

Heterogeneity of Genes Encoding the Structural Proteins of Avian Infectious Bronchitis Virus

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Abstract : Infectious bronchitis is an acute, highly contagious respiratory, nephropathogenic and reproductive disease of poultry that is caused by infectious bronchitis virus (IBV). The present study used a large data set of structural gene sequences, including newly generated ones and sequences available in the GenBank database to further analyze the diversity and to identify selective pressures and recombination spots. There were some deletions or insertions in the analyzed regions in isolates of the Italy-02 and D274 genotypes. Whereas, there were no insertions or deletions observed in the isolates of the Massachusetts and 4/91 genotype. The hypervariable nucleotide sequence regions spanned positions 152-239, 554-582, 686-737 and 802-912 in the S1 sub-unit of the all analyzed genotypes. The nucleotide sequence data of the E gene showed that this gene was comparatively unstable and subjected to a high frequency of mutations. The M gene showed substitutions consistently distributed except for a region between nucleotide positions 250-680 that remained conserved. The lowest variation in the nucleotide sequences of ORF5a was observed in the isolates of the D274 genotype. While, ORF5b and N gene sequences showed highly conserved regions and were less subjected to variation. Genes ORF3a, ORF3b, M, ORF5a, ORF5b and N presented negative selective pressure among the analyzed isolates. However, some regions of the ORFs showed favorable selective pressure(s). The S1 and E proteins were subjected to a high rate of mutational substitutions and non-synonymous amino acids. Strong signals of recombination breakpoints and ending break point were observed in the S and N genes. Overall, the results of this study revealed that very likely the strong selective pressures in E, M and the high frequency of substitutions in the S gene can probably be considered the main determinants in the evolution of IBV.

Keywords : IBV, avian infectious bronchitis, structural genes, genotypes, genetic diversity

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