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This study shows for the first time PoNoV circulating in Brazilian pig herds and the high genetic diversity presented by those agents. Circulation of PEC mainly in asymptomatic animals might be a mechanism of virus persistence in pig population important on CaV epidemiology and evolution. The role played by CaV on animal and public health remains unknown.

Financial support: CAPES, CNPq, Instituto Oswaldo Cruz

059 - CURRENT SITUATION OF CLASSICAL SWINE FEVER IN BRAZIL.

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Classical Swine Fever (CSF) is a highly contagious viral disease of Suidae caused by CSF Virus (CSFV), a positive single-strand RNA virus (*Pestivirus*-Flaviviridae). CSF is considered the major cause of economic losses to the swine industries and pig farmers. The efficacy of CSF combat Programs developments in Brazil was studied yet in FREITAS et al. (2007). In present study the CSF - Control and Eradication program (CSFCEP) was evaluated from 2000 until July, 2009 including CSF outbreaks in North and North-East regions (out of CSF-Free Zone or infected area) and compared with CSF–Free Zone in the same period. The survey of CSF outbreaks and the tendency line were analyzed by quadratic trend model. Mann-Whitney test was applied to demonstrate the efficacy of CSFCEP. Around the world many programs to control and eradicate CSF were applied but without plain outcome (TERPSTRA et al., 1993). The advance on CSFCEP was evidenced by the number of CSF outbreaks drastically reduced in all country. In the Brazilian CSF-free zone established in 2001 the virus, was never reintroduced, proving that the zone is secure and stimulated others states to intensify all measures to be included in CSF Free-Zone. Nowadays, the CSF Free- Zone comprises 15 states from center-west, south, southeast, north and northeast regions, account for almost the totality of commercial swine farms. Mann Whitney analysis showed at 95% confidence level a significant difference ($p < 0.05$) of efficacy results of CSFCEP and oldest control program to control CSF. In contrast, at North and North-East regions (out of CSF-Free Zone, some CSF outbreaks still occur. The comparison of profiles from CSF outbreaks data (2000-2009) plotted showed an oscillatory curve with peaks of 12, 04, 07, 01, and 01 CSF outbreaks in 2001, 2003, 2007, and 2008, respectively. But, 21 CSF outbreaks were registered until July 2009. All CSF outbreaks were eliminated by stamping out measures. The emergence vaccination was recurred to avoid new outbreaks. Those results suggest that the efficacy of CSF eradication programs depends on the continuity of preventive strategies as rigorous vigilance for quick adequate action upon CSFV detection. But, to eradicate CSF beyond those measures a rigorous control of animal movement, backed up with serological investigations need to continue until no more outbreaks could be cited in all country.

060 - BARLEY AND CEREAL YELLOW DWARF VIRUS GENETIC DIVERSITY IN BRAZIL

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Yellow dwarf disease (YDD) of wheat (*Triticum aestivum*), barley (*Hordeum vulgare*) and oat (*Avena* spp.) is one of the most important viral diseases of cereals worldwide. YDD is caused by virus transmitted by aphids in a circulative manner and limited to the phloem tissues of plants. The virus-vector relationship was used to discriminate virus species. Nowadays, based on genomic sequences, species are positioned in the genus *Luteovirus* (*Barley yellow dwarf virus* species) and *Polerovirus* (*Cereal yellow dwarf virus* species) in the family *Luteoviridae*. Surveys based on ELISA analysis indicated that *Barley yellow dwarf virus* – PAV are the predominant specie in Brazilian winter cereal crop regions. The objective of this study was to determine the coat protein (cp) sequence of Brazilian B/CYDVs isolates and to study their relationship in comparison to other isolates in the family *Luteoviridae*. In 2007 (14) and 2008 (28), 42 isolates from Brazilian South region (Rio Grande do Sul - 33, Santa Catarina - 2 and Paraná -7) were collected from *Avena* sp (26), *T. aestivum* (10), *H. vulgare* (4), *Lolium multiflorum* (1) and *Zea mays* (1). Viral isolates were propagated on oat (*Avena sativa*) or wheat (*T. aestivum* cv. Embrapa 16) using aphids (*Rhopalosiphum padi* or *Sitobion avenae*). After total RNA extraction from source plants, viral cDNA was synthesized by primers witch are specific to virus sequence. PCR amplified products were inserted into pGEM-T easy vector. The clones were sequenced using ABI 3700 DNA sequencer. Sequences identities were verified by a BLAST search of the GenBank nucleotide database. Nucleotide sequences were aligned, analyzed and compared with those of the other virus isolates from the family *Luteoviridae* using CLUSTAL W. From the 42 isolates, 3 from oat collected

