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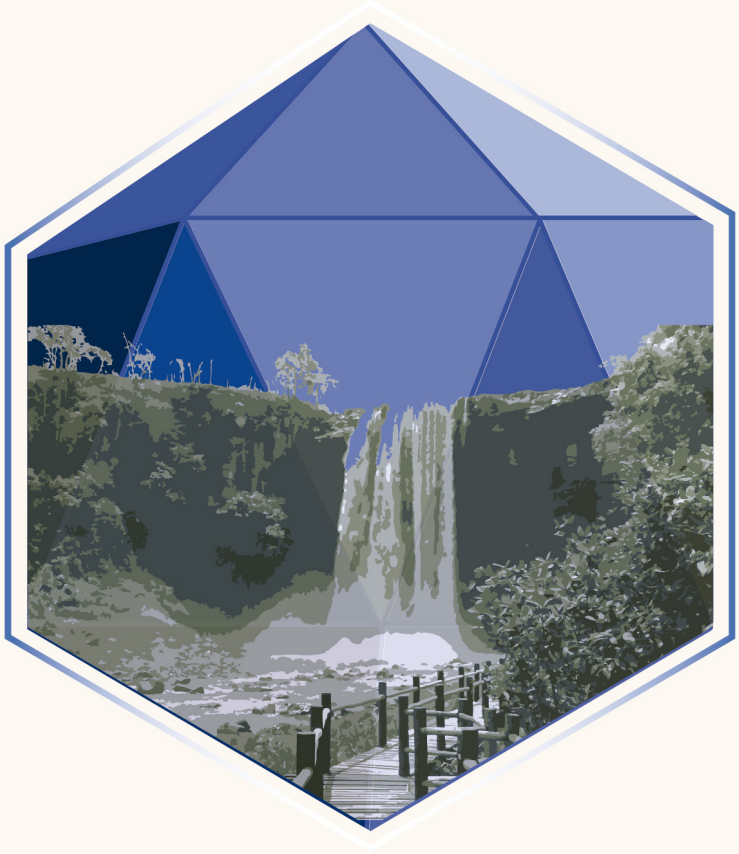
# VIRUS Reviews and Research



## XXVII Congresso Brasileiro de Virologia

XI Encontro de Virologia do Mercosul

18 a 21 de setembro de 2016

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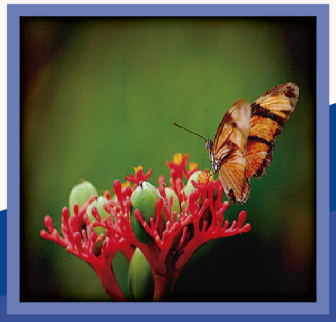

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are classified into nine groups or species designated from A to I, although in birds the infections have been characterizing by groups A, D, F and G and widely distributed. The RV belong to the Reoviridae family, genus Rotavirus have segmented genome with 11 double-stranded RNA (dsRNA). This study aimed to detect RV by multiplex RTPCR in fecal birds specimens collected from different locations from State of Pará. Nine two fecal specimens have been selected randomly, of different bird's species, from the samples animals Bank been of Rotaviruses Laboratory of the Instituto Evandro Chagas IEC. There specimens have subjected to Polyacrylamide Gel Electrophoresis and Multiplex (RTPCR). All samples from this study were negative by Polyacrylamide gel Electrophoresis, however showed positivity in 10.9% (10/92) by Multiplex (RTPCR), which 6.9% (2/29) represented the Group A, 13.8% (4/29) Group D, 10.3% (3/29) Group F and 3.4% (1/29) to the Group G. Subsequently all positive samples have sequenced to characterization of groups. The results presented record simultaneously detection about RVA, RVD, RVF and RVG from fecal birds specimens in the State of Pará, and show to the multiplex RTPCR efficiency as diagnostic test, noticing the largest necessity investigation of these animals like RV reservoirs and possible chance of zoonotic transmission.

## VV78 MOLECULAR CHARACTERIZATION OF GLYCOPROTEIN G OF RABIES VIRUS FROM CATTLE IN THE CENTRAL RIO GRANDE DO SUL STATE, BRAZIL

