Genetic Diversity and Evolution of Infectious Bronchitis Virus in Southern Thailand: Dominance of QX-like (GI-19) and Emergence of GI-19/GI-7 Recombinants (2014-2025)

Pattaramon Suanin[1,*], Sasiwimol Thongmee[1], Nusara Pathan[1], Wongkae Watjiranon[1], Khanistar Rattanaburee[1], Khwansanee Suknao[1], Gamonsiri Bhumibhamon[1] and Wandee Kongkaew[1]

Abstract

Background: Avian infectious bronchitis virus (IBV) poses a continuous threat to the poultry industry due to its rapid evolution. High mutation rates, particularly within the S1 gene, drive significant genetic diversity, leading to the emergence of new variants and potential vaccine failure. Previous studies (2008-2016) identified the QX-like lineage (GI-19) as the predominant genotype in Thailand since 2009, co-circulating with 4/91-like (GI-13), Massachusetts (GI-1), and vaccine-related strains.

Objectives: This study aimed to characterize the genetic diversity and phylogenetic relationships of IBV isolates collected from chickens in Southern Thailand between 2014 and 2025 using partial S1 gene analysis.

Methods: Viral RNA was extracted from 12 confirmed IBV clinical cases. Partial S1 gene fragments (980 and 1065 bp) were amplified via reverse transcription polymerase chain reaction (RT-PCR). Phylogenetic trees were constructed using MEGA software (v.12) to determine lineage classification. Potential recombination events were further analyzed and confirmed using RDP software (v.5).

Results: Phylogenetic analysis revealed that the QX-like lineage (GI-19) remained predominant, accounting for 9 out of 12 isolates. Other isolates were identified as 4/91-like (GI-13) and DLD vaccine-like strains. Notably, one isolate showed discordant phylogenetic clustering and was confirmed as a GI-19/GI-7 recombinant. Most genotype assignments were supported by high bootstrap values.

Conclusion: The QX-like (GI-19) genotype remains the predominant IBV strain circulating in Southern Thailand. The identification of a novel GI-19/GI-7 recombinant underscores the high genetic diversity and ongoing evolution of IBV in the region. These findings emphasize the necessity of continuous molecular surveillance. Furthermore, the combined analysis of 980 and 1065 bp S1 fragments proved highly effective for accurate genotyping and recombination detection.

Keywords: Avian infectious bronchitis virus, S1 gene, GI-19 (QX-like), GI-19/GI-7 recombinant, Molecular epidemiology

[1] Veterinary Research and Development Center (Upper Southern Region), Nakhon Si Thammarat, Thailand
[*] Corresponding author; E-mail: cogygift@gmail.com