

# **Infectious Bronchitis Virus (Gamma coronavirus) in Poultry: Genomic Architecture, Post-Translational Modifications, and Structural Motifs**

## **ABSTRACT**

Infectious bronchitis virus (IBV) is an avian coronavirus (CoV) that belongs to the genus Gamma coronavirus and has been listed as an important disease by the World Organization for Animal Health (WOAH). It causes highly contagious respiratory, reproductive, and renal diseases in commercial poultry farms. Multiple IBV serotypes and genotypes have been identified in many countries and many detected variants do not provide cross-protection against infection, resulting in repeated outbreaks and significant economic losses worldwide. In addition, the high genetic mutations and recombination events in the prominent genomic regions of IBV, particularly in the spike glycoprotein (S) and nucleocapsid (N) proteins, are directly involved in the evolutionary processes of IBV and lead to increased pathogenicity and tissue tropism. The characterization of the different genotypes and the relationship between the structure, function, post-translational modifications (PTMs), and structural motifs will elucidate the mechanisms that promote replication and pathogenicity and affect the host's immune response during infection. In this review, we discuss the molecular features of various IBV genes and proteins that contribute to the infection process. We also highlight the common PTMs and structural motifs that occur during protein synthesis and are essential components of IBV ecology.