The Evolutionary Landscape and Serotypic Dynamics of Avian Infectious Bronchitis Virus from Spike Protein

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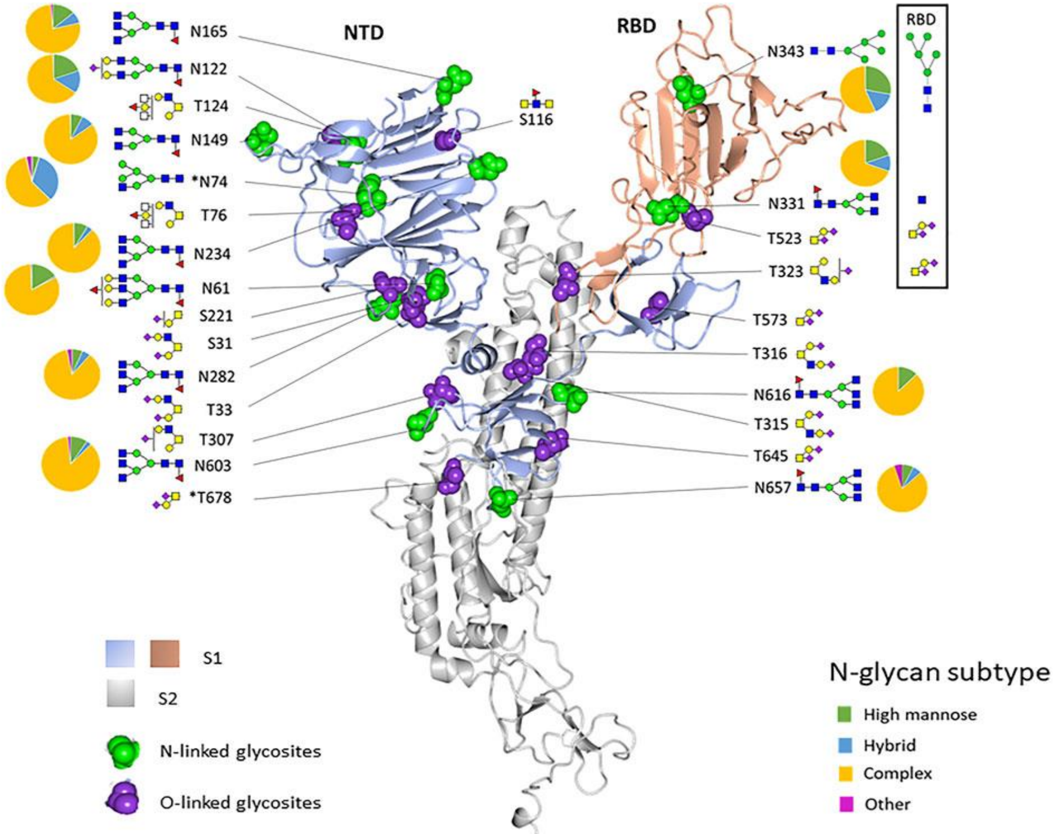
Background

- **Infectious bronchitis (IB)**
- **A highly contagious disease**

It is especially severe in chicks, leading to high mortality rates, and in laying hens, resulting in reduced egg quality.

IBV exhibits rapid mutation and numerous serotypes. Vaccination shows limited efficacy, and no effective drugs are currently available, highlighting the urgent need for novel control strategies.

