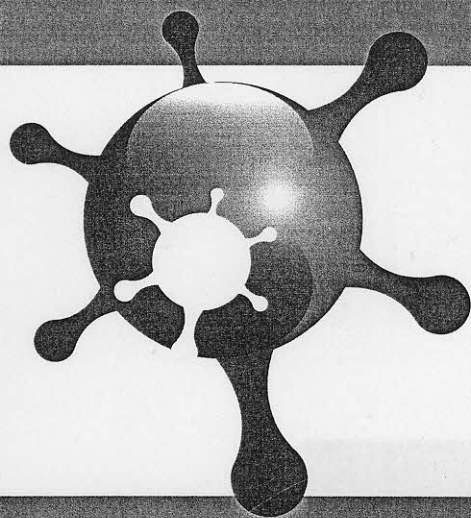


VIRUS

Reviews & Research



XXI Encontro Nacional de Virologia

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**XXI NATIONAL MEETING OF VIROLOGY
& V MERCOSUR MEETING OF VIROLOGY**

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TTV in pigs in intensive swine raising system (ISRS), 47 serum samples from pigs between 20 and 121 days old, were analyzed by polymerase chain reaction (PCR) using primers for identification of PCV-2, TTV-1 and TTV-2 DNA. Prior, all samples were submitted to a phenol-based protocol for DNA extraction. PCV2 was detected in association with TTV in 17 (36.2%) samples. PCV-2 DNA associated to TTV1 was identified in six (12.8%) samples and the association of PCV2 DNA only with TTV2 was found in six (12.8%) samples. PCV-2 DNA associated with both TTV-1 and TTV-2 DNA was detected in five (10.6%) samples. The serum samples, in which we observed co-infection with any TTV and PCV2, coincide with those animals that showed clinical signs suggestive of PMWS syndrome, such as progressive weight loss and respiratory signs. Further studies are needed to better understand the role of this co-infection in occurrence of PMWS syndrome or other PCVAD. To our knowledge, this is the first identification of co-infection between TTV and PCV2 in the state of Goiás.

Palavras-chave: Circovirose, suínos, torque teno vírus.

HIGH-RESOLUTION MOLECULAR EPIDEMIOLOGY OF HIV-1 SUBTYPE C EPIDEMIC HISTORY IN SOUTH AMERICA.

ID: 00593-00001

Área: 05 - Virologia Humana e Saúde Pública

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HIV-1 subtype C represents 30% to 65% of HIV infections in Southern Brazil and, more recently, isolated cases of HIV-1 subtype C infection were also reported in Argentina, Uruguay, Paraguay and Venezuela. Phylogenetic studies suggested that the Brazilian subtype C epidemic was initiated by an introduction of closely related strains. Nevertheless, the point of entry and the timing of subtype C introduction in Brazil, as well as the origin of the founder lineage are still controversial. The present study investigated in depth the origin, spread and phylogeography of HIV-1C in South America, by analyzing carefully assembled datasets covering four South American countries, six Brazilian states and three genomic regions (*p24*, *reverse transcriptase* and *gp41*). High-resolution phylogenetic analysis consistently showed a well supported monophyletic clade including all available strains from Brazil, Uruguay and Argentina

close related to different eastern and central African countries (Democratic Republic of Congo, Burundi, Kenya and Tanzania), depending on the gene region analyzed. Only one lineage from Venezuela was completely unrelated to the epidemic involving the other three countries. Molecular clock and likelihood mapping analysis showed that HIV-1C introduction in Brazil dated back to the 1960-1970s, approximately fifteen years earlier than previous estimates, and was followed by a nearly simultaneous star-like outburst of viral lineages indicating a subsequent rapid spread. Phylogeographic patterns suggested Paraná as the entrance point of subtype C and an asymmetrical gene-flow from Paraná to Santa Catarina and Rio Grande do Sul fostered by the strong inter-connectivity between population centers in Southern Brazil. The study illustrates how coupling phylogeography inference with geographic information system data is critical to understand the origin and dissemination of HIV-1 subtype C in South America and potentially predict its future spread.

Palavras-chave: Human Immunodeficiency Virus, Evolutionary history, Subtype C.

OCCURRENCE AND GENETIC DIVERSITY OF BEGOMOVIRUS IN SOUTH OF BRAZIL

ID: 00594-00001

Área: 06 - Virologia Vegetal

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Begomoviruses (Fam. Geminiviridae) transmitted by the whitefly *Bemisia tabaci* (Fam. Aleyrodidae) are widespread in Brazil. In order to estimate begomovirus occurrence and genetic diversity in the main crops and associated weeds in the south region of Brazil, samples of 114 plants including *Euphorbia heterophylla*, *Sida* sp., *Leonurus sibiricus*, *Sidastrum micranthum*, *Leucas martinicensis*, *Oxalis* sp., *Crotalaria* sp., *Bidens pilosa*, *Glycine max* and *Phaseolus vulgaris* showing typical symptoms of virus infection or infested by the vector were collected from two consecutive years (2009 and 2010) between latitude S28 and S22 (states of Rio Grande do Sul, Santa Catarina, Paraná and Mato Grosso do Sul). DNA extracted from plants was used as template in PCR reactions, containing pairs of primers identified as A1978F and A496R. Fifty-eight samples were positive (35 *E. heterophylla*, 10 *Sida* sp., 9 *L. sibiricus*, 1 *L. martinicensis*, 1 *Oxalis* sp., 1 *Crotalaria* sp., 1 *G. max*). Genetic diversity of the detected begomovirus was analyzed by restriction fragment length polymorphism

on PCR – amplified DNA with *Hinf*I. Genetic diversity of begomovirus was found within and between the hosts. At least four restriction patterns were found for each of the following hosts: *E. heterophylla*, *Sida* sp. and *L. sibiricus*. Co-infections were also observed. Some RFLP patterns had a wide distribution and were predominant in geographic areas while others were restricted.

Financial support: Embrapa, CNPq.

Palavras-chave: Geminiviridae, PCR-RFLP, weed hosts.

PREVALENCE OF HEPATITIS A INFECTION IN CHILDREN AND ADOLESCENTS IN SANTOS COUNTY, SÃO PAULO STATE – BRAZIL.

ID: 00763-00001

Área: 05 - Virologia Humana e Saúde Pública

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Hepatitis A infection is found all over the world, and the high prevalence is associated with poor socioeconomic conditions. Brazil has been considered a country with high endemicity for HAV. Brazilian health Ministry estimates that at least 70% of the population has antibodies against this infection. The objective of this study was to estimate the prevalence of hepatitis A infection among children and adolescents from Santos County. We evaluated 4,677 children and adolescents from nursery schools, elementary schools and high schools from Santos County. Serum samples were collected in filter paper, eluted in PBS and screened for anti HAV – IgG and IgM antibodies -, employing commercial kits (DiaSorin™, Saluggia, Italy). The prevalence of hepatitis A infection was 11,7%. In nursery schools the prevalence was 4,4%; in elementary schools it was 6,1% and in the high schools the prevalence was 16,6%. Detecting anti-HAV IgM it was observed 4,2% of new infection during the study period. The prevalence of hepatitis A infection was low in this study, and also showed that HAV infection increased with age, depending on environmental exposures. These data are important to show that young population could be susceptible to HAV infection, acquiring the infection later in life developing more severe disease, with more public health implications.

Palavras-chave: epidemiology, HAV, prevalence, Santos.

PHYLOGENETIC ANALYSIS OF NEWCASTLE DISEASE VIRUS BY TWO DIFFERENT GENES

ID: 00764-00001

Área: 03 - Virologia Animal

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The Newcastle disease is one of the most important zoonosis in the world economy today. In Brazil, despite being considered free of the disease, the NDV (virus that causes Newcastle disease) is mandatory reporting because of the risk that it represents to the largest exporter and the major producer of chicken meat in the world. The pathogenicity of NDV is closely related to the antigenic fusion protein (F), highly variable. Most phylogenetic studies, including sub-typing, is based on analysis of this encoding gene. This study was done with genome sequences of NDV isolated from penguins in Antarctica. The sequences were aligned with others from GenBank using Blast in the NCBI Home page. Nucleotide sequence editing, analysis, prediction of amino acid sequences, and alignments were conducted by using Bioedit Sequence Alignment Editor Software version 6.0.7. Additionally, phylogenetic trees were constructed by use of PAUP* software (Distance method, version 4.0) with a heuristic search and 1,000 bootstrap replicates. The figure was obtained with the Tree Figure Drawing Tool FigTree version 1.2.1. Data showed that using small fragments of 121pb of the matrix gene (M) obtained the same basic topology of the tree produced by F gene fragments of 172pb, which in turn showed genetic relationship equivalent to that found in the literature, considering the total sequences of F and HN genes. Therefore, the use of relatively short sequences from different sub-genetics regions is suitable for identifying genotypes and does not significantly influence the values of genetic distances in the case of NDV. Financial support: CNPq.

Palavras-chave: APMV-1, PHYLOGENETIC ANALYSIS, Newcastle disease virus, F protein, M protein.

PHYLOGENETIC ANALYSIS OF RABIES VIRUS PHOSPHOPROTEIN AND MATRIX PROTEIN FROM BRAZILIAN VARIANT MAINTAINED BY HAEMATOPHAGOUS BATS *Desmodus rotundus*.

ID: 00765-00001

Área: 03 - Virologia Animal

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