RESUMO - VETERINÁRIA

ANALYSIS OF THE EIAV P26 GENE AND PROTEIN VARIABILITY

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Equine infectious anemia virus (EIAV) is a retrovirus from genus Lentivirus that affects horses. The transmission of this virus occurs by blood-sucking insects of the genus Tabanidae, ingestion of secretions, excretions and contact with contaminated objects. Infected animals may present three stages of Equine infectious Anemia (EIA): acute, chronic and asymptomatic, with clinical signs varying from mild to death. The viral genome is composed of three main structures: gag, pol and env. The EIAV is a notifiable disease according to the International Animal Health Organization (OIE); in Brazil, euthanasia of infected animals is mandatory, except in the Pantanal region, an endemic area with a specific legislation. The gold standard diagnostic tests for EIA are AGID (Agar Gel Immunodiffusion) and ELISA (Enzyme Linked Immunosorbent Assay), but there are other tests that can contribute to the EIA diagnosis as, for example, viral isolation and molecular methods. However, studies have reported conflicting results between serological and molecular tests. Indications of this divergence may be related to variations in the viral envelope gp90 glycoproteins

and gag p26 proteins. This work aimed to identify the variability of the p26 gene and protein to improve and develop new techniques and also clarify the molecular epidemiology of EIAV at the Pantanal region based on 35 blood plasma from affected horses. These samples were previously submitted to IDGA, ELISA, seminested and real-time PCR (qPCR) tests. Following, 24 samples that presented positive results in serological and molecular tests were grouped separately from the remaining 11 samples which showed negative IDGA and/or ELISA and positive seminested and qPCR results. These two groups were submitted to nucleic acid extraction procedure and amplification of the gag region of the EIAV genomic DNA. After Sanger sequencing, the partial gag sequences were aligned and compared to the reference proteins BRA1 (MN560970) and BRA2 (MN560971). The identity analysis of BRA1 in relation to sequences of this study ranged 86.24% to 93.61%, and BRA2 the variation was 87.66% to 99.57%. Additionally, total of five known p26 protein linear epitopes were then compared based on the aligned amino acid sequences. This analysis showed no significative differences between the epitopes of the two groups of samples, therefore indicating these p26 protein segments are probably not determinant to the discrepancy observed between the serological and molecular tests results in one of the sample groups. So it can be inferred that these epitopes do not contribute to the modification of the protein, and probably other regions may induce some structural modification. Thus, a more detailed study is needed to elucidate the factors that interfere with the alteration of p26.

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