

Molecular reconstruction of Newcastle disease history in Nigeria

Since its first records in the 1950s in West Africa, Newcastle disease virus (NDV) has been the target of several surveillance campaigns that have provided large datasets of samples. In order to understand the transmission dynamics of NDV in the region, better knowledge of the temporal and the spatial evolution of the virus and their association with poultry trade is needed.

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Methods

We analysed the phylogenetic relationship among African NDV samples. We combined spatial and genetic analyses using Bayesian stochastic search variable selection (BSSVS) procedure to identify most likely virus transmission pathways in the Nigerian region. These diffusion pathways were compared with national commercial poultry networks.

Results

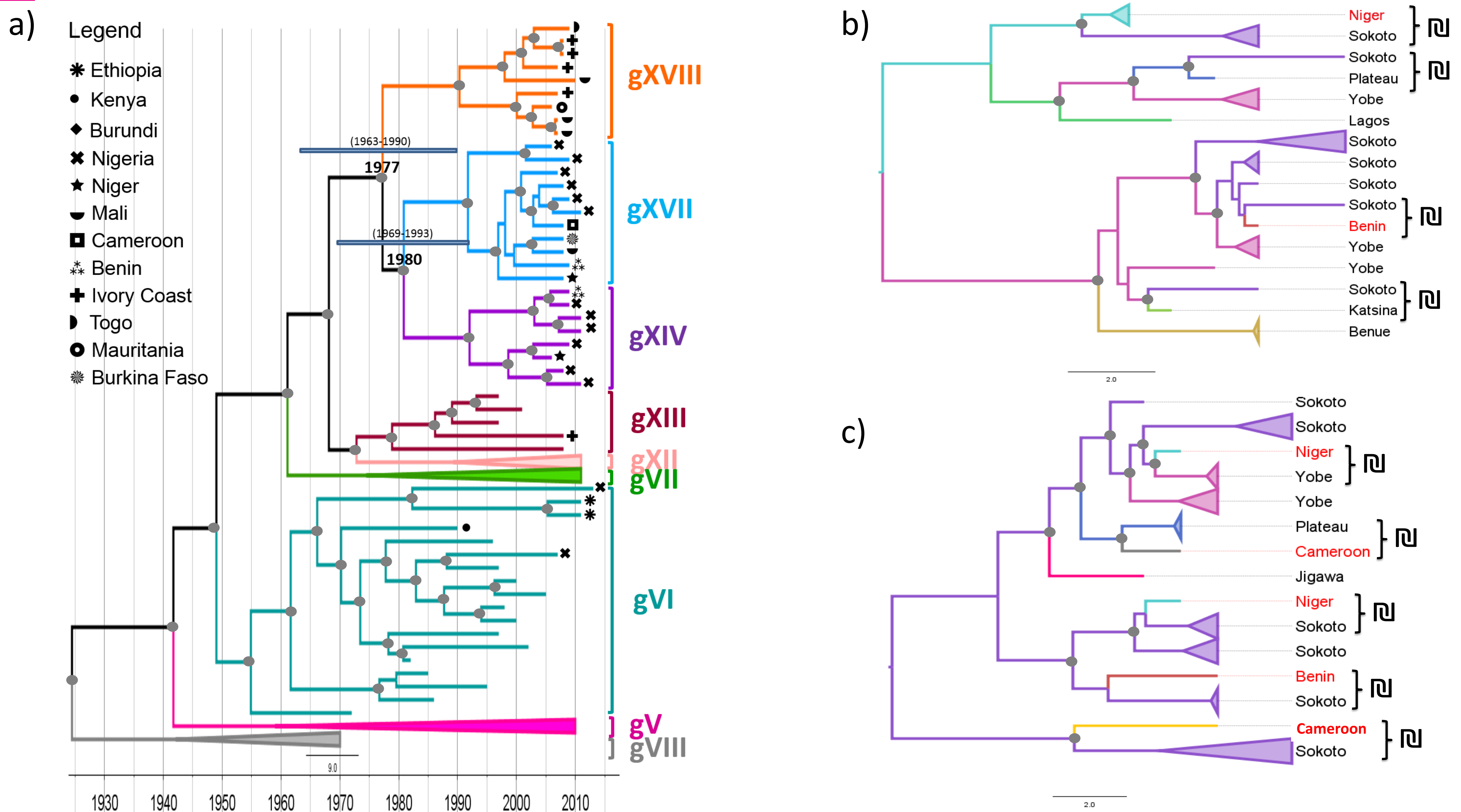


Fig 1: Phylogenetic trees of complete fusion protein gene representing the most recent genotypes (a), the genotypes XIV (b) and XVII (c) of NDV. Nodes with posterior probability support above 0.70 are indicated with (●).

