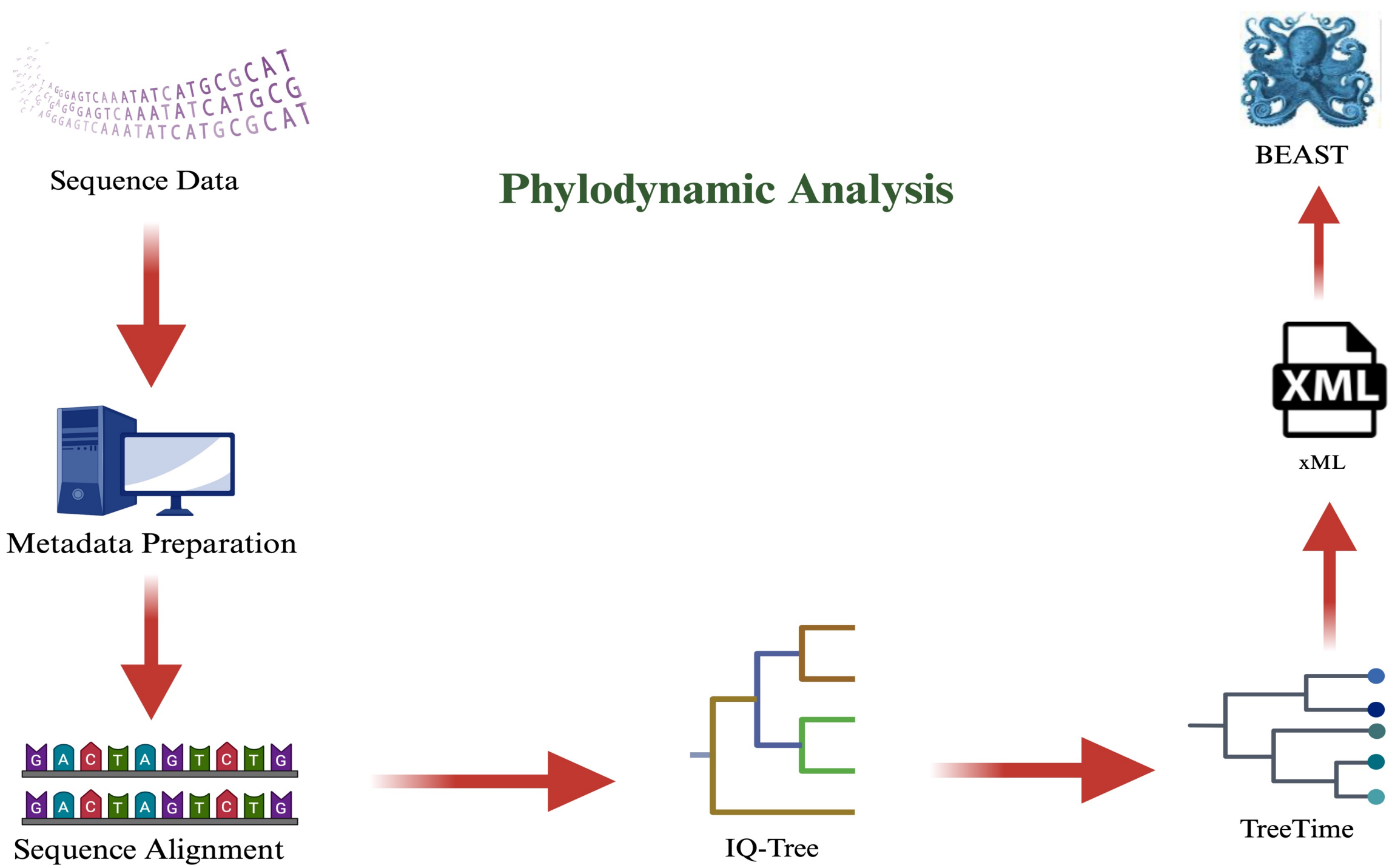


## INTRODUCTION

- ✓ 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



- ✓ Complete sequences of the HA genes from Influenza Virus A(H5Nx) belonging to clade 2.3.4.4b in Europe was retrieved from GISAID genome database.
- ✓ Sequence alignment was performed using MAFFT and Phylogeny was built using IQ-TREE.
- ✓ Time-scaled phylogenetic trees were provided by TreeTime.
- ✓ Bayesian phylogenetic analysis was conducted to generate a maximum clade credibility (MCC) tree.
- ✓ Bayesian discrete trait diffusion models were summarized using Bayesian stochastic search variable selection (BSSVS).

## RESULTS

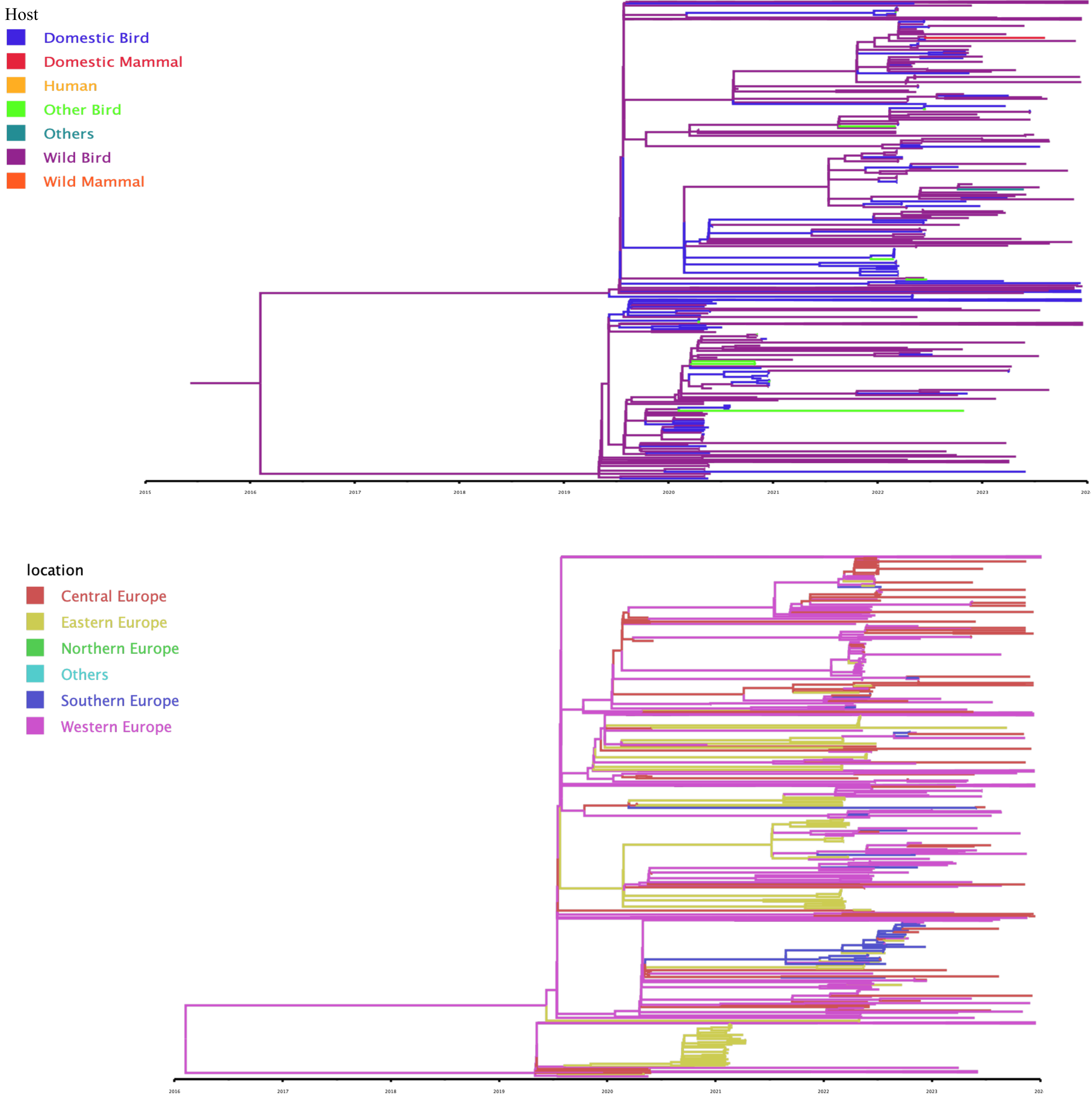


Figure 1: Maximum Clade Credibility tree of H5Nx clade 2.3.4.4b in Europe

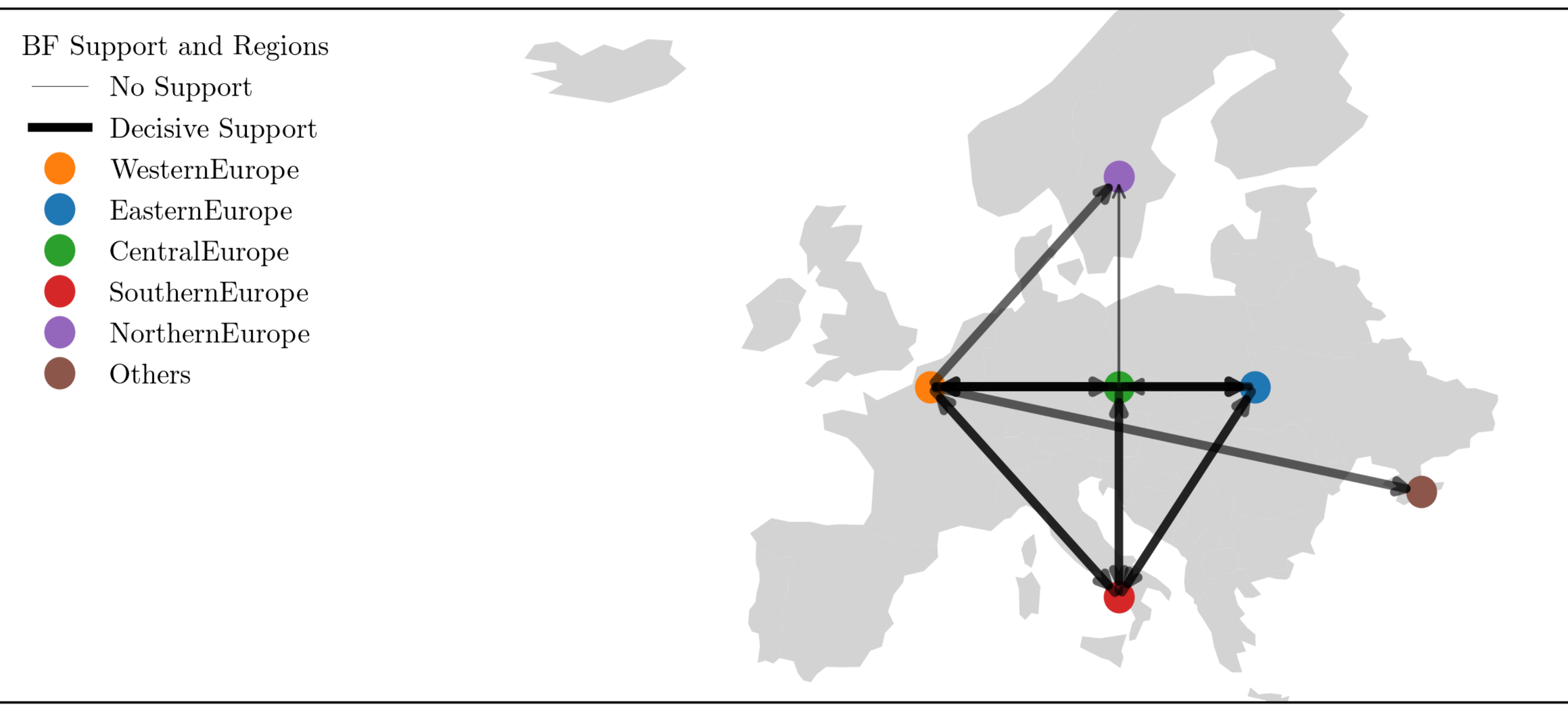


Figure 2: Network of Regional Connections in Europe Based on Bayes Factor

## RESULTS

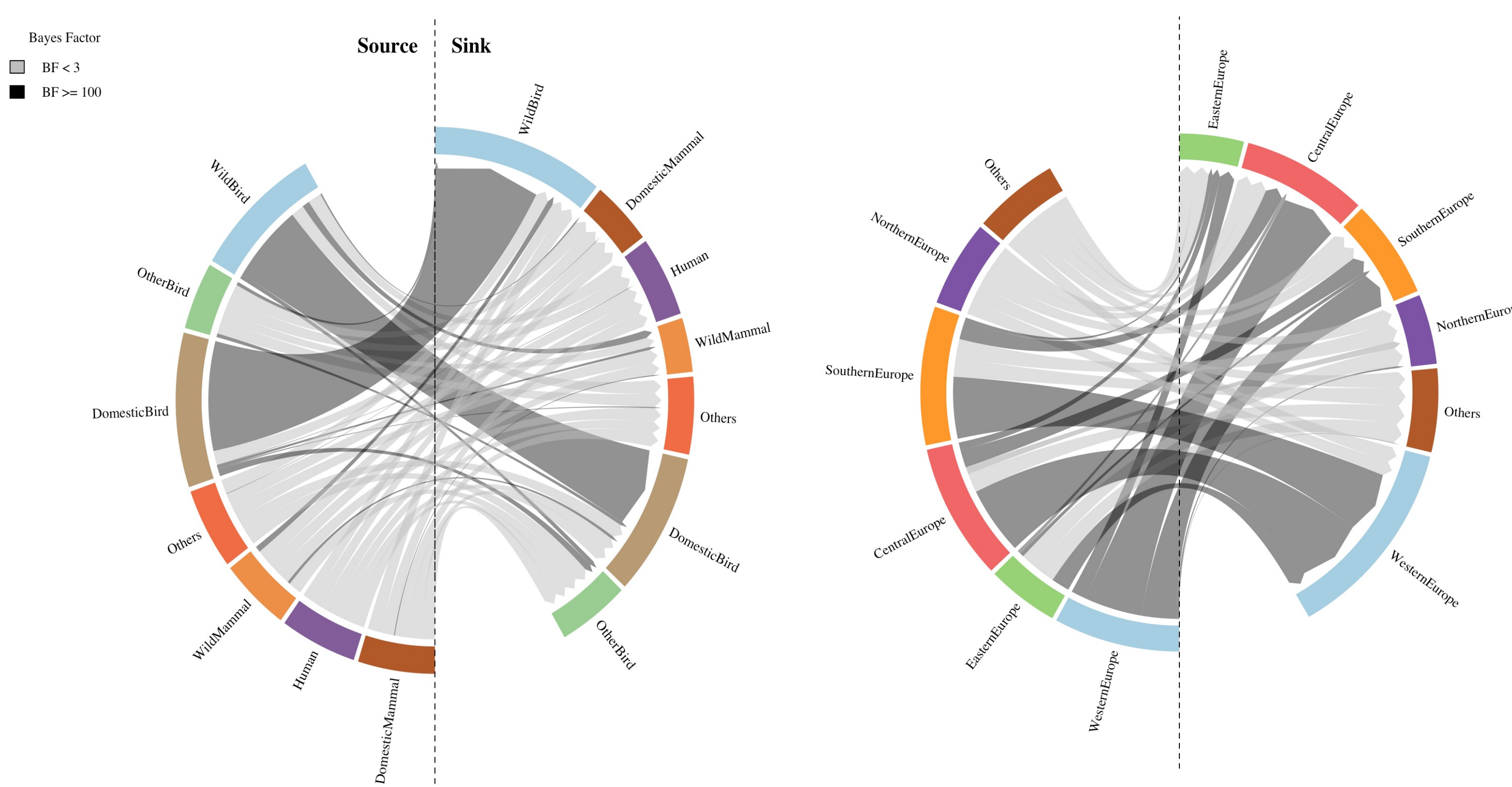


Figure 3: Host and Region models with source on the left of the chord diagrams contribute viral diversity to sink on the right

## DISCUSSIONS

- ✓ Wild birds frequently transmit the virus to other bird species, domestic birds, and wild mammals, underscoring their significant role in the virus's spread.
- ✓ Our analysis also revealed 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.

## CONCLUSION

- ✓ Domestic birds frequently transmit the virus to humans, highlighting the need to monitor and control interactions between domestic birds and humans to mitigate public health risks.
- ✓ We plan to incorporate European bird migration data in future studies to deepen our understanding of the virus's spread across Europe.

## ACKNOWLEDGEMENTS

