

Genome Sequencing of Infectious Bronchitis Virus QX-Like Strain Isolated in Malaysia

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Abstract : Respiratory diseases are the most important infectious diseases affecting poultry worldwide. One of the avian respiratory virus of global importance causing significant economic losses is Infectious Bronchitis Virus (IBV). The virus causes a wide spectrum disease known as Infectious Bronchitis (IB), affecting not only the respiratory system but also the kidney and the reproductive system, depending on its strain. IB and Newcastle disease are two of the most prevalent diseases affecting poultry in Malaysia. However, a study on the molecular characterization of Malaysian IBV is lacking. In this study, an IBV strain IBS130 which was isolated in 2015 was fully sequenced using next-generation sequencing approach. Sequence analysis of IBS130 based on the complete genome, polyprotein 1ab and S1 genes were compared with other IBV sequences available in Genbank, National Center for Biotechnology Information (NCBI). IBV strain IBS130 is characterised as QX-like strain based on whole genome and S1 gene sequence analysis. Comparisons of the virus with other IBV strains showed that the nucleotide identity ranged from 67% to 99.2%, depending on the region analysed. The similarity in whole genome nucleotide ranging from 84.9% to 90.7% with the least similar was from Singapore strains (84.9%) and highly similar with China QX-like strains. Meanwhile, the similarity in polyprotein 1ab ranging from 85.3% to 89.9% with the least similar to Singapore strains (85.3%) and highly similar with Mass strains from USA.

Keywords : infectious bronchitis virus, phylogenetic analysis, chicken, Malaysia

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