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Phylogeographic Diffusion and Host Dynamics of HPAI H5Nx Virus Clade 2.3.4.4b in Europe



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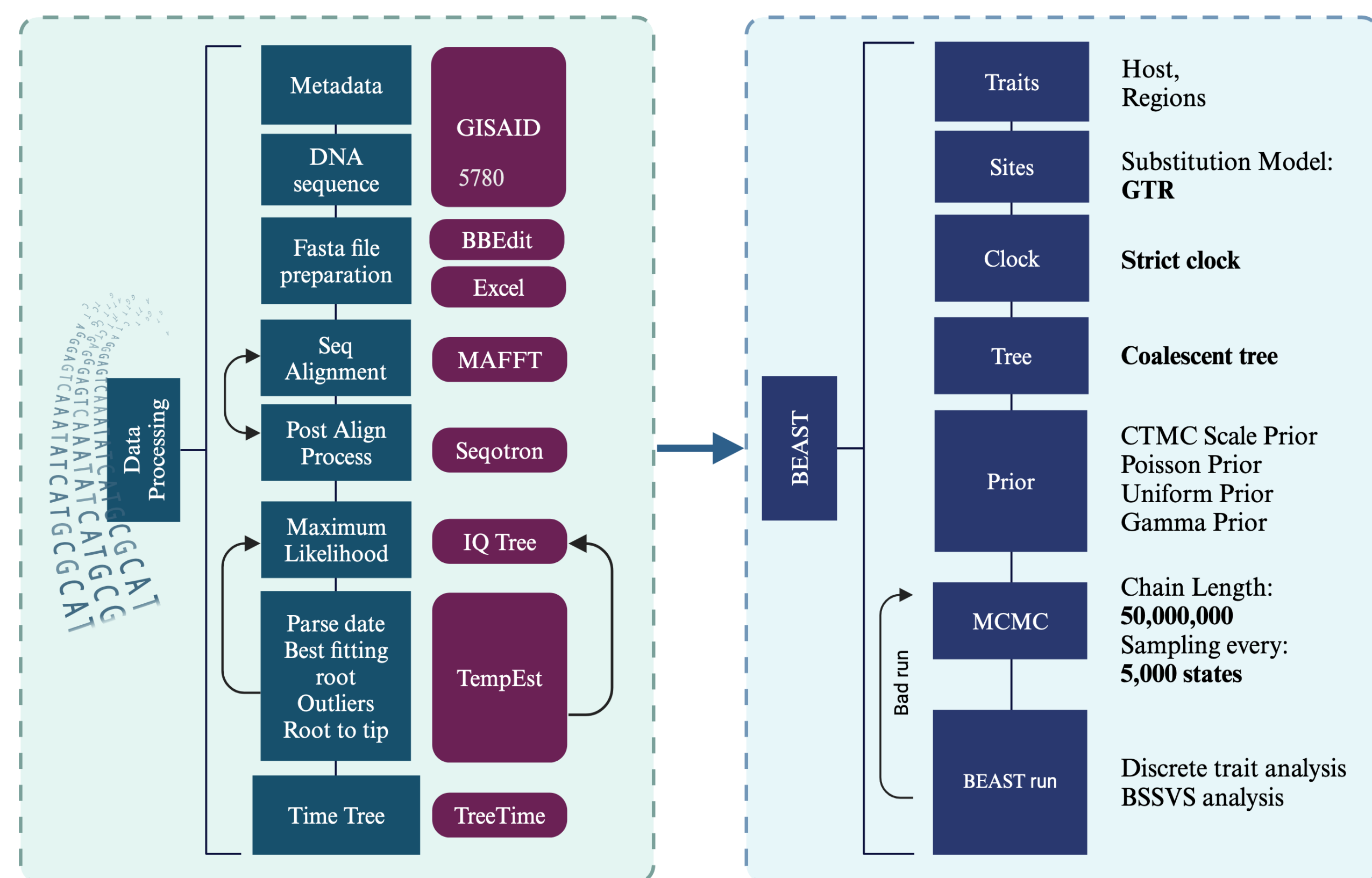
Introduction

The HPAI H5Nx virus, belonging to the clade 2.3.4.4b of the Gs/GD lineage, has presented significant risks to poultry enterprises and the broader community across various countries since its initial emergence.

