

Enhancing Animal Disease Surveillance with Virus Sequences and Phylodynamics

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Introduction

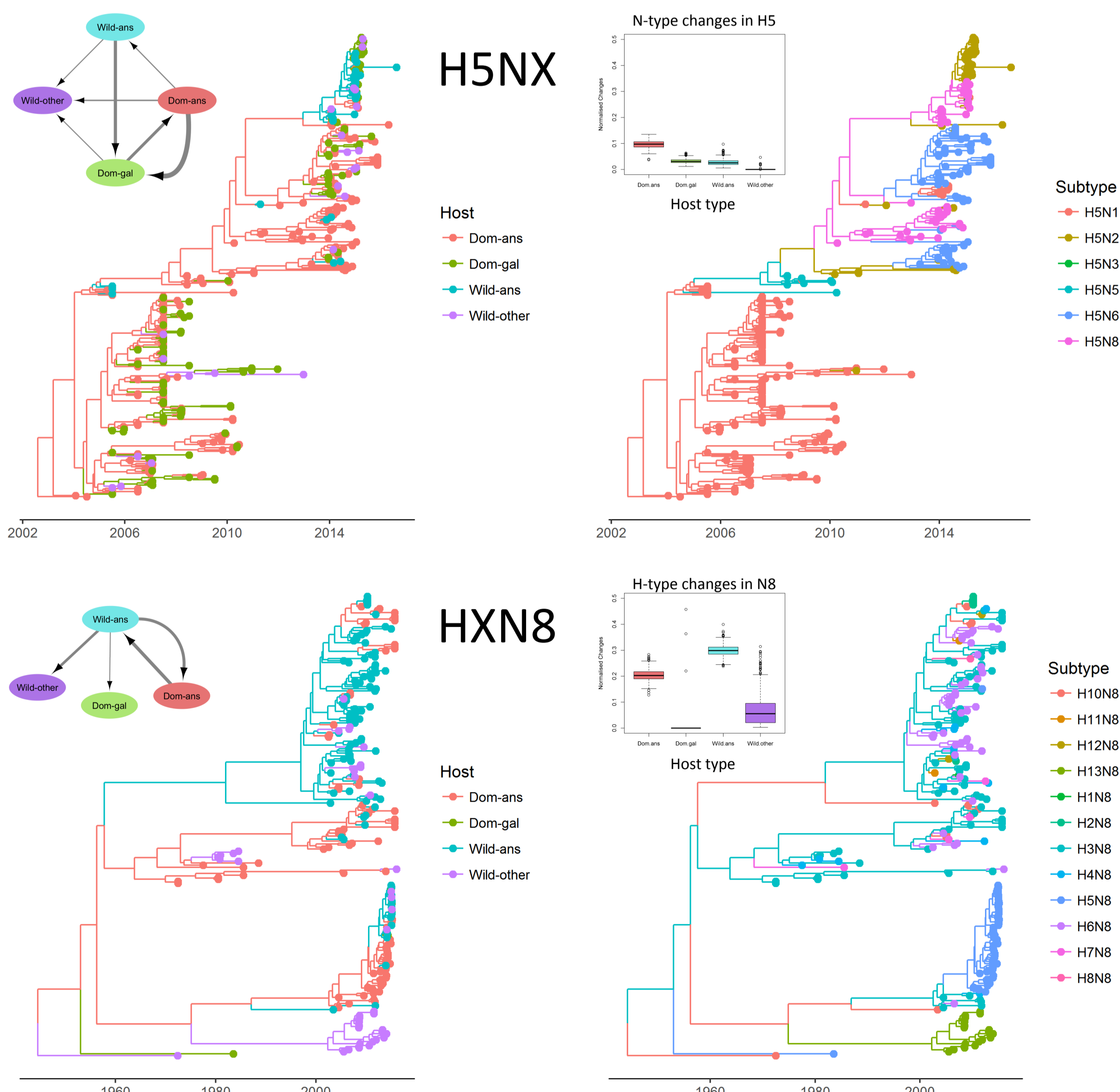
- Virus genomes accumulate mutations over time
- Sequences have detailed information on subtype; markers for virulence, host adaptation and drug resistance
- Sequences used to track infections in populations

Phylodynamic and Phylogeographic Methods

- Whole genome, individual genes or variable regions can be used to infer set of phylogenetic trees
- Molecular clock signal provides time scale
- Model discrete or continuous traits on the trees to infer ancestral states and pattern of who infected whom