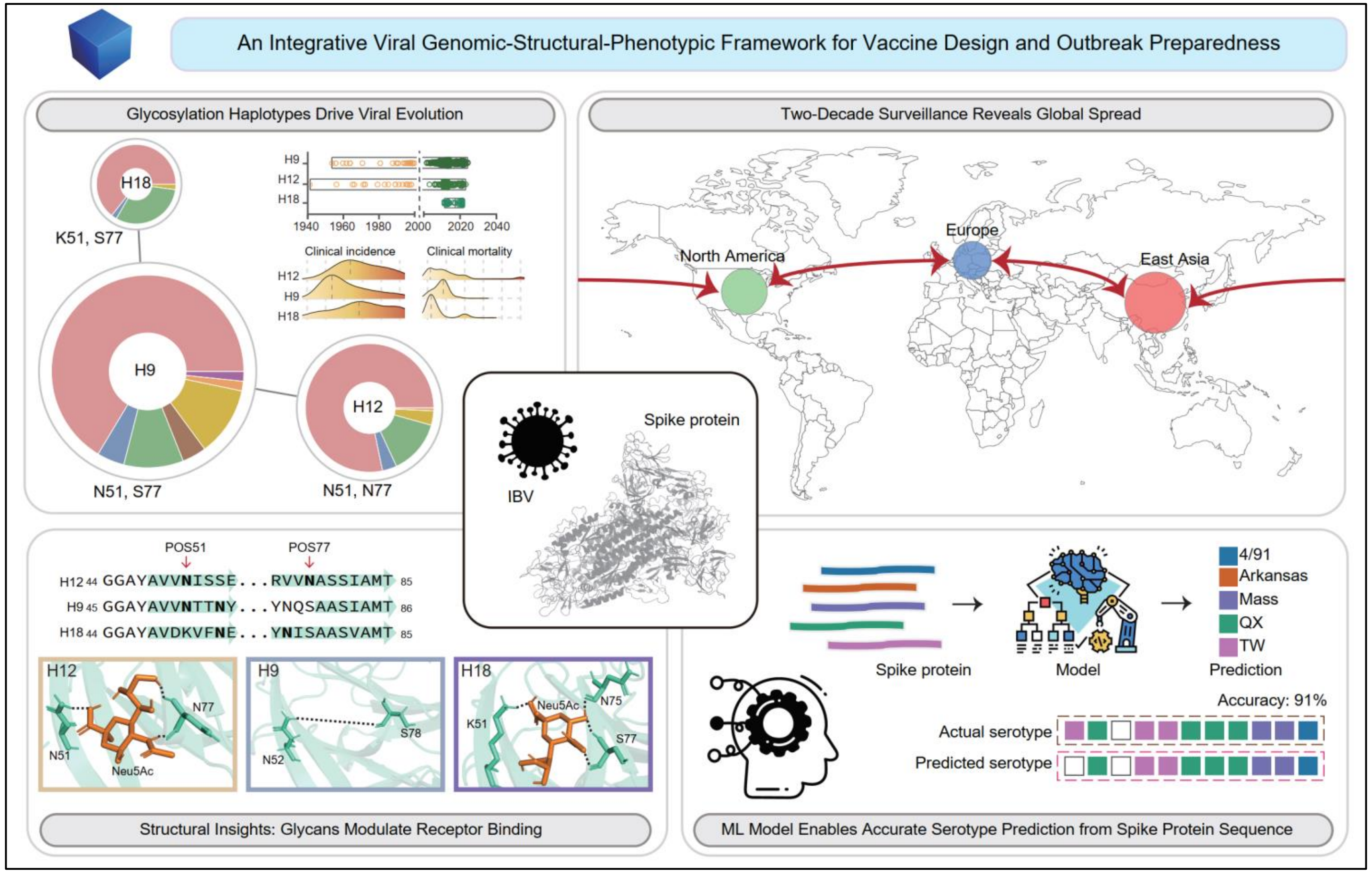
It poses a serious threat to the global poultry industry.



(Tian et al., 2023)

N-glycosylation of the S protein may mask antigenic epitopes and modulate receptor binding. However, the evolutionary dynamics of S protein N glycosylation in IBV and its association with viral clinical phenotype and transmission remain unclear.

Highlights



- Epidemiological surveillance and evolutionary analysis reveal the complex spatiotemporal transmission dynamics of avian infectious bronchitis virus (IBV) across the whole world.
- Key spike protein glycosylation haplotypes are associated with receptor-binding specificity and are linked to distinct clinical outcomes.
- Glycosylation motifs serve as structural-genomic markers, offering a scalable framework for predicting coronavirus evolution and spread.
- Spike protein-based machine learning method enables reliable prediction of IBV serotypes.

