

Esox flaviae, population genomics revealed entangled origin and differentiation of the Italian populations

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Introduction and scope

The **Southern pike (*Esox flaviae*)** was identified as a distinct species from the **Northern pike (*Esox lucius*)** in 2011. It is endangered due to the threat of habitat degradation and hybridization with the invasive *E. lucius*.

Limited ecological and genetic data make it challenging to define **Conservation Units (CU)** or **Evolutionary Significant Unit (ESU)**.

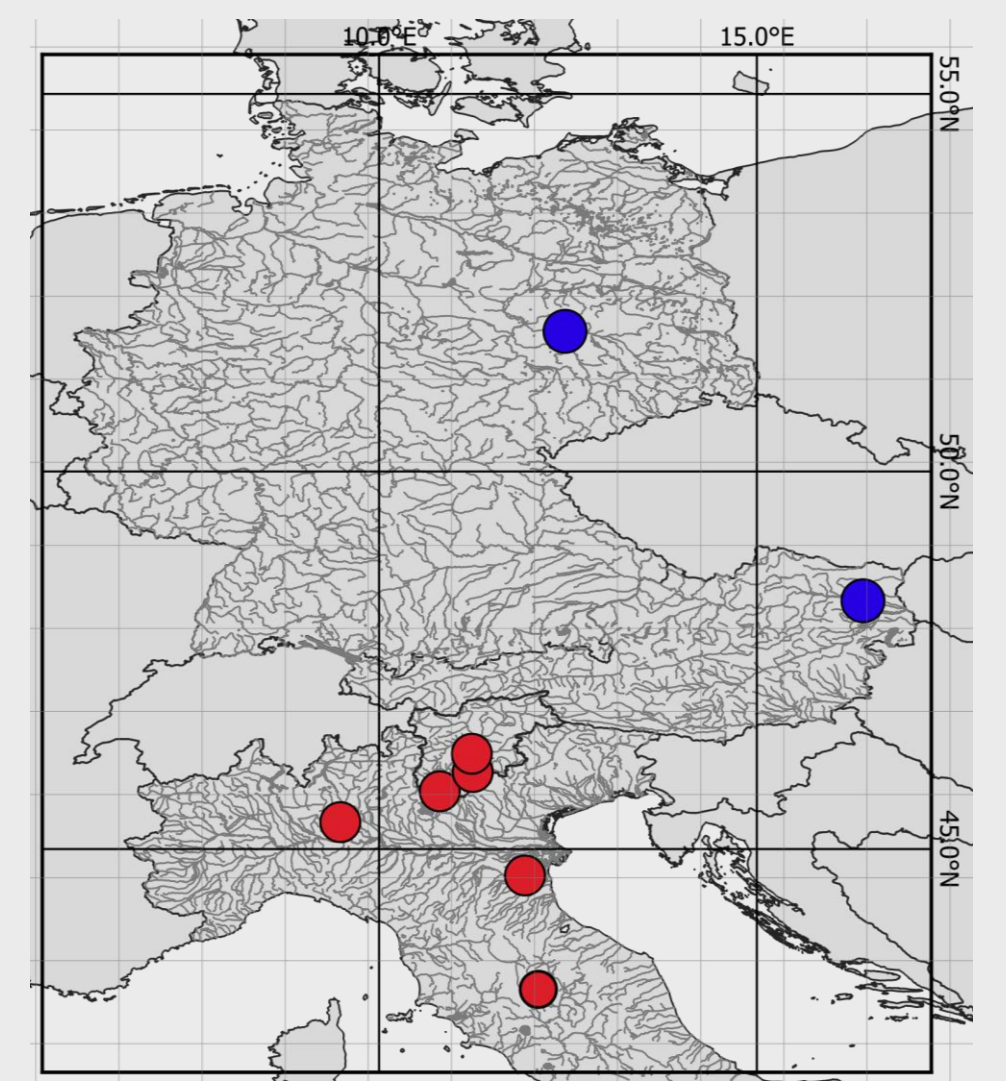
We aim to investigate the population structure and phylogenetic dynamics of 5 Italian populations using a **whole genome** approach to provide insight for **defining proper CUs**.

Methods

Samples and filtering: 62 pike samples (*E. lucius*: blue, *E. flaviae*: red dots), snp whole genome (WGS), 10 million SNPs, 1 million SNPs after filtering

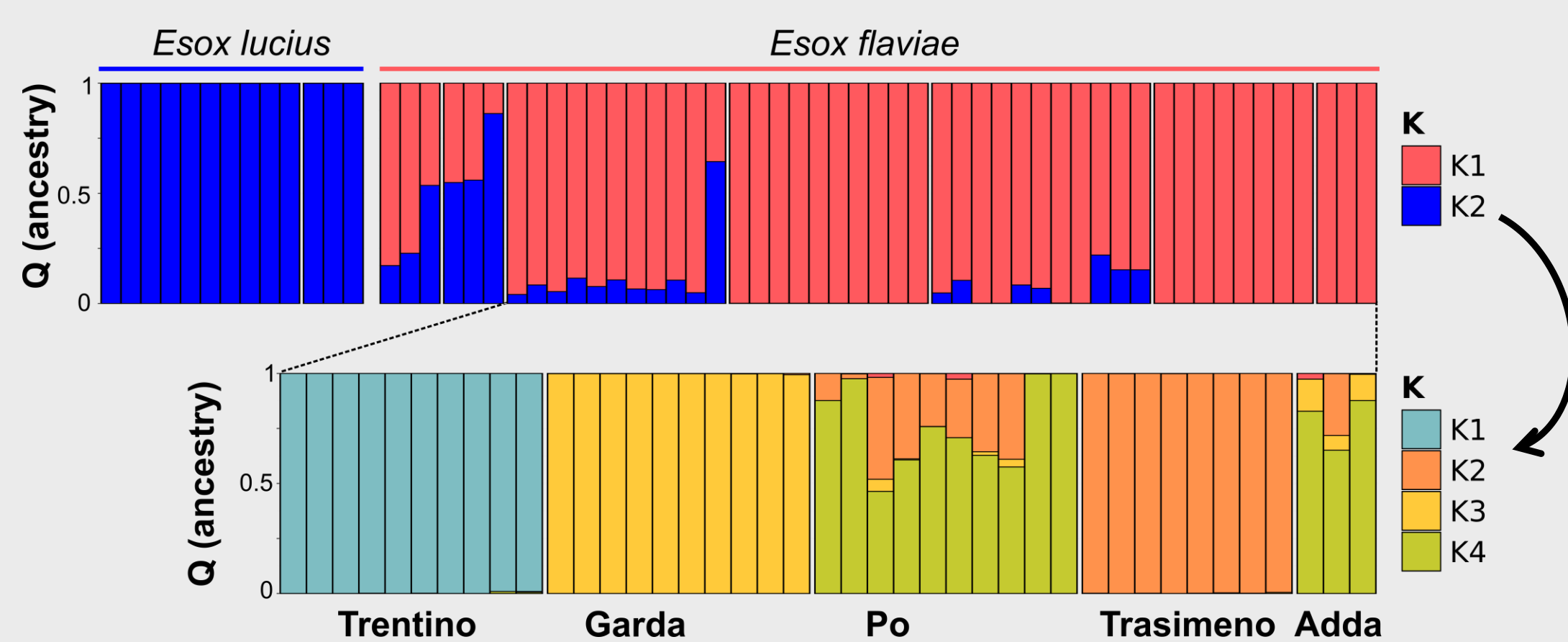
Population structure: PCA analysis, structure analysis using PopCluster.

Evolutionary dynamics: network analysis on mitochondrial and nuclear genome, **phylogenetic**, **population constrained phylogeny**, admixture (**D statistic**).



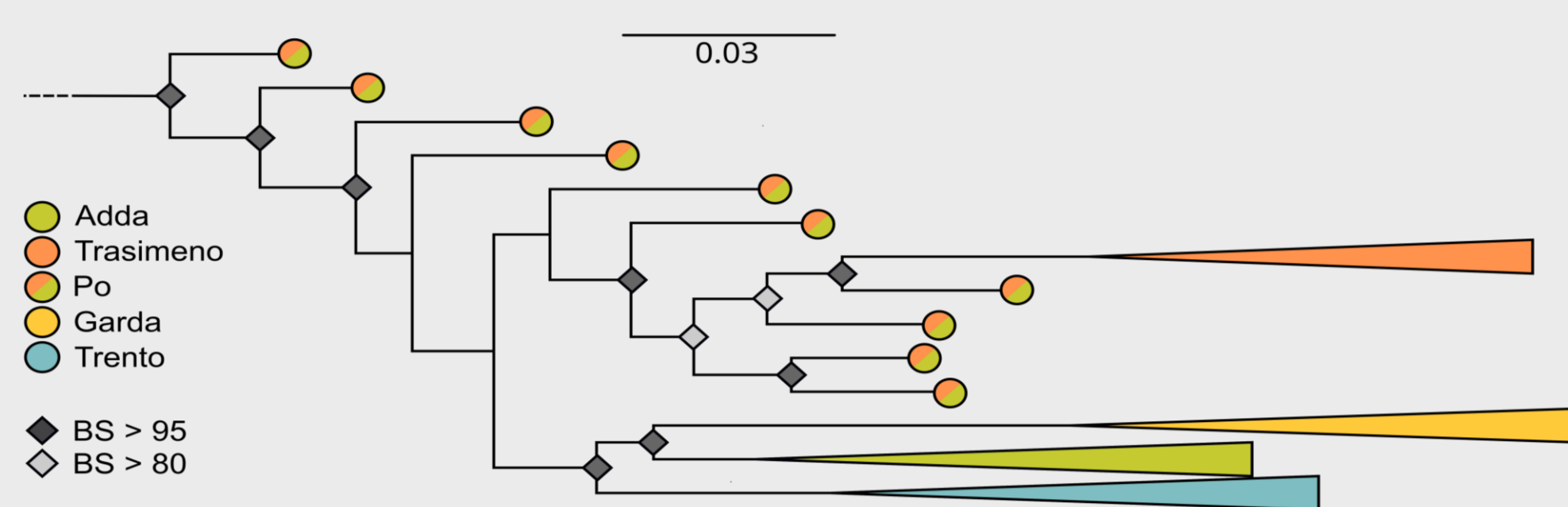
Introgression and Admixture in Southern Pike

The population structure suggests **hybridization** between *E. lucius* and *E. flaviae*. The structure of *E. flaviae* alone revealed a strong structure for **Trentino, Garda, and Trasimeno**. However, the **Po** population showed a poor structure, indicating a probable **admixed event** in the recent past.

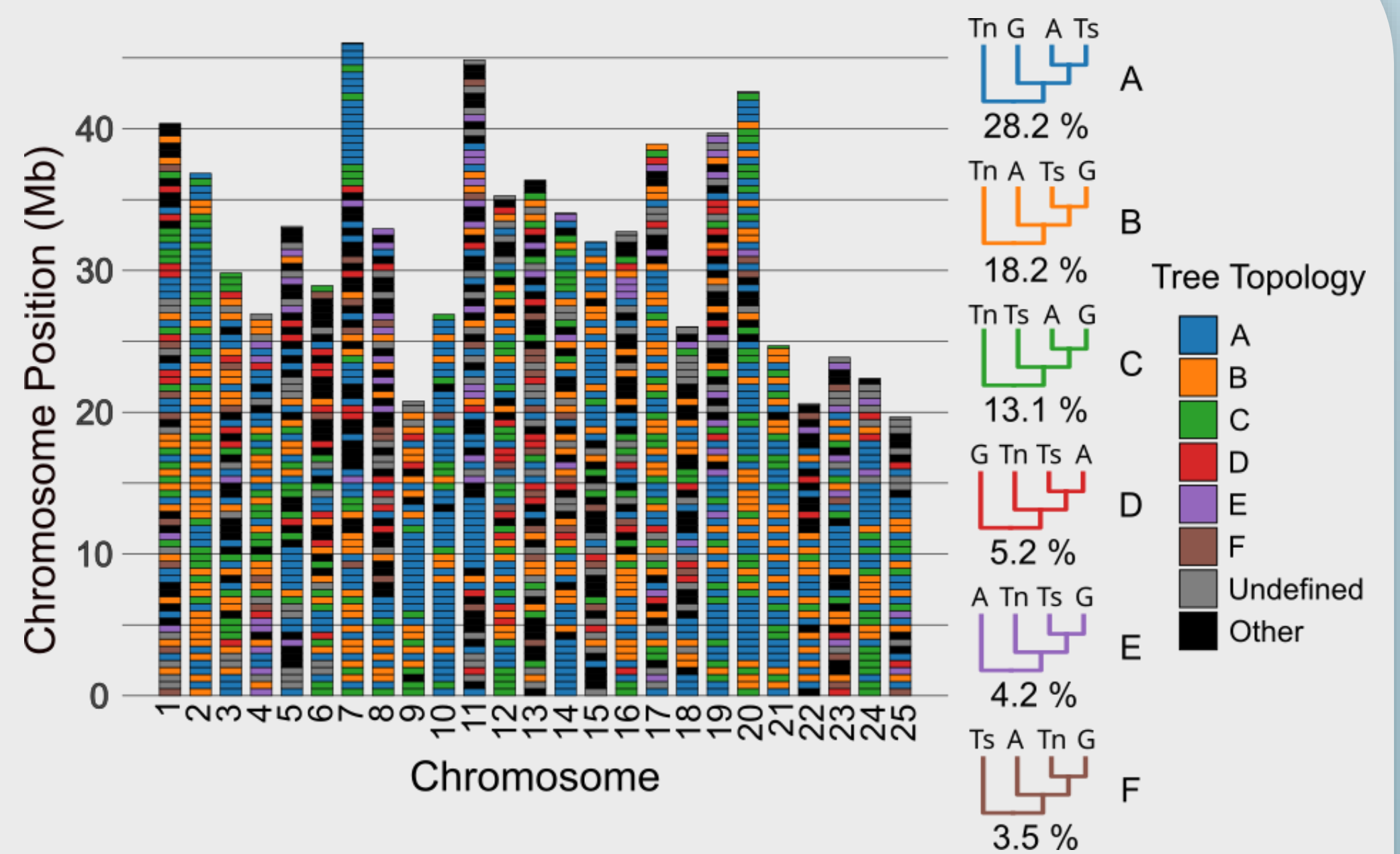


Are these populations monophyletic?

Phylogeny of the populations can offer insight into past dynamics, including **admixture, ILS**, or **rapid population differentiation**. **Po** samples show a strong **polyphyletic** origin. The Adda, Trasimeno, Garda and Trento **population monophyly** suggest isolated populations.

