

MOLECULAR CHARACTERIZATION OF IBDV FROM OUTBREAK IN A BROILER FLOCK IN MINAS GERAIS - BRAZIL

**ELLER, M.R.^{3,2}; OLIVEIRA, C. R.^{3,2}; DIAS, C.C.A.^{1,2}; SILVA, E.S.M.^{1,2};
SOUZA, M.B.^{3,2}; OLIVEIRA, F.S.^{3,2}; SANTOS, B.M.^{1,2}; MORAES, M.P.^{1,2}
ALMEIDA, M.R.^{3,2}.**

¹Departamento de Veterinária, UFV, Viçosa/MG; ²Laboratório de Virologia Molecular Animal/BIOAGRO, UFV, Viçosa/MG; ³Departamento de Bioquímica e Biologia Molecular, UFV, Viçosa/MG. marcia@ufv.br

Infectious bursal disease (IBD) has been a great concern for the poultry industry for a long time. Genome sequencing investigations have been used to characterize IBDV strains molecularly, allowing analysis variations that happen naturally or by attenuation in different strains. The aim of this study was to characterize molecularly a hypervariable region of VP2 gene of two strains of IBDV isolated in Minas Gerais State. Total RNA was extracted from IBDV infected bursal tissues samples and RT-PCR reaction was conducted using specific primers to amplify hypervariable parcial region of VP2. The amplified fragment was cloned in pGEM[®] T Easy Vector System and purified in accordance to manufactures recommendations to posterior sequencing. Sequence of VP2 was obtained and compared to twenty-six IBDV sequences retrieved from GeneBank. Alignment was performed with multiple alignment program CLUSTALW 1.8 and phylogenetic analysis were performed with MEGA 3.1 and an unrooted tree was constructed using the distance-based neighbor-joining method and 2000 bootstrap replicates. IBDV strains analyzed were closely related to European and Chinese strains and showed an antigenic variation when compared to vaccine strains, and classical and variant strains described in the U.S.A. Palavras-chaves: IBDV, VP2, phylogenetic analysis.