Epidemic of avian viruses in China during the last two decades (2003-2023)

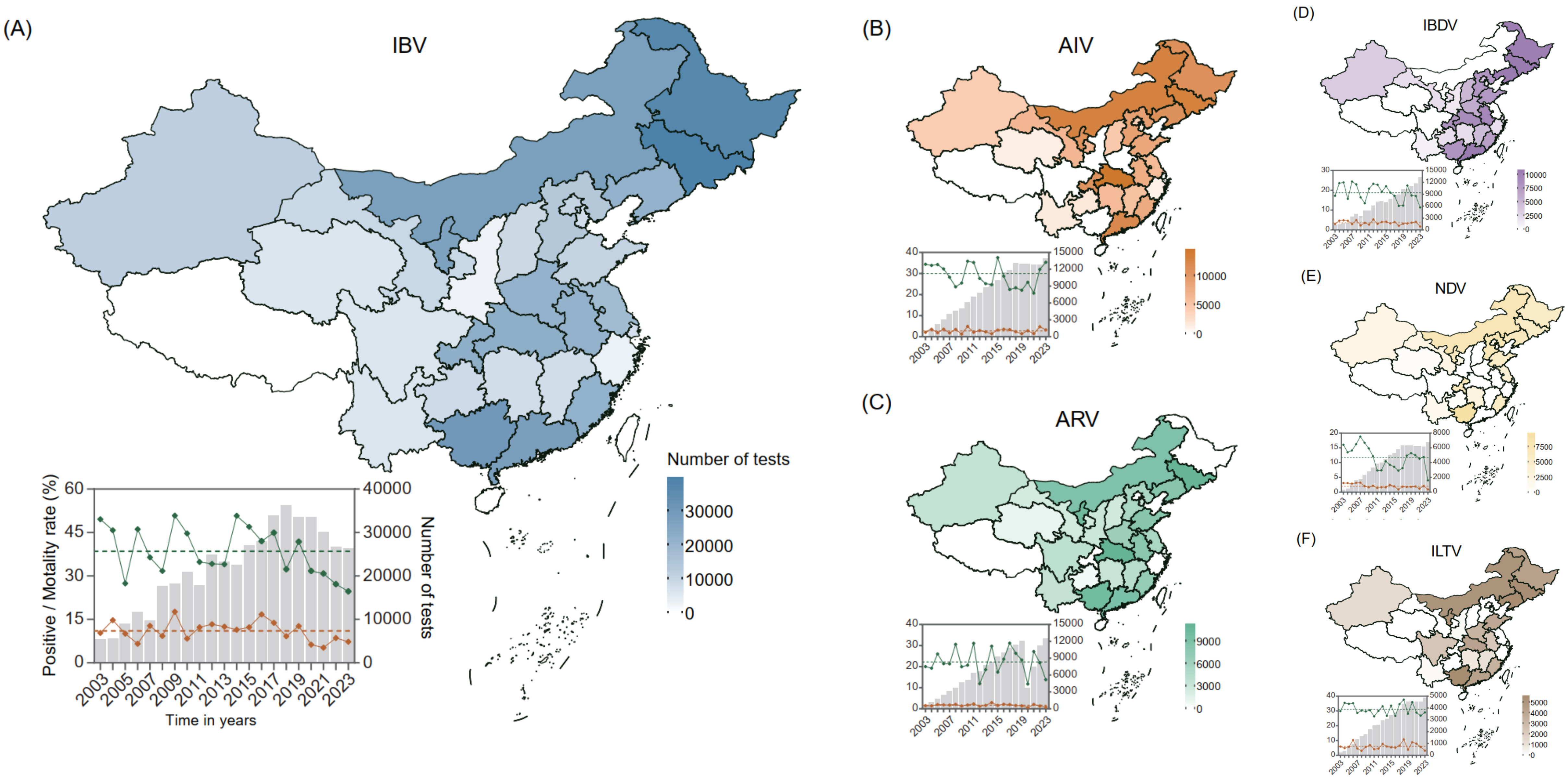


Figure 1 Spatiotemporal patterns of major avian viral pathogens in China, 2003–2023.

