1]Embrapa Suínos e Aves, Concórdia, Brazil. [2]Programa de Pós-Graduação em Ciências Veterinárias, Universidade Estadual do Centro-Oeste (Unicentro), Guarapuava, Brazil. [3]Departamento de Microbiologia, Imunologia e Parasitologia, Instituto de Ciências Básicas da Saúde, Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil. [4]Embrapa Pecuária Sudeste, São Carlos, Brazil. [5]Secretaria de Inovação e Negócios, Embrapa, Parque Estação Biológica - PqEB s/nº, 70770-901, Brasília, Brazil. [6]Programa de Pós-Graduação em Zootecnica, Udesc Oeste, R. Beloni Trombeta Zanin, 680E - Santo Antônio, Chapecó, Brazil

Influenza A virus (IAV) causes a major economic concern for the swine industry and represents a pandemic threat for humans. Vaccination with IAV strains is the main strategy to control the disease in pig herds. Although some influenza vaccines were developed and tested in field trials, molecular mechanisms underlying nanovaccine-induced protection are still unknown. Here, we evaluated the gene expression profile in mediastinal lymph nodes (LMD) of 8 non-vaccinated specific-pathogen free pigs and 16 vaccinated pigs with an adjuvanted nanovaccine for IAV containing the surface glycoproteins (hemagglutinin and neuraminidase) of H1N1pdm, H1N2 and H3N2 viruses. The LMD of the 24 pigs were submitted to the RNA-Seq analysis with the Truseq Stranded mRNA (Illumina) and sequencing in NextSeq 2000 sequencer (lllumina) using 2x100bp paired-end reads protocol. Reads were submitted to quality control using Trimmomatic, mapped and counted with STAR against the swine reference genome (Ensembl 109) and analyzed with limma package considering differentially expressed (DE) genes when a false discovery rate (FDR) was <0.05 and a logFC > |1.5|. The functional annotation of the DE genes was performed using DAVID database. Seventeen genes were DE, all of them upregulated in the vaccinated group, and enriched biological processes (BP) involved with positive regulation of cell cycle. Among them, several genes were related to humoral (GCSAM, MYBL1, MYBL2, ELL3, SIPR2) and cellular (AFF2, POU2AF1, ASF1B) immune response. Furthermore, BP involved with cellular to lipid (AICDA, NUGGC, SCIMP) were also identified, relating them to the phospholipid envelope of the influenza virus present in the nanovaccine. Therefore, in this study, the gene expression profile involved with a virosome-based vaccine immunogenicity was highlighted, showing significant activation of humoral and cellular responses through different biological processes that are related with virus clearance and sustained protection.

Poster Session 3 – Monday 20 November

---

078 - Identification of new antigens as potential sub-unit vaccine candidates for ECF control

Hannah Chege[1,2], Samuel Githigia[1], James Gathumbi[1], Harriet Oboge[3,2], Naomi Chege[4], Rose Ojuok[2], Vishvanath Nene[2], Anna Lacasta[2]

[1]University of Nairobi(Department of Veterinary Pathology and Microbiology), Nairobi, Kenya. [2]International Livestock Research Institute (Department of Animal and Human Health), Nairobi, Kenya. [3]University of Nairobi(Department of Puclic Health and Toxicology), Nairobi, Kenya. [4]University of Calgary, Calgary, Canada