

Phylogenetic analysis of Infectious Bursal Diseases Virus in South Brazil.

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Infectious bursal disease (IBD) is caused by a virus that is a member of the genus Avibirnavirus of the family Birnaviridae which is one of the most important viral diseases of poultry linked to immunosuppression. In the early nineties a new strain called Very Virulent IBDV (vvIBDV) was isolated in several countries including in Brazil, where this strain caused severe losses for the poultry industry. The aim of this work was to run a phylogenetic analysis of IBDV isolates from four main poultry producers States (Rio Grande do Sul, Santa Catarina, Paraná and Minas Gerais) to determine if the standard strains from the early nineties are in the field in the present days. To achieve this goal all 10 isolates (egg embryo's) from clinical field cases were submitted to RT-PCR, followed by sequencing. From these samples were obtained good quality sequences of seven samples which were analyzed by MEGA 5 software GEN COMP NJ 1000 bootstraps Kimura-2 constructing a tree of the VP2 gene where 2 isolates were grouped with Very Virulent IBDV (A162/09 and A1451/10), but all the others were grouped with the classical and vaccines strains (A3923/10, A-296/11, A453/11, A3600/10 and 3892/10). These results indicate that very virulent strains of IBDV are still circulating in Brazilian flocks and the vaccination strategies of breeders and chicks are fundamental for the control of the disease. The strains grouped as classical or vaccine strains, might be the vaccine virus because these flocks were vaccinated with IBDV, even though the isolation has been performed from clinical cases.

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