Complex phylogeny, homology, and evolutionary dynamics of IBV strains

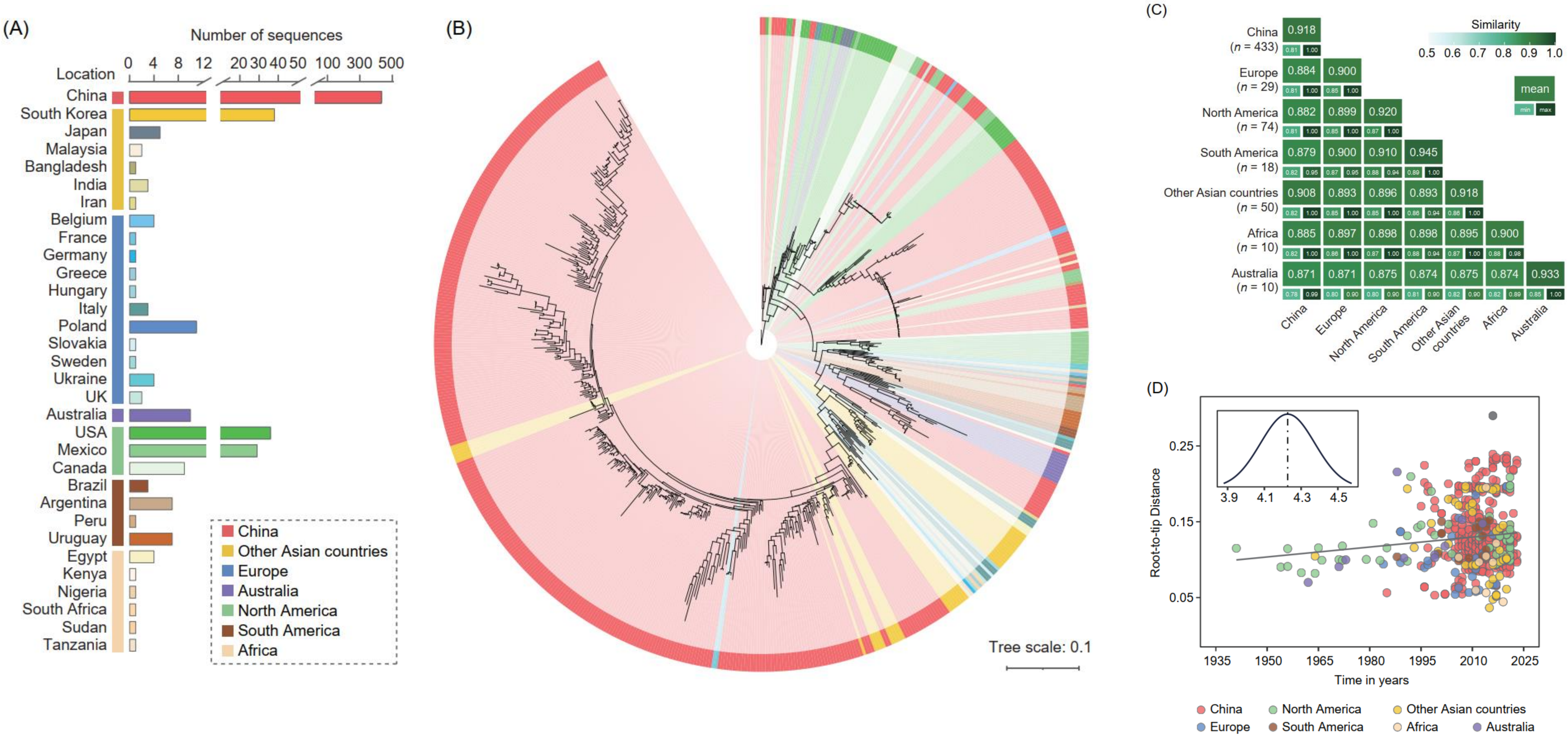


Figure 2 Global genetic diversity and evolutionary dynamics of IBV.

