PHYLOGENETIC ANALYSIS OF ISOLATES OF AVIAN INFECTIOUS BRONCHITIS VIRUS (IBV) IN BRAZIL BASED ON THE 3'-TERMINAL SEQUENCE OF THE NUCLEOPROTEIN GENE

(ANÁLISE FILOGENÉTICA DE ISOLADOS DO VÍRUS DA BRONQUITE INFECCIOSA AVIÁRIA (VBI) NO BRASIL COM BASE NA SEQUÊNCIA 3'-TERMINAL DO GENE DA NUCLEOPROTEÍNA)

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Infectious bronchitis is caused by IBV, which is classified in the genus *Gammacoronavirus,* Family *Coronaviridae*. This disease is distributed worldwide and stands as one of the most important health problems for the poultry industry. Recently, researchers in Brazil have identified a large number of IBV variants, the phylogenetic analysis based on the S1 gene shows that they differ from the American, European, Asian and Australian strains. However, little research has been conducted about other encoding genes of important proteins such as the nucleoprotein (N), which is a key factor in replication and assembly processes of new viral particles, and contains epitopes important for interaction with T and B cells. The aim of this study was to determine the 3'-terminal sequences of the N protein gene isolated from IBV in Brazil and compare them with those of IBV strains from other regions of the world. So, 15 IBV isolates obtained from 1988 to 2000, during outbreaks of Infectious Bronchitis (IB) in broilers or laying birds in Southern and Southeastern Brazil, were submitted to molecular analysis. Phylogenetic analysis of partial sequences of the N gene resulted in the separation of the 15 Brazilian IBV isolates in five different groups while three of these groups are related to strains of the Massachusetts genotypes, whereas the other two groups are associated with the Connecticut genotypes or a Brazilian variant. These genotypic groups mostly coincided with those previously determined by phylogenetic analysis based on the S1 gene. In conclusion, the phylogenetic analysis of the N gene can differentiate Brazilian strains of IBV and evaluate its development, especially in cases where the S1 gene amplification is more difficult due to wide variability between different IBV strains.

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