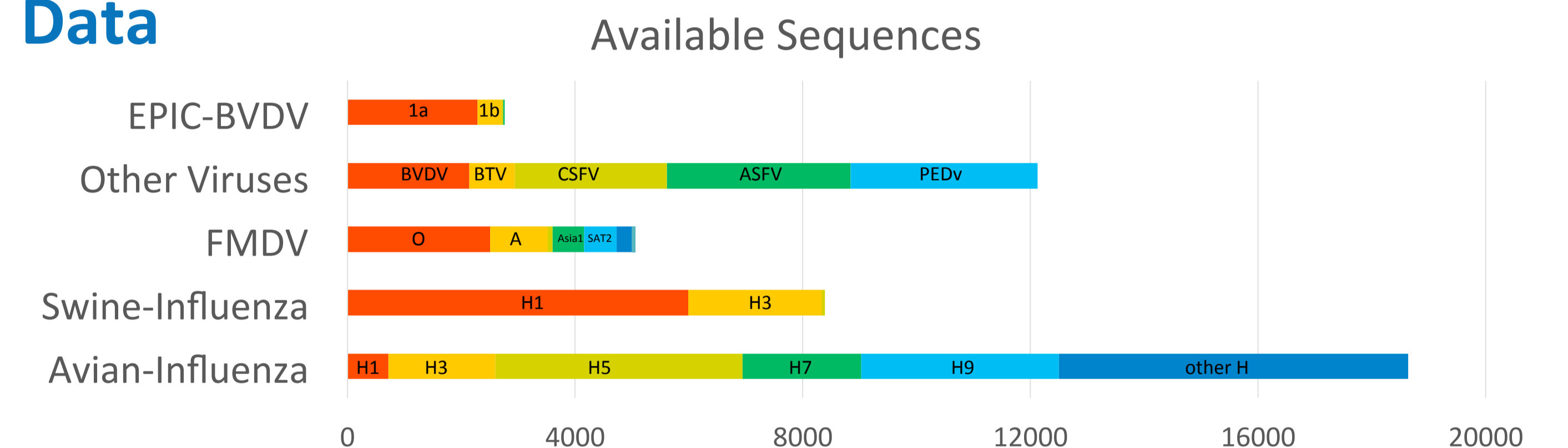
Reassortments and cross species transmissions Avian Influenza Virus

- Trees of Highly pathogenic H5N8/X Hemagglutinin and corresponding HXN8 Neuraminidase
- Use Host and Subtype discrete trait models



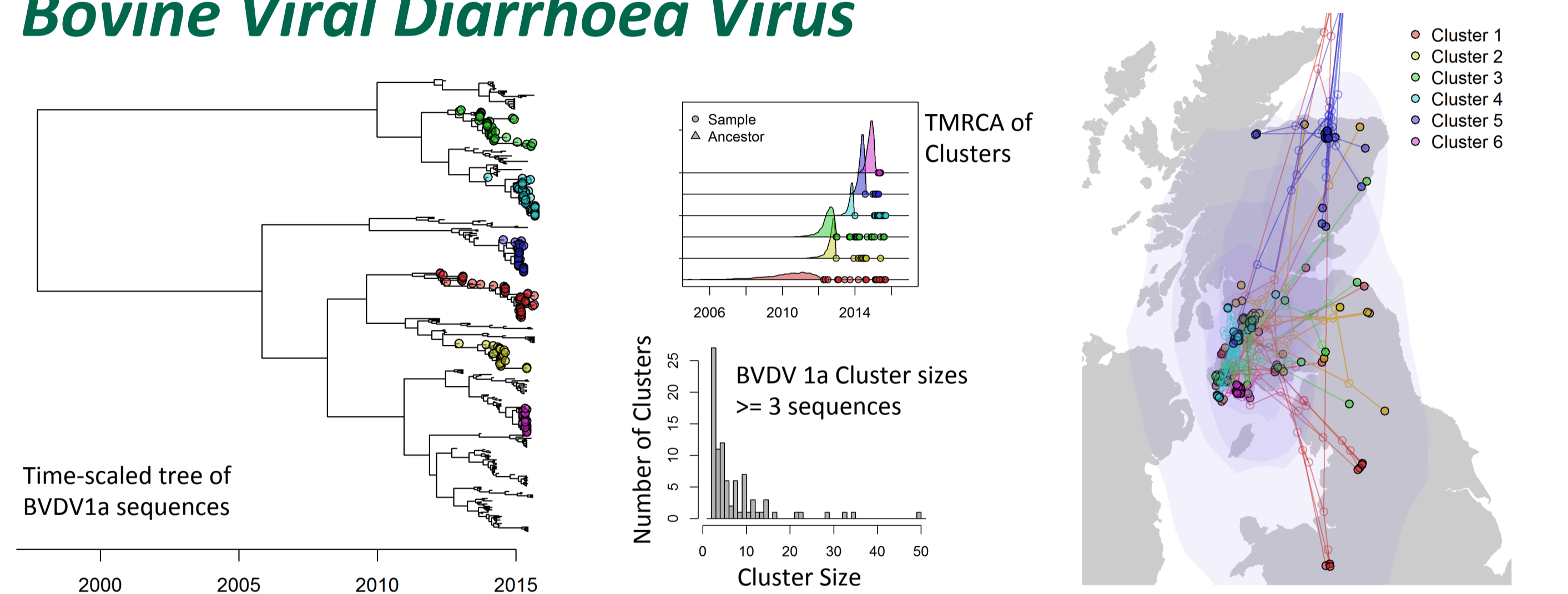
- Two way transmission: domestic and wild populations
- Rapid reassortment for low pathogenic strains in wild populations
- Domestic ducks and geese responsible for reassortment of highly pathogenic strains