The genotypes XIV, XVII and XVIII, exclusively found in West and Central Africa, were closely related, with a common ancestor placed in late 1970's.

The phylogeny revealed transmission pathways (⌞) of NDV between Nigeria and neighbouring countries and among Nigerian states.

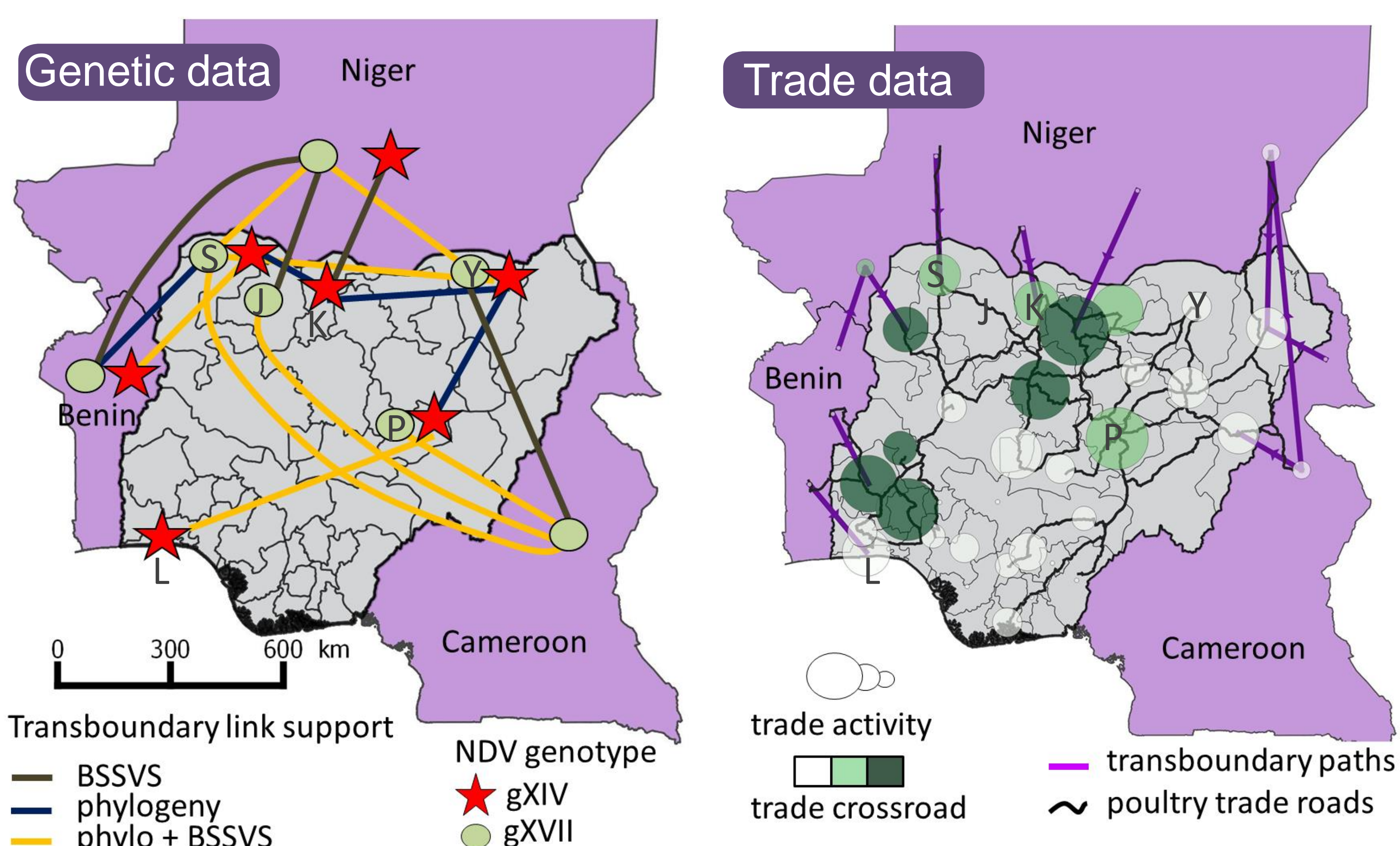


Fig 3: Comparison of NDV phylogenetic data with major poultry movement in between Nigeria and neighbouring countries and among Nigerian states (J= Jigawa, K=Katsina, L=Lagos, P=Plateau, S=Sokoto, Y=Yobe)

Most transmission pathways were confirmed by BSSVS and a strong correlation between these pathways and the commercial poultry networks linking West Africa countries and into Nigerian states, was denoted.

CONCLUSION

West Africa hosts a complex group of endemic NDV strains. Evolution and phylodynamics of these strains appears closely associated with poultry trade. More thorough sampling and phylogenetic analyses can help improve regional NDV control effort.

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