These viruses continue to evolve globally, and the migration of birds facilitates the spread of new strains, which may carry mutations that allow for better adaptation to mammals.

We aim to study phylogeographic diffusion patterns of HPAI H5Nx virus 2.3.4.4b clade and perform discrete phylogeographic analysis to identify source-sink dynamics and virus diffusion in Europe.

Methodology

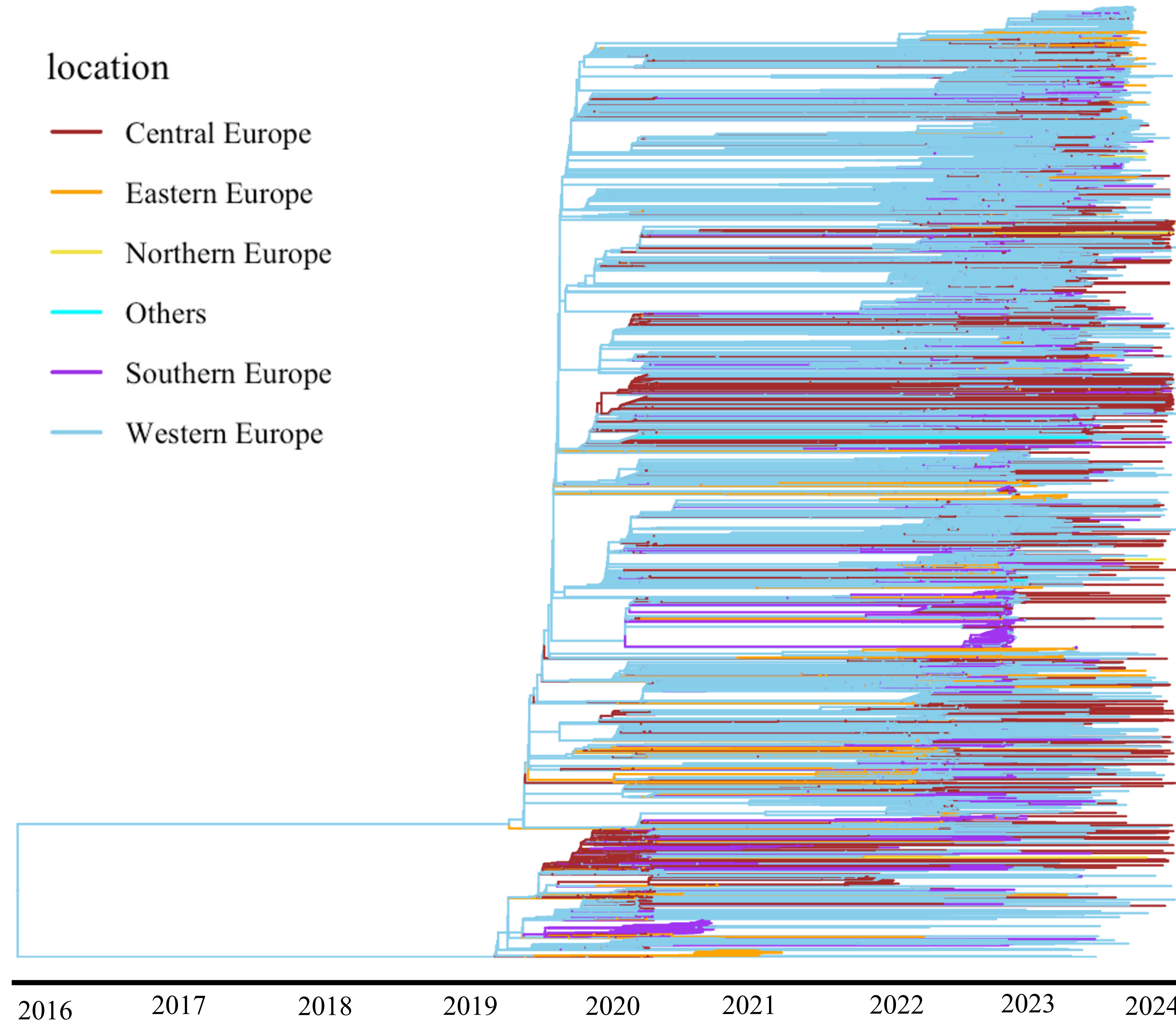