Haplotype dynamics of N-glycosylated sites within the spike (S) protein

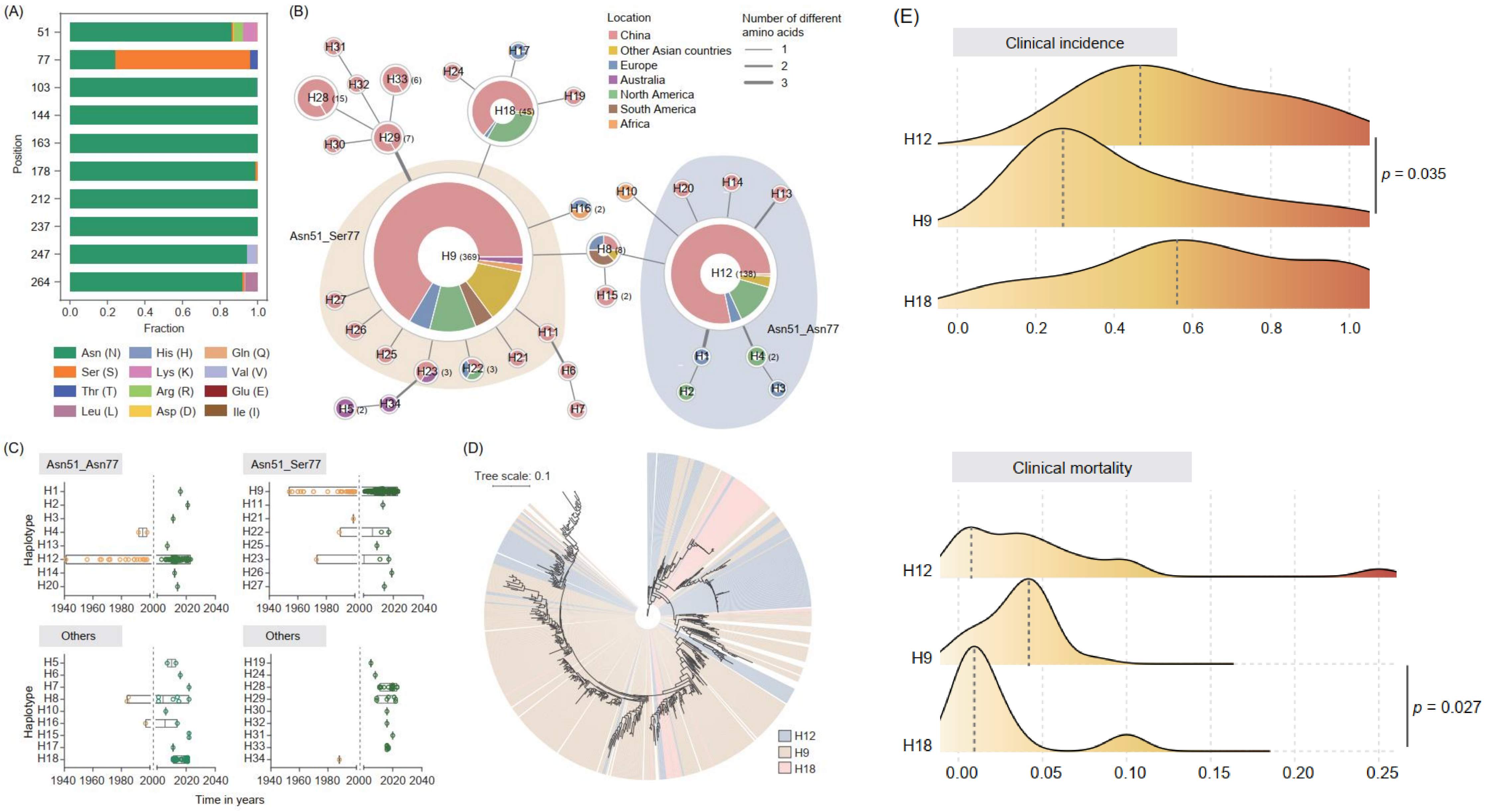


Figure 3 Evolutionary diversification of N-linked glycosylation haplotypes in the NTD of IBV S protein.

