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Arenaviruses are members of the family Arenaviridae that consists of a unique genus (Arenavirus) that currently comprises 23 viral species. It is assumed that humans usually become infected with arenaviruses contact with infected rodents or inhalation of virus in aerosolized droplets of secretions or excretions from infected rodents. South America arenaviruses belong to the Tacaribe sorocomplex and five members are known to cause hemorrhagic fever in Argentina, Brazil, Bolivia and Venezuela. In Brazil, the first report of a hemorrhagic fever associated to Sabia virus, whose reservoir is still unknown, was done in 1990. There are three other arenavirus circulating in Brazil: Amapari, Flexal and Cupixi virus. In this study, the presence of arenavirus were investigated among small mammals from Dois Irmãos do Buriti and Sidrolândia municipalities. Those municipalities are situated in Mato Grosso do Sul State where there is no description of arenavirus-associated hemorrhagic fever, although they are near areas where circulation of those viruses are well documented. Two fieldworks were conducted for rodent trapping, the rodents were captured in Sherman and Tomahawk live traps, and processed in a laboratory installed in the field. Rodent spleen and liver samples were submitted to RT-PCR amplification of partial S segment

using oligonucleotide primers of the S segment of Junin virus. Twenty of the 76 collected animals were positive by molecular testing. The positives animals compromise six different species, and only one of them has been recognized as a host for arenavirus. These initial results showed a strong evidence of arenavirus circulation in Mato Grosso do Sul State, as well as a high prevalence of these viruses among the rodents from this region. Further analyses must be made to identify the specie or species of arenavirus, here described, and the role played by the positive rodents as hosts of these viruses. Financial support : FIOCRUZ and CNPq

#### **VV1427 - POPULATION DYNAMIC OF PORCINE PARVOVIRUS INDICATES DECREASE OF VARIABILITY**

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The porcine parvovirus (PPV) is considered to be a major cause of reproductive failure in swine. In the last 15 years, several reports described new PPV biotypes containing amino acid substitutions located in the capsid surface. Analysis of the PPV evolutionary dynamic revealed that the virus displays a substitution rate in the structural protein gene close to those usually finding in RNA viruses. That facts raise concern about the commercial vaccines, leading to the hypothesis that the emerging biotypes are a result of an escape mechanism from the current vaccine used. To address these

questions, the population dynamic of PPV isolates from swine herds was analyzed using all PPV viral protein gene complete and partial sequences originated from swine and deposited in GenBank. The population dynamic history of the virus was calculated using Bayesian Markov Chain Monte Carlo method with a Bayesian skyline coalescent model. Additionally, an in vitro model was performed by twenty consecutive passages of the Challenge strain (a virulent field strain) and NADL2 strain (a vaccine strain) in PK15 cell-line supplemented with polyclonal antibodies raised against the vaccine strain. The Bayesian analysis indicated a decrease in the population diversity over the years and in consequence the presence of around eleven dominant PPV strains. In agreement, the in vitro study revealed that a lower number of mutations appear for both viruses in the presence of anti-PPV antibodies in comparison with the control passages without antibodies. As hypothesis, the antibodies pressure may reduce the neutral selection, which should play a major role in the new mutations drift. In swine, the PPV vaccines largely used in the last 30 years probably reduced the genetic diversity of the virus. In this scenario, vaccine failures and the non-vaccinated populations (e.g. wild boars) may have an important impact in the emergence of new biotypes. Financial support: Capes and DAAD.

**VV1463 - CROSS-SECTIONAL STUDY FOR THE SEROLOGICAL PROFILE TO INFLUENZA H1N1 VIRUSES IN SWINE HERDS IN BRAZIL**

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Influenza A virus (IAV) is one of the main pathogens that causes respiratory disease in pigs and the humoral immune response is important to prevent the infection and to decrease clinical manifestation of the disease. The circulation dynamics of specific pathogens in a herd can be accessed by the analysis of its serological profile. Therefore, the objective of this work was to study the serological profile of influenza virus in commercial swineherds in Brazil. A cross-sectional study was performed in seven Brazilian herds located in Minas Gerais, São Paulo, and Paraná states, sampled before (H1 to H3a) and after the human influenza H1N1 2009 pandemic (H3b to H6). Serum samples from 10 animals in each production category (sows, lactating piglets, nursery, grower, and finisher pigs) were evaluated by hemagglutination inhibition test (HI) against classical swine (cH1N1) and pandemic (pH1N1) H1N1 influenza viruses. All herds sampled before the pandemic (H1 to H3a) were seronegative. Serological profile patterns were similar in all herds evaluated after 2009 H1N1 pandemic (H3b to H6), in which maternal derived antibodies (MDA) seemed to decay in nursery phase. Seropositive animals were detected in all categories, with