Phylogeographic Reconstructions and Discrete Trait Analysis

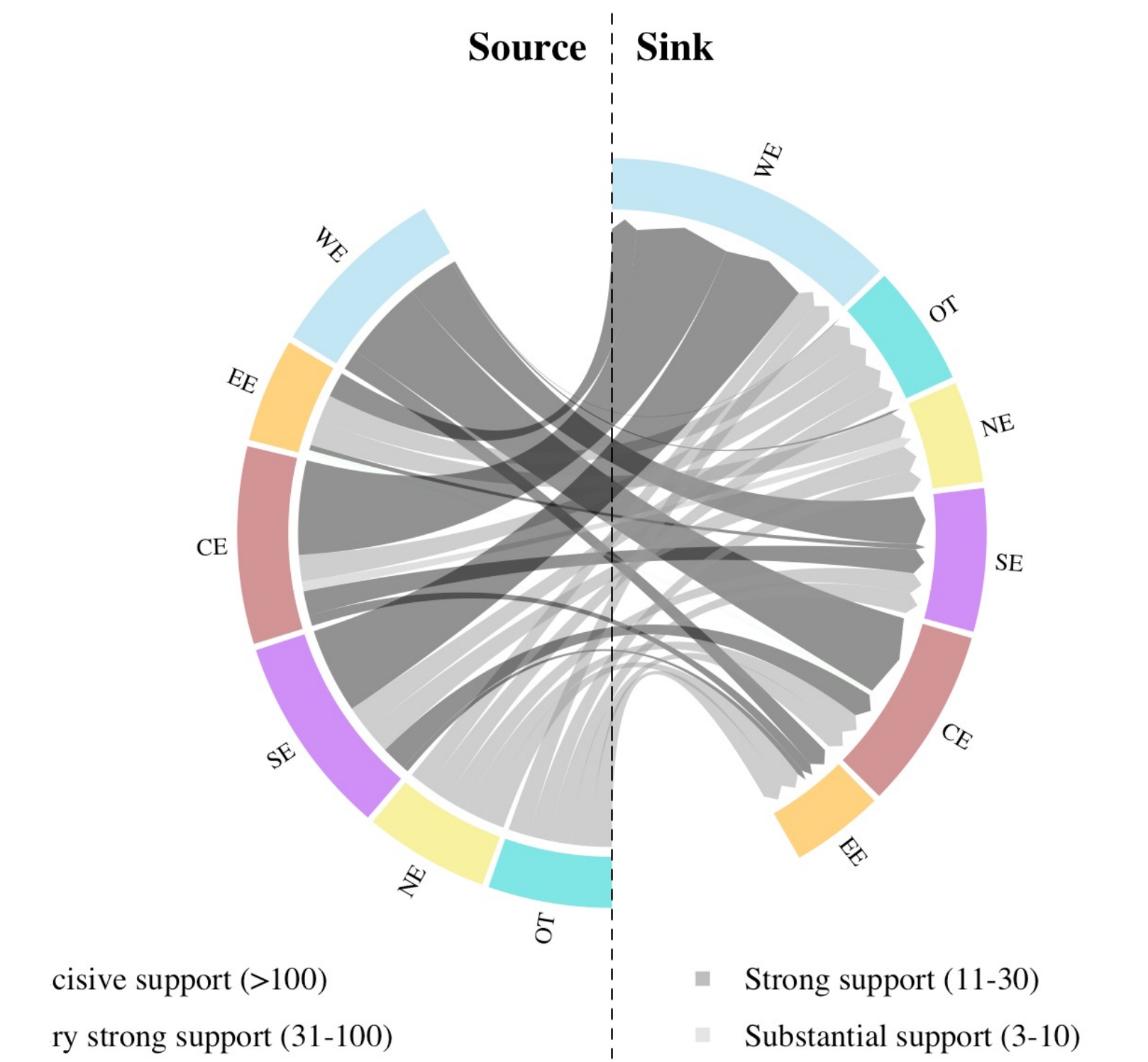
A

location

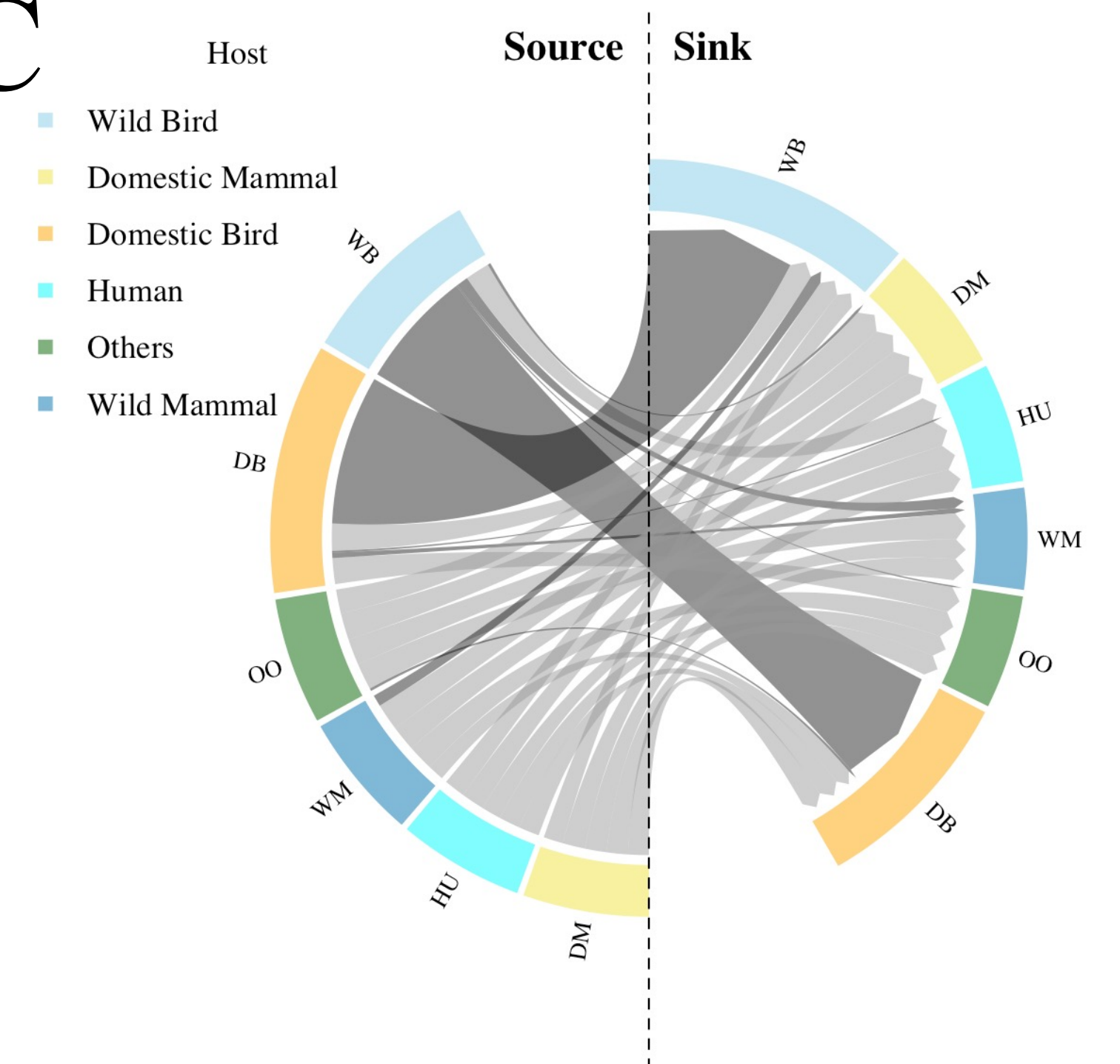
- Central Europe
- Eastern Europe
- Northern Europe
- Others
- Southern Europe
- Western Europe