The N-glycosylation substitutions alter the docking of N-acetylneuraminic acid

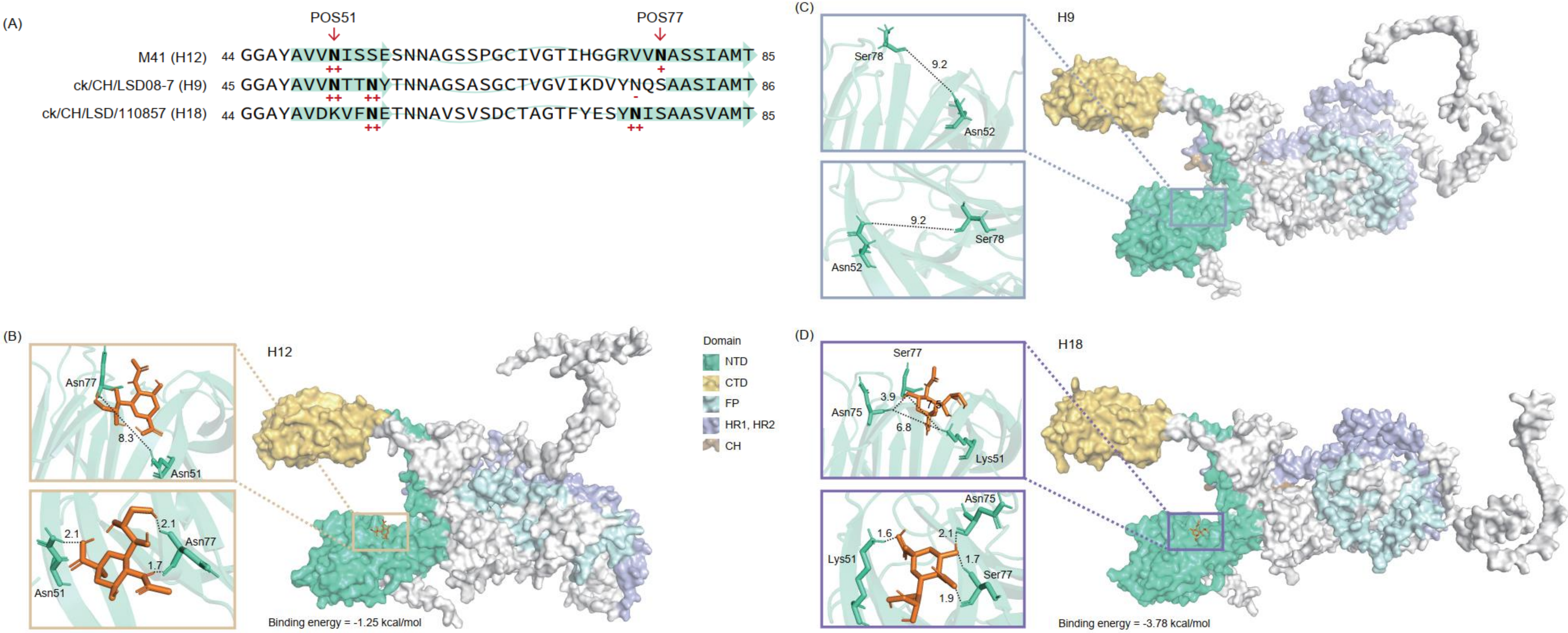


Figure 4 Structural insights into N-glycosylation-mediated modulation of receptor binding in IBV S NTD haplotypes.

