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Molecular characterization of infectious bronchitis virus

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Infectious bronchitis virus (IB) is an acute, highly contagious respiratory and urogenital disease of chickens. It is very significant to the economic importance to the poultry industry. IB is of economic important because it is a cause of poor weight gain and feed efficiency, also a component of mixed infection that produce air-sacculitis resulting in condemnations of broilers at processing (King and Cavanagh, 1991). IBV is the type species of the family *Coronaviridae* (Cavanagh *et al*., 1994 ; Siddel *et al*., 1983). It is envelope, about 120nm in diameter and contains a non-segmented positive-stranded RNA genome (Cavanagh, 1995). It possesses prominent surface spikes and has 3 major structural proteins ; the spike (S) glycoprotein, the small integral membrane (M) glycoprotein and nucleocapsid (N) protein. The main objectives of this study are diagnosis IBV by RT-PCR, differentiation of IBV isolate and sequencing of the S1 region. One-step and the two-step RT-PCR technique with two kind of RT-enzyme ; AMV reverse transcriptase and Superscript II™ reverse transcriptase enzyme were used to amplify the particular gene region by using universal and designed primers. This study conducted to screen IBV isolates from year 1991 until 2003 obtained from MDPJ, MVP and VRI for vaccine strain namely Massachusetts (M41) serotype and the positive Massachusetts was no further work to carry out. Otherwise, the non-Massachusetts were amplified by using RT-PCR-RFLP to screen for nephropathogenic strain for obtained new isolates that was non-Massachusetts and non-nephropathogenic strain. Out of 30 isolates, all was shown positive for IBV and nine are found to be of Mass serotype analyzed from agarose gel electrophoresis. Based on RT-PCR-RFLP, only one was suspected neither Mass nor nephropathogenic serotypes and was cloned and sequenced for S1 region.