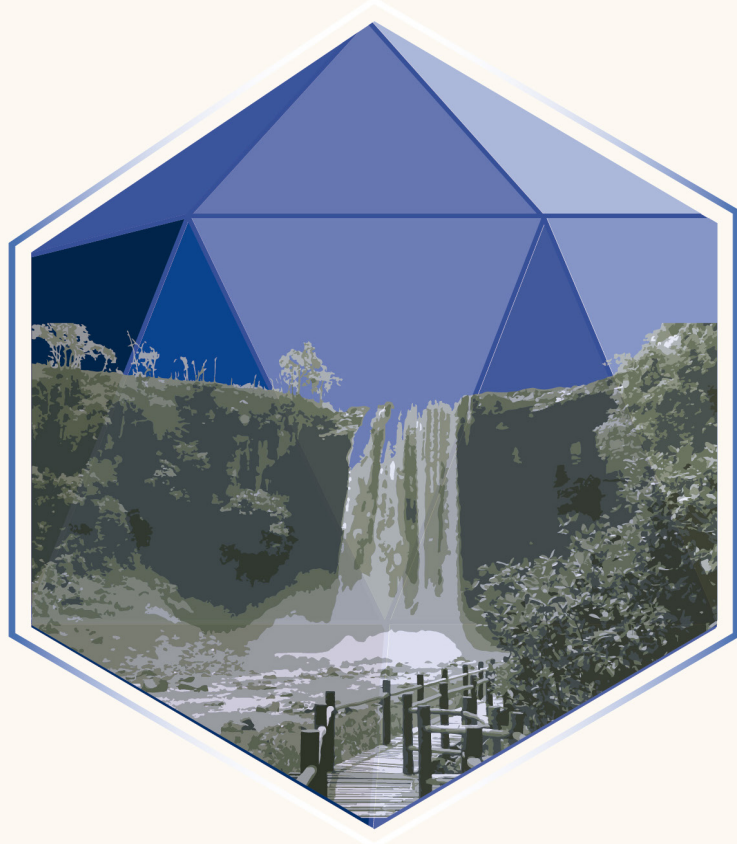


VIRUS

Reviews and Research



XXVII Congresso Brasileiro de Virologia

XI Encontro de Virologia do Mercosul

18 a 21 de setembro de 2016

PIRENÓPOLIS • GO

POUSADA DOS PIRENEUS RESORT

sbv.org.br/congresso



Vol 20 (2), August-December 2016

JOURNAL OF THE BRAZILIAN SOCIETY FOR VIROLOGY

2016 (July), a total of 1952 nasal swabs and 1871 sera collected from nursery and growing pigs, and 165 lung tissue samples collected from suckling, nursery and fattening pigs from 171 pig farms located in the southern, midwest and southeast regions of Brazil were submitted to ELISA, HI assay, RTqPCR, virus isolation and genomic sequencing. Swine from all tested farms had antibodies to FLUAV. Seventyfive percent (75.2%) of sera tested by ELISA were positive for FLUAV antibodies. The HI analysis revealed specific antibodies for H1N1/2009, H1N2 and H3N2/2015 in pig sera from 24 out of 48 of the tested pig farms. Antibodies against two or more influenza virus subtypes were detected in pigs in seven of those 24 farms. Influenza A virus was detected by RTqPCR in 306 (14.45%) of the 2117 tested samples (nasal swabs and lungs). Virus isolation of the influenza positive samples by RTqPCR was performed by the inoculation of lung tissue supernatant or nasal swab samples into MDCK cells or into SPF embryonated chicken eggs and resulted in 162 virus isolates. Complete and partial sequences of 58 FLUAVs were obtained by genetic sequencing and together with RTPCR subtyping results, revealed 23 H1N1/2009, 15 H1N2 and seven H3N2 FLUAVs. The sequence analysis showed that the HA genes of subtypes H3N2 and H1N2 are most closely related to human seasonal H3N2 and H1N2 viruses that circulated in humans in the 1990s and early 2000s, respectively. A novel N1 gene closely related to a human influenza virus that circulated in 2007 was detected in three H1N1 viruses isolated in 2014 and 2015. These findings highlight the importance of humant-swine transmission in the evolution of influenza virus diversity in swine in Brazil and represent a challenge for the design of effective crossprotective vaccines.

VV85 - NEONATAL PIG MORTALITY ASSOCIATED WITH SENECAVIRUS A

Gava, D.; Lorenzett, M.P.; Haach, V. Driemeier, D.; Joshi, L.R.; Mohr, K.A.; Diel, D.G.; Caron, L.; Morés, N.; Morés, M. A. Z.; Schaefer, R.

Senecavirus A (SVA) is an emerging picornavirus that has been associated with outbreaks of vesicular disease in swine. In 2015, neonatal mortality affecting piglets of 07 days of age correlated with SVA, was reported in Brazil. Here, we present an investigation carried on during 2015-2016 in five farrow-to-finish swine

operations in Southern Brazil showing an increased neonatal mortality and also vesicular disease that have been associated to SVA infection. Piglets were lethargic and had a watery diarrhea. The mortality rate increased in 23% and in some littermates a 100% of mortality was observed. Despite of a relatively fast onset of wasting syndrome progressing to mortality, all herds recovered to baseline mortality levels within 410 days. Piglets were necropsied and tissue samples were collected for histopathology, RTPCR for SVA detection targeting the VP1 VP3 region, and for viral isolation in H1299 cell culture. Genome sequences of VP1 gene of five SVA isolates were compared to other SVA sequences available on GenBank. Necropsy of six piglets revealed empty stomach and mesocolonic edema. In general, it was observed enlargement and edema of inguinal lymph nodes, pulmonary edema, ascites and ulcerative lesions on the snout and coronary band. Microscopic lesions were characterized by necrotic epidermitis and dermatitis of coronary band, mild enteritis with villus degeneration on small intestine, marked mesocolon edema and multifocal hemorrhage with lung edema. Senecavirus A was detected by RTPCR in tonsil, lung, liver, intestine and coronary band. SVA was isolated in cell culture from tonsil, lung, intestine and coronary band from piglets of all farms. Sequence comparisons based on a region of the VP1 gene (541 base pairs) revealed that the Brazilian isolates characterized here share 96-99% of nucleotide (nt) identity with contemporary Brazilian isolates, 95-98% nt identity with US and 90-93% nt identity with the prototype strain SVV001. SVA was associated with neonatal mortality based on RT-PCR, virus isolation and sequencing results. The genetic analysis shows the diversity of the Brazilian SVA isolates and that more studies are needed to demonstrate if there are differences between SVA from neonatal mortality and vesicular cases. SVA is clinically and economically important due to its resemblance with vesicular diseases, so the diagnosis tools are critical to confirm the initial investigation.