Spatiotemporal reconstruction of IBV dissemination across the world

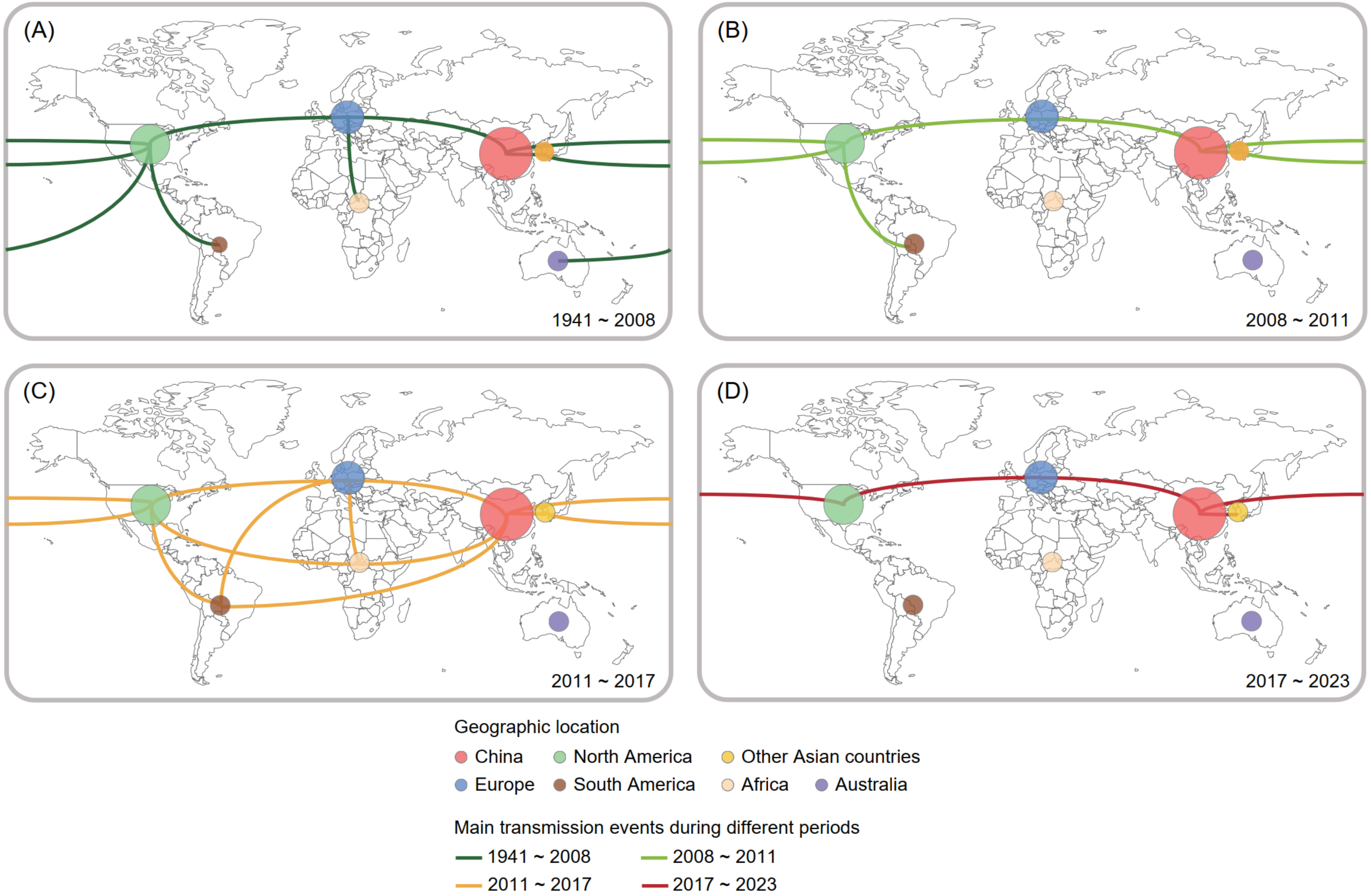


Figure 5 Spatiotemporal dissemination of IBV Strains globally.

