VETERINARY VIROLOGY - VV

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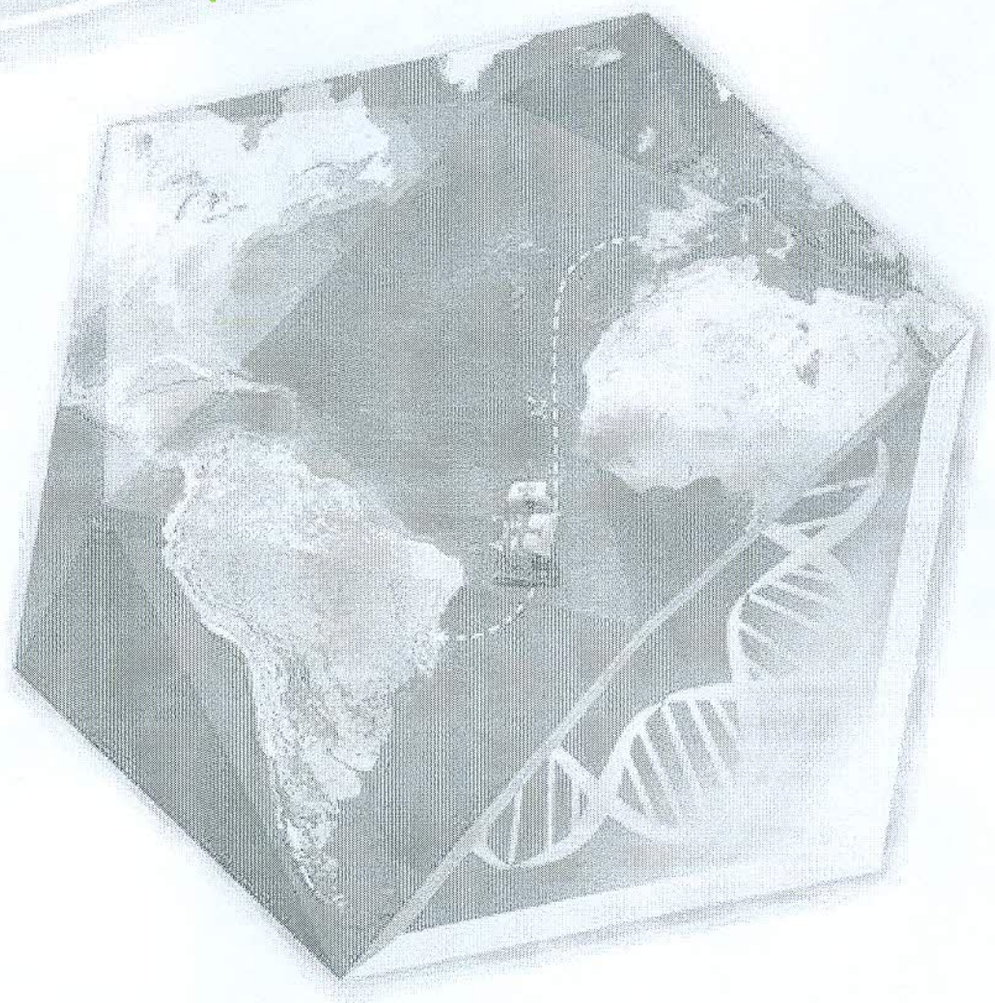
(Repro - 3 resumos)