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Rabies is a worldwide, generally fatal, zoonosis of mammals, caused by the rhabdovirus rabies virus (RabV). Rabies is endemic in Southern Brazil, especially in Rio Grande do Sul (RS), Brazil where thousands of bovine cases have been reported every year. Molecular and epidemiological investigations of RabV infection have been performed, mainly to identify the virus variants involved in the disease and their geographic distribution. In the present study we performed a molecular characterization of the glycoprotein G (gG) of 78 RabV identified in clinical specimens obtained from bovine in RS between 2012 and 2016. Glycoprotein G is an important RabV protein involved in virulence and it the interactions with the immune system. The gG gene was amplified by RT PCR; nucleotide and amino acid sequences were analyzed. To date, total nucleotide/amino acid sequences were obtained of 22 RabV obtained from cattle from central RS. The amino acid analyzed showed the high conservation of gG from all samples (97.6 to 100% of amino acid identity), mainly in all six antigenic sites (I, IIa and IIb, III, IV, G5 and G1). For phylogeny, all samples clustered together with herbivorous and vampire bat RabV obtained from Genbank and apart of dog, cat, wild animals and human RabV sequences. Three sublineages were detected, clustering two samples from Pinhal Grande county (sublineage 1), identified in 2012 and 2016; three samples of Ivorá, Pinhal Grande and Jaguari counties obtained in 2015 and 2016 (sublineage 2); and two samples obtained from São Pedro do Sul county (sublineage 3) in 2014, indicating divergent virus circulating in central region of RS. Some amino acid mutations were identified in gG sequences, and two sublineages were determined by some mutations: lineage 2, at amino acid position 375 (aspartic acid to asparagine); and lineage 3, at amino acid position 376 (glycine to arginine). The results showed the high conservation of gG among the analyzed samples, mainly in the antigenic sites. On the other hand, our data demonstrate that different RabV variants are circulating among herbivorous of central RS.

## 81 GENETIC CHARACTERIZATION AND PHYLOGENETIC ANALYSIS OF SENECAVIRUS A CIRCULATING IN THE US AND IN BRAZIL

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Senecavirus A (SVA) has been associated with sporadic outbreaks of vesicular disease in pigs in the US since the late 1980's. Recently, however, an increased number of reports have described the association of SVA with

vesicular disease and neonatal mortality in swine. Notably, the number of SVA cases have jumped from two in 2014 to over 100 in 2015, which represents a significant increase in the incidence of infection. Since November 2014, SVA has also been frequently reported in swine in Brazil. However, the factors that contributed for the emergence of SVA remain unknown. The overall goal of our study was to characterize contemporary SVA isolates to determine the genetic diversity of the strains circulating in the US and Brazil. The complete genome sequences of seventeen SVA isolates obtained in the US and four SVA isolates obtained in Brazil were compared to other SVA sequences available on GenBank. Sequence comparisons revealed that the US contemporary isolates characterized here share 9193% of nucleotide (nt) identity with the prototype US SVA strain SVV001 and an isolate obtained in Canada in 2007 (SVA11559103), 9899% nt identity with other contemporary isolates recently obtained in the US, 9597% nt identity with contemporary Brazilian isolates and 9496% nt identity with a recent Chinese isolate (CH12015). Comparison of the amino acid (aa) sequences of SVA polyprotein (2181 aa) revealed that the US contemporary isolates here share 9799% aa identity with other SVA strains. Comparisons based on a 541 nt region of the VP1 gene revealed a similar genetic heterogeneity between these isolates. A greater genetic divergence (8688% nt identity), however, was observed when the contemporary SVA isolates were compare to historical US isolates obtained prior to 2002. Sequence comparisons between the isolates obtained here and other contemporary or historical strains available on GenBank revealed a high degree of sequence homology between contemporary isolates. Additionally, both US and Brazilian SVA isolates share a high degree of homology with a recent SVA strain obtained in China. Phylogenetic analysis using complete genome sequences of contemporary SVA isolates and a limited number of historical sequences suggest a constant evolution of SVA. Results here provide important information on the genetic diversity of contemporary SVA isolates that have been recently associated with outbreaks of vesicular disease in swine.

## VV101 NEUTRALIZING ANTIBODIES TO BOVINE ADENOVIRUS TYPE 3 IN CATTLE, RIO GRANDE DO SUL, BRAZIL

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Adenovirus infections are mostly characterized by ubiquitous nature in many host species, thus being expected that seroprevalence to bovine adenovirus (BAV3) may be high in cattle herds worldwide. However, there is no information regarding the presence of BAV3 specific antibodies in Brazilian cattle. BAV3 is associated with respiratory disorders, conjunctivitis, and pneumonia, and also with enteritis, lymphadenopathy and polyarthritis disease, comprising the so called “weak calf syndrome”. Transmission mainly occurs by the fecal-oral route, but can also occur by aerolized droplets. The objective of the present study was to survey the presence of neutralizing antibodies to BAV3 in cattle herds from Rio Grande do Sul State, Brazil. One hundred and seven (n=107) serum samples were analyzed by Virus Neutralization (VN) assay. Serum samples were provided by Setor de Virologia da Universidade Federal de Santa Maria and came from central, north and northwest region of State, both from beef and milk cattle herd and from female gender. The serum samples were diluted from 1:2 until 1:256 in microplates assayed against 100 – 200 TCID50/mL of a prototype BAV3 strain. Nearly all samples, 91% (97/107) were positive for antiBAV antibodies. One percent of serum of these animals had 1:4 of titers; however, 60% of serum samples showed titers > 1:256. From these results, we can conclude that indeed BAV3 is circulating among southern Brazilian cattle herds and further attention have to be taken for the presence of typical clinical signs in calves.

## VV110 ANTIBLUETONGUE ANTIBODIES IN DAIRY CATTLE FROM THE STATE OF PERNAMBUCO, BRAZIL

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Bluetongue is a noncontagious infectious disease, caused by an Orbivirus from the Reoviridae family,