

**Characterization of S1 gene sequence variations of attenuated QX-like and variant infectious bronchitis virus strains and the pathogenicity of the viruses in specific-pathogen-free chickens**

**ABSTRACT**

Besides the vaccine strains, the Malaysian variant (MV) and QX-like are the predominant IBVs detected on commercial poultry farms. These two virus strains are distinct based on genomic and pathogenicity studies. In this study, we determined the sequence of the S1 gene and compared the pathogenicity of serial passage 70 (P70) of Malaysian QX-like (QX/P70) and MV (MV/P70) strains with that of their respective wild-type viruses. The nucleotide and amino acid sequences of the complete S1 genes of QX/P70 and MV/P70 showed 1.4 to 1.6% and 3.0 to 3.3% variation, respectively, when compared to the wild-type virus. Most of the mutations were insertions and substitutions in the hypervariable regions (HVRs), primarily in HVR 3. Furthermore, selection pressure analysis showed that both viruses are under purifying selection. A pathogenicity study in specific-pathogen-free (SPF) chickens showed a reduction in respiratory and kidney lesions in chickens inoculated with MV/P70, but not with QX/P70, when compared to the respective wild-type viruses. However, MV/P70 is still pathogenic and can cause ciliary damage. In conclusion, the MV IBV strain is more responsive than the QX-like IBV strain following the attenuation process used for the development of a live attenuated IBV vaccine.