



TRABALHOS APROVADOS PARA APRESENTAÇÃO EM FORMA DE PÔSTER

206 - ÁREA: VETERINÁRIA

NOVEL HUMAN-LIKE H1N1 SWINE INFLUENZA VIRUS WITH THE SIX INTERNAL GENES DERIVED FROM H1N1/2009 VIRUS

REJANE SCHAEFFER, DANIELLE GAVA, VANESSA HAACH, MAURÍCIO EGIDIO CANTÃO, MARTHA IRENE NELSON
¹ EMBRAPA SUÍNOS E AVES - Empresa Brasileira de Pesquisa Agropecuária, ² FIC/NIH - Fogarty International Center of the National Institutes of Health, ³ ICBS/UFRGS - Departamento de Microbiologia, Imunologia e Parasitologia, Instituto de Ciências Básicas da Saúde, Universidade Federal do Rio Grande do Sul
rejane.schaefer@embrapa.br

Resumo

Influenza A viruses (IAVs) circulating in swine are of major economic concern for the swine industry and a pandemic threat for humans. The segmented RNA genome of IAV allows the occurrence of genetic exchange or reassortment among distinct influenza viruses during mixed infections. Recently, after spreading in humans, the 2009 pandemic H1N1 influenza virus (H1N1/2009) was re-introduced in pig populations globally, as well as in Brazil, and re-assorted with other virus lineages. Currently, H1N1/2009 and human-like H1N2 and H3N2 viruses circulate in swine in several Brazilian states. Herein, we describe the whole-genome sequencing of a novel human-like H1N1 IAV isolated from nursing pigs in 2014 in Santa Catarina State. Nasal swabs collected from pigs with respiratory clinical signs tested positive for IAV by reverse-transcription PCR targeting the matrix gene. Virus isolation was performed in SPF chicken eggs and the isolated virus was subtyped by RT-PCR. Virus RNA was extracted from nasal swabs and the eight gene segments were amplified by RT-PCR using PathAmp FluA reagents. DNA libraries were prepared and submitted for sequencing using Ion Torrent system at Embrapa Swine and Poultry. Influenza genome was assembled using Newbler V 2.9 with high coverage (180x). Nucleotide alignments of the NA and NA segments were generated for related human and swine IAVs, collected globally and downloaded from the Influenza Virus Resource available in GenBank. The phylogenetic relationships of the datasets were inferred by using the Neighbour Joining method. Analysis of the HA and NA segment of this virus revealed a novel introduction of human H1N1 influenza virus into swine in Brazil. Besides, the H1 and N1 probably represent the same human-to-swine transmission event in the early 2000s. The six internal gene segments (PB2, PB1, PA, NP, M and NS) of the novel virus showed a high similarity (98-99%) to H1N1/2009 virus. The detection of a novel reassortant human-swine influenza virus shows the very dynamic epidemiology of influenza virus in pigs in Brazil and highlights the importance of performing full genome sequencing of pig isolates in order to enhance genetic information about influenza virus circulating in pigs.

Palavras-chave: H1N1 influenza virus, Pandemic H1N1/2009 influenza virus, Swine, Reassortant