

VACCINIA VIRUS STRAINS ISOLATED FROM OUTBREAKS IN BRAZIL: GENETIC POLYMORPHISM AND VARIATIONS OF PATHOGENICITY IN MICE MODEL.

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Since 1999, outbreaks of bovine variola caused by *Vaccinia virus* strains have been consistently occurring in different regions of Brazil. The characterization of the viruses isolated by our group, as well as the three viruses isolated from rodents (BAV, SPAn232 and VBH) was done by serologic, biologic and molecular assays. The genetic diversity and variations of pathogenicity in mice model found in our studies proves that there are different *Vaccine virus* strains circulating in the nature in Brazil, leading to new questions. Have these samples evolved from a common source or not? What is the ancestral virus of these Brazilian VACV samples: a different vaccine strain or an autochthonous virus? This fact makes this zoonosis a very important model to study the epidemiology, pathogenesis, and molecular characteristics of these viruses. This understanding would also be essential to establish ways to prevent and control these infections caused by these viruses.

Keywords – orthopoxvirus, *Vaccinia virus*, bovine variola