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Rotaviruses (RVs) are members of the Reoviridae family, and classified into eight species (A-H). RV species A (RVA) are the main etiologic agents of acute gastroenteritis and responsible for nearly 400,000 deaths worldwide. The viral genome is enclosed within a three-layered particle and consists of 11 segments dsRNA. The outer capsid proteins VP7 and VP4 carry independent neutralization and protective antigens. A binary system is used to classify RVA into P and G genotypes based on the specificity of the VP4 and VP7-encoding genes, respectively. Thus far, 37 P genotypes and, 27 G genotypes have been identified. Among the VP4 genotypes, P[8] accounts for 73.8% of global prevalence of human RVA infections and hence its importance as an effective vaccine candidate. VP4 is a trimeric protein involved in cell attachment and membrane penetration. High-level infectivity requires that VP4 be cleaved by trypsin into two fragments, designated VP8* and VP5*. Five important epitopes have been mapped on the VP8* peptide: M1L10 (aa 1-10), I35R44 (aa 35-44), I55D66 (aa 55-66), V115G123 (aa 115-123) and L223P234 (aa 223-234). A major challenge in immunization is the vast inter- and intragenotypic diversity accomplished by RVA. Two currently available RVA vaccines includes P[8] as an antigenic component. Therefore, it is possible that genetic mutations and antigenic variations on the VP4 gene of P[8] strains will influence the efficacy of the RVA vaccines. The polymorphism of RVA-P[8] strains circulating in Rio de Janeiro between 1996 and 2004 was evaluated. The partial VP4 encoding gene of 20 P[8] strains was sequenced and compared to reference strains. The deduced amino acid sequences were used as basis for in silico analysis of the VP4 protein. We observed the circulation of three major P[8] lineages during the studied period. Comparison between the VP8* trimeric structures of a RVA reference strain (Wa) and Brazilian P[8] strains showed mutations at amino acid residues located at the epitopes I55D66 (aa 64) and V115G123 (aa 120-121). Although the RVA vaccine program has clearly been successful in Brazil, these results suggest the possibility of the emergence of P[8] strains that could evade the immune response elicited by a RVA vaccine and cause a vaccine breakthrough. Consequently, continuous monitoring of RVA intragenotypes diversity is critical to understand how it could affect vaccine effectiveness. Financial support: CAPES, CNPq, FAPERJ

VV316 - NOVEL H1N2 AND H3N2 INFLUENZA A VIRUSES IN SWINE IN BRAZIL

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Influenza A virus (IAV) infection is endemic in swine in Brazil. Previous serological studies have indicated the circulation of H1N1, H3N2 and H1N2 influenza virus subtypes, although no signs of influenza infection was observed in pigs before 2009. This scenario has changed after the onset of pandemic H1N1 influenza virus (pdmH1N1) in pigs in 2009. Since then, outbreaks of mild to moderate respiratory disease have been frequently observed in growing-finishing pigs. We have analyzed 1875 nasal swabs and 86 lung tissue samples collected from pigs from 2009 to 2012. Fifty IAVs were isolated in SPF chicken eggs or in MDCK cells and 25 IAVs were submitted to DNA sequencing. So far, the analysis of the HA, NA and M gene segments showed a high identity and clustered with gene sequences from the pdmH1N1. One H1N2 influenza virus isolated in early 2011 was grouped with samples of influenza viruses of human origin (δ cluster). Seventeen other influenza viruses, isolated from pigs during 2011 and analized by subtype-specific RT-PCR were identified as being of subtypes H1N2 and H3N2. We have detected eight H1N2 influenza viruses and one H3N2 influenza virus, isolated for the first time in pigs in Brazil. Eight virus isolates had or HA or NA not subtyped by RT-PCR (three H1N* and five H*N2). Furthermore, these novel influenza virus isolates have the matrix (M) gene derived from the pdmH1N1, indicating that a reassortment event between endemic influenza viruses and the pdmH1N1 has occurred in pigs in Brazil. More information about the gene segments composition of the novel swine influenza viruses will be available with the whole genome sequencing that is in progress at Embrapa Swine and Poultry. The results generated so far allow us to conclude that influenza A viruses circulating in pigs are in constant evolution leading to the emergence of new virus subtypes. So, the monitoring of pigs is very important to detect changes in influenza viruses over time. Financial support: Embrapa (Process nº. 02.11.10600-01)

VV324 - RT-PCR IDENTIFICATION OF INFECTIOUS MYONECROSIS VIRUS (IMNV) IN FARMED SHRIMP IN THE STATE OF SANTA CATARINA