Data



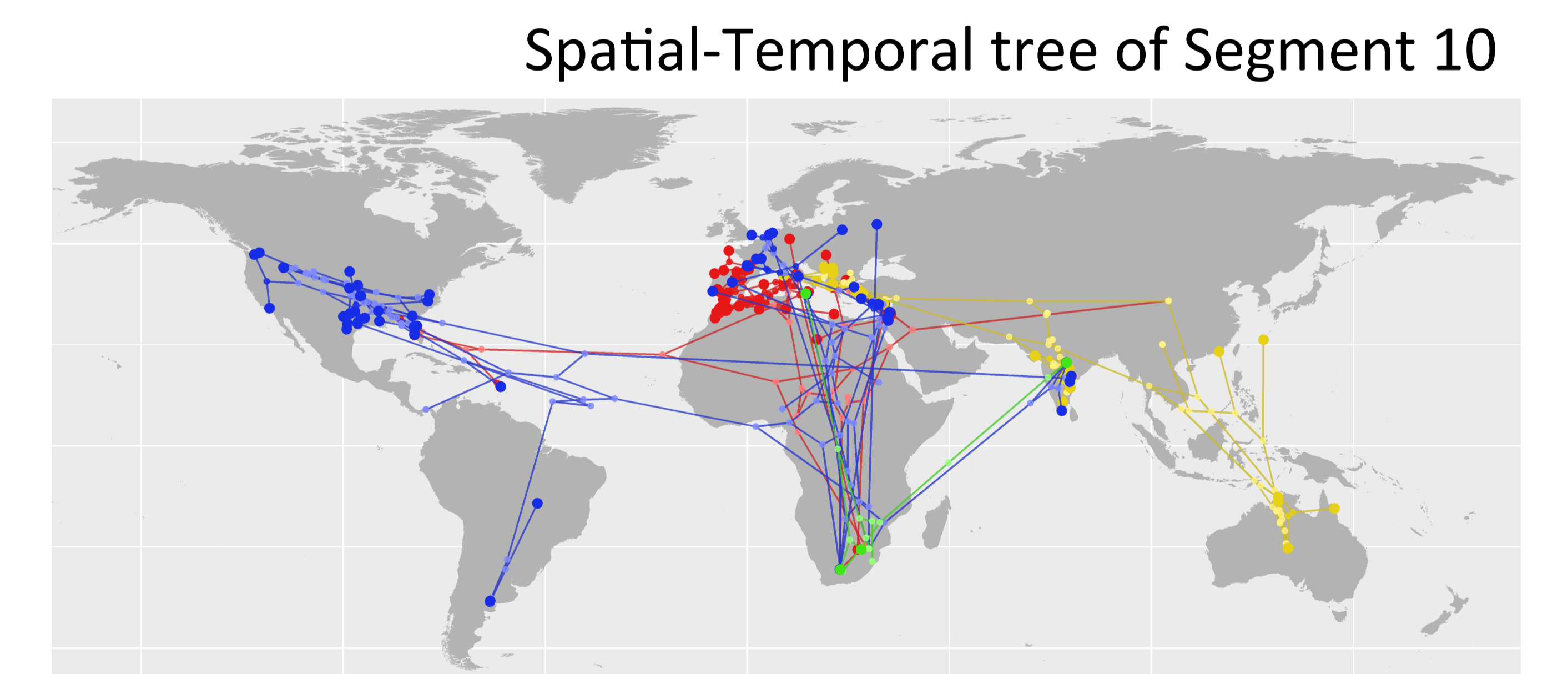
- Publically available virus sequences on GenBank
- EPIC BVDV sequences generated from GB samples submitted for routine testing

Similar sequences imply recent transmission Bovine Viral Diarrhoea Virus



- 1000+ BVDV1a 5'UTR with postcodes and dates
- Clusters of 5'UTR sequences with genetic distance 0
- Big clusters ≥ 20 sequences are spatially distributed, implying transmission via infected animal movements

Global Spread and Incursions Bluetongue Virus



- Tree of internal protein coding gene of BTV
- Widespread reassortment in BTV, similar to influenza
- Four main clusters for internal protein coding segment, regardless of subtype
- Spatial coordinates modelled as continuous traits
- Transmission routes: African-Europe, Asian-Europe and American
- Long range transmissions due to international trade