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The herpes simplex virus type 1 (HSV-1) is a ubiquitous virus, that may cause keratoconjunctivitis or even encephalitis. Viral replication initiates when virus enters into the host cell. This is followed by viral macromolecule synthesis, comprehended by phases α , β and γ of virus replication. Finally, virus particles bud through the nuclear membrane and are released. Acyclovir (ACV), an aciclo-nucleoside that acts as a DNA chain terminator, is the main anti-HSV drug in clinical use. However, ACV resistant strains of HSV-1 have been identified. This motivates the search for new antiviral molecules. Through an empirical approach in which we screened library of 129 compounds, we identified the triazole derivative (NFTOSIL; 9d) as a potent inhibitor of HSV-1 replication ($EC_{50} = 1.3\mu M$), endowed with low cytotoxicity ($CC_{50} = 1266\mu M$). We found that the compound 9d does not affect viral adsorption and penetration. By means of time-of-addition assays, we observed that compound 9d addition to the infected cultures could be up to very late times points after infection without losing its effectiveness over 90% inhibition at 5 μM . For comparison, the antiviral activity of ACV is maintained up to 6 hours post-infection, when the peak of action of viral DNA polymerase and thymidine kinase occur. Together, these data suggest that

ACV and compound 9d exhibit distinct mechanisms of action. Moreover, after three passages of virus in the presence of our drug, an increase of 2.5 to 3 times in viral titers was observed, suggesting an accumulation of antiviral resistance mutations. Our next approaches are to sequence the genome of compound 9d resistant strains of HSV-1 and to analyze the ability of ACV to cross-inhibit these mutant strains. Together, our data suggest that the compound 9d appears to have a novel mechanism of action, differently than ACV. Financial Support: CNPq, FAPERJ.

VV911 - SEROLOGICAL AND MOLECULAR EVIDENCE OF HEPATITIS B VIRUS INFECTION IN SWINE FROM BRAZIL

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The hepatitis B virus (HBV) belongs to the Hepadnaviridae family, which can be found in both mammals (Orthohepadnavirus genus) and birds (Avihepadnavirus genus). The Orthohepadnavirus genus includes HBV that infects humans, rodents such as woodchuck and squirrels, and non-human primates including chimpanzees, gibbons, gorillas, orangutans and woolly monkeys. Avihepadnavirus genus has been reported to infect ducks, geese, herons, storks and, recently, chickens. Like most hepadnavirus, HBV displays a narrow host range, being restricted to limited or closely related naturally infected species. Although host-specific, many studies demonstrated the ability of HBV to cross species barriers. Recently, investigations in a swine herd in China identified an evidence of the existence of a novel member of the hepadnavirus family endemic in swine using human HBV diagnostic kits including enzyme-linked immunosorbent assay (ELISA), immunohistochemical staining and transmission electron microscopy. The aim of this study was to investigate the serological and molecular markers of HBV circulation in Brazilian domestic swine and wild boars herds. For this purpose, 376 swine were screened for HBV serological markers. Analyses were performed in serum samples using commercial ELISA kits

(DiaSorin®) for anti-HBc, HBsAg and anti-HBs. Reactive and indeterminate swine serum samples were selected to perform partial genome amplification, viral load quantification and genome sequencing. From 376 swine samples analyzed, 28 (7.45%) were reactive to anti-HBc, 3 (0.80%) to HBsAg and 6 (1.6%) to anti-HBs. Besides, more 17 (4.52%) swine samples analyzed were classified in gray zone of EIA test to anti-HBc and 2 (0.53%) to HBsAg. HBV viral load could be measured in two samples and ranged from 4.43×10^3 to 4.55×10^3 copies/ mL. Partial genome sequencing (252-365 bp) of another 3 samples confirmed HBV sequence, sharing 93-96.3% of identity with human HBV. Serological and molecular data demonstrate evidence of HBV infection in Brazilian swine. Financial support: IOC/Capes Area: Animal Virology

VV912 - MOLECULAR ANALYSIS IN EQUINE SERUM POOLS OF MATO GROSSO STATE TO INVESTIGATE THE PRESENCE OF WEST NILE VIRUS IN BRAZIL

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The West Nile Virus (WNV) became known in 1937 in Uganda, Africa, and appeared in the American continent only in 1999. Since then, evidence of circulation was obtained in a growing