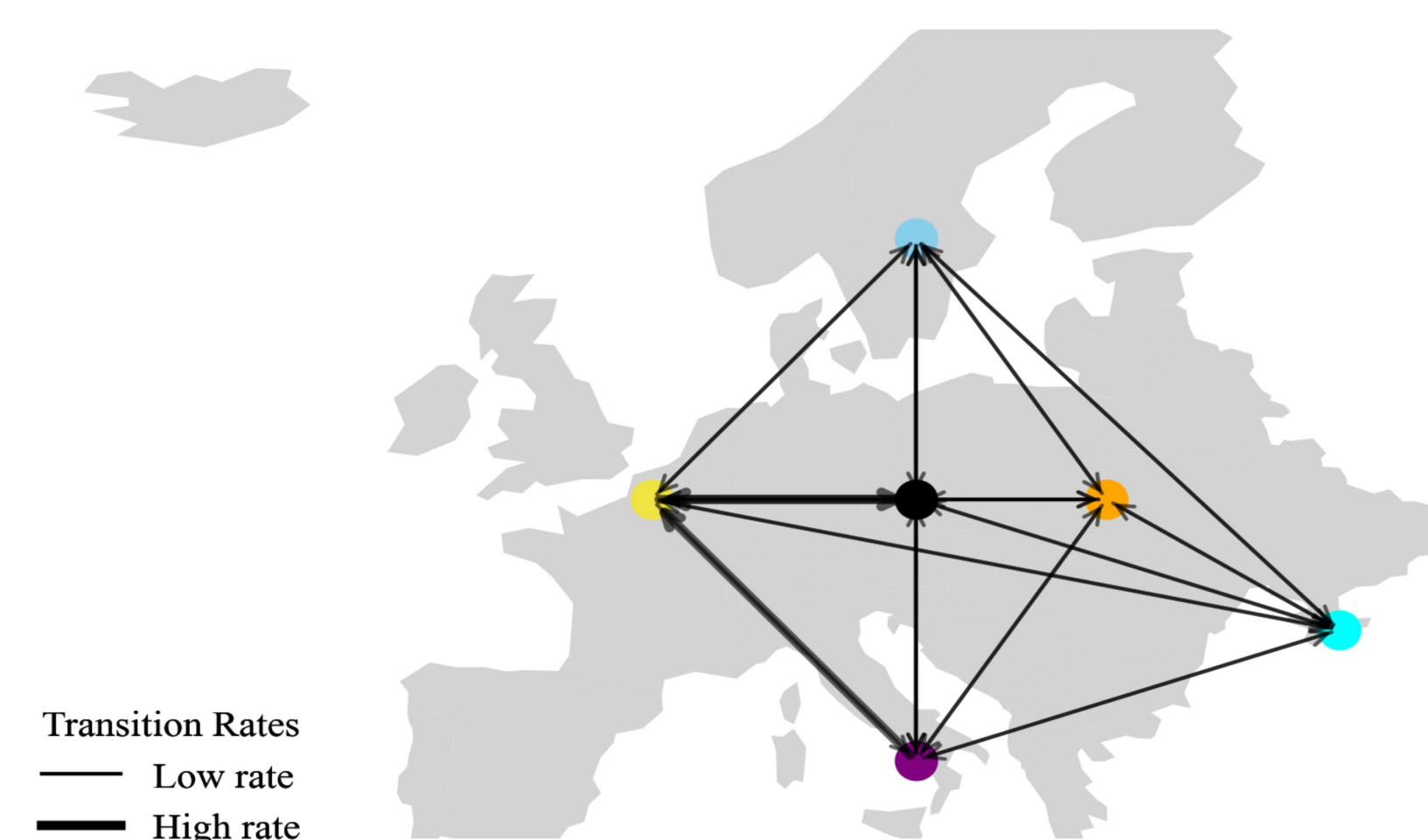
B



C



D



Conclusion and Future Work

Decisive support for significant virus spread from Western Europe to Eastern, Northern, Southern, Central Europe, and other regions, indicating critical pathways for the virus's geographic diffusion. Wild birds frequently transmit the virus to other bird species, domestic birds, and wild mammals, underscoring their significant role in the virus's spread.

We plan to incorporate European bird migration data in future studies to deepen our understanding of the virus's spread across Europe.