Machine learning (ML)-based IBV serotype model construction and validation

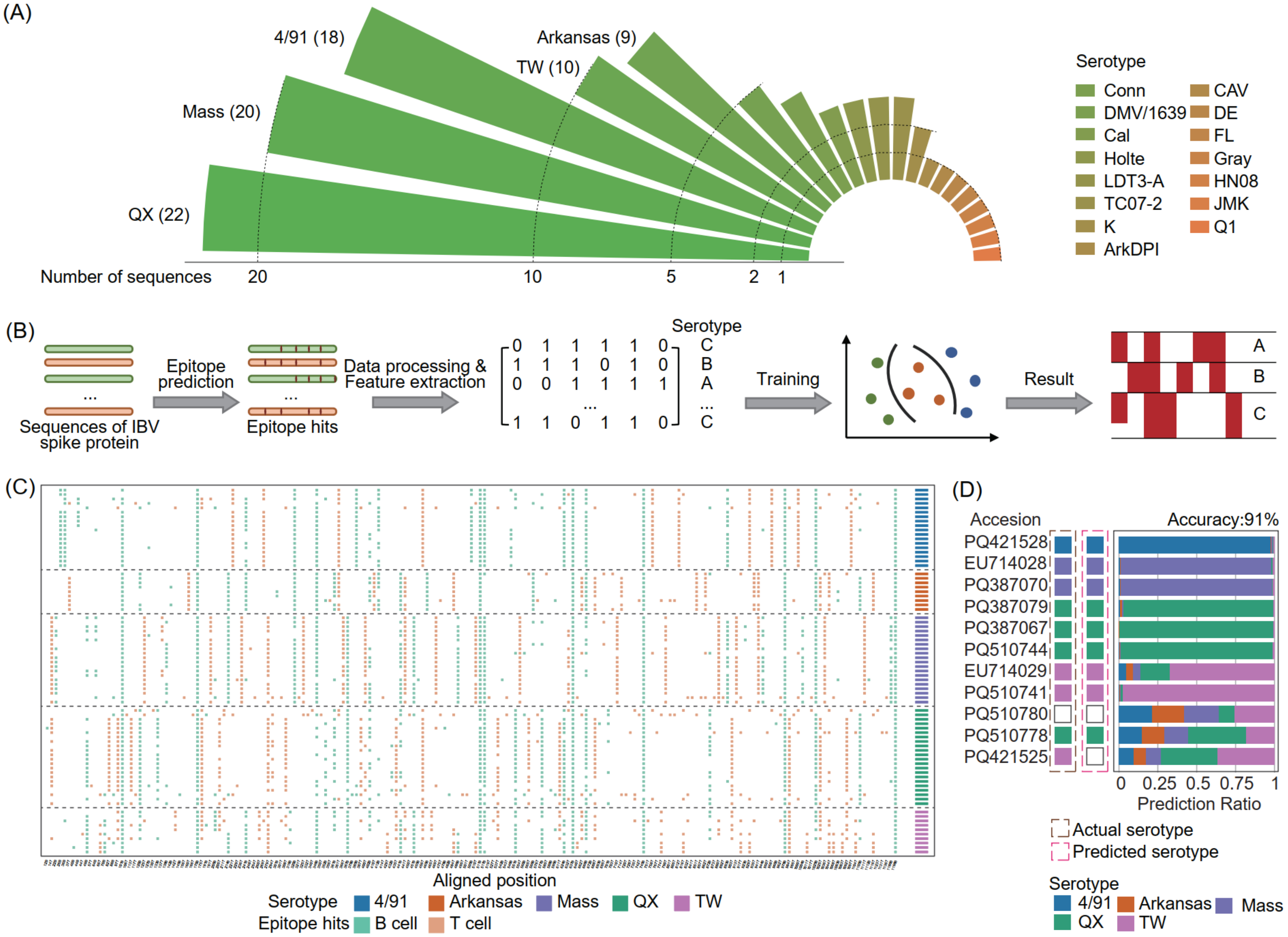


Figure 6 Machine learning models elucidating the relationship between viral sequences and their corresponding serotypes.

Summary

- ❑ By integrating genomics, structural biology, and machine learning, this work constructs a predictive framework for coronavirus evolution.
- ❑ We demonstrate that glycosylation haplotypes in the spike protein serve as evolutionary and epidemiological markers, may contribute to receptor binding, clinical severity, and transmission.
- ❑ Our computational model enables highly reliable serotype prediction directly from viral sequence data.

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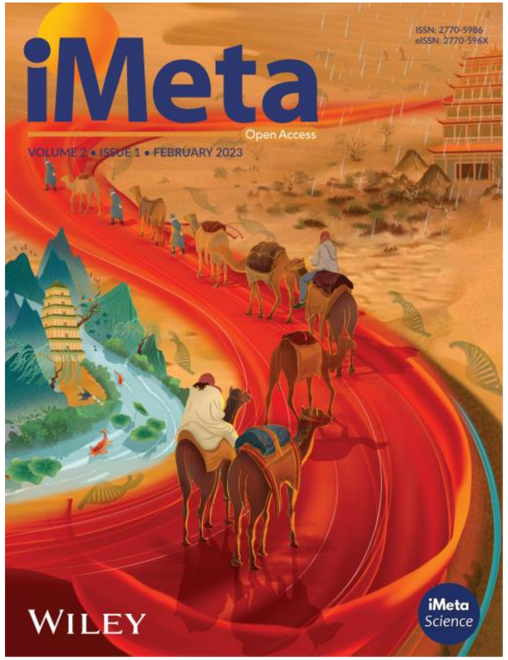

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