in 2007 were identified as *Cereal yellow dwarf virus* (CYDV) – RMV (93% to 94% identity with "Illinois" - Z14123 isolate). Other 39 isolates were identified as *Barley yellow dwarf virus* (BYDV) – PAV. The cp gene nucleotide average identity compared to other BYDV-PAV isolates was higher than 90%. The Brazilian isolates established a very homogeneous cluster (identity between 99-100%, independent from locality, year and host) and formed a node within subgroup A2 of BYDV-PAV. The prevalence of BYDV-PAV in Brazilian population as previously appointed by ELISA surveys, and the low genetic variability may indicate the prevalence of A2 subgroup of BYDV-PAV in Brazil.
Financial support: Embrapa, CNPq

061 - DETECTION OF HUMAN ROTAVIRUS-A IN LABORATORY SURFACE SAMPLES IN RIO DE JANEIRO, BRAZIL

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Rotavirus A (RV-A) are the leading cause of gastroenteritis in children under 5 years of age worldwide. These viruses are frequently associated with diarrhea and vomiting in this age group and sporadic cases have been described in hospitalized children. They are usually transmitted through person to person spread by the fecal oral route. Environmental transmission of RV-A has been described in hospitals, and involves contaminated work surfaces, floors, light switches, taps and door handles. The aim of this study was to examine environmental contamination with RV-A in laboratory in Rio de Janeiro, Brazil by analyzing surfaces and fomites. Sites were chosen to represent areas commonly in contact with hands. Laboratory surface samples were obtained by dipped swabs in PBS collected from 26 different surface sites as: taps, elevator button, personal protective equipment (PPE) drawer and door handle. Viral nucleic acid was extracted from swabs using a guanidinium isothiocyanate/silica procedure, followed by cDNA synthesis using random primers. Detection of RV-A was performed using RT-PCR and/or nested-RT-PCR for VP6 gene. All procedures to avoid cross-contamination were performed in four different rooms. Positive and negative controls were included during all steps. RV-A were detected in 4 (15%) and 10 (38%) out of 26 environmental swabs by single round PCR and by nested-RT-PCR, respectively. Nucleotide sequencing was performed on nested-PCR amplicons, confirming RV-A VP6 gene. It was shown that environmental sites contaminated with RV-A were often associated with sites frequently in contact with hands, which may indicate that more strict practices of hand washing should be implemented in laboratories .
Financial support: CNPq, CGVAM

062 - *CHLAMYDIA TRACHOMATIS* AND *C. PNEUMONIAE* AMONG *HUMAN IMMUNODEFICIENCY VIRUS 1* (HIV-1) INFECTED INDIVIDUALS FROM THE STATE OF PARA, BRAZIL.

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Chlamydia trachomatis share the sexual route of transmission with HIV-1. As a consequence of the compromise of the immune response among HIV-1 carriers, *Chlamydia pneumoniae* is a potential infectious harassment within their respiratory tracts. The present study intended the description of the seroprevalence of these two agents among 430 HIV-1 infected persons residing in the State of Para, Brazil, attending the State Reference Unit for Infectious Diseases (URE-DIPE), between September 2007 to June 2008. Plasma samples were tested using an enzyme immunoassay for the detection of IgM and IgG antibodies to *Chlamydia*, and those which elicited positive results were ramdomly selected (15%) for serotyping through a microimmunofluorescence assay for both agents. Results were compared statistically using the Chi square test ($\div^2$). The general prevalence to *Chlamydia* was 64.2% (51.6% IgG reactivity and 4% to IgM). Serotyping showed 100% reactivity to *C. trachomatis* (for both IgG and IgM), a large distribution of reactivity to strains of *C. trachomatis* that cause genital infections (L_1, E, G, F) and a high prevalence to *C. pneumoniae* (73.5% IgG and 70.5% to IgM). The infection with both pathogens were associated to several characteristics which included: higher prevalence among males, high age, high number of sexual partners and anal sexual relations. It is necessary not only the individual attention for prevention, but also the continuous monitoring to block transmission and the improvement of the well being of HIV-1 infected persons.
Financial Support: PN-DST/AIDS, CAPES, UFPA, FADESP

063 - ANTIHERPES SCREENING OF DIFFERENT TAXA OF BRAZILIAN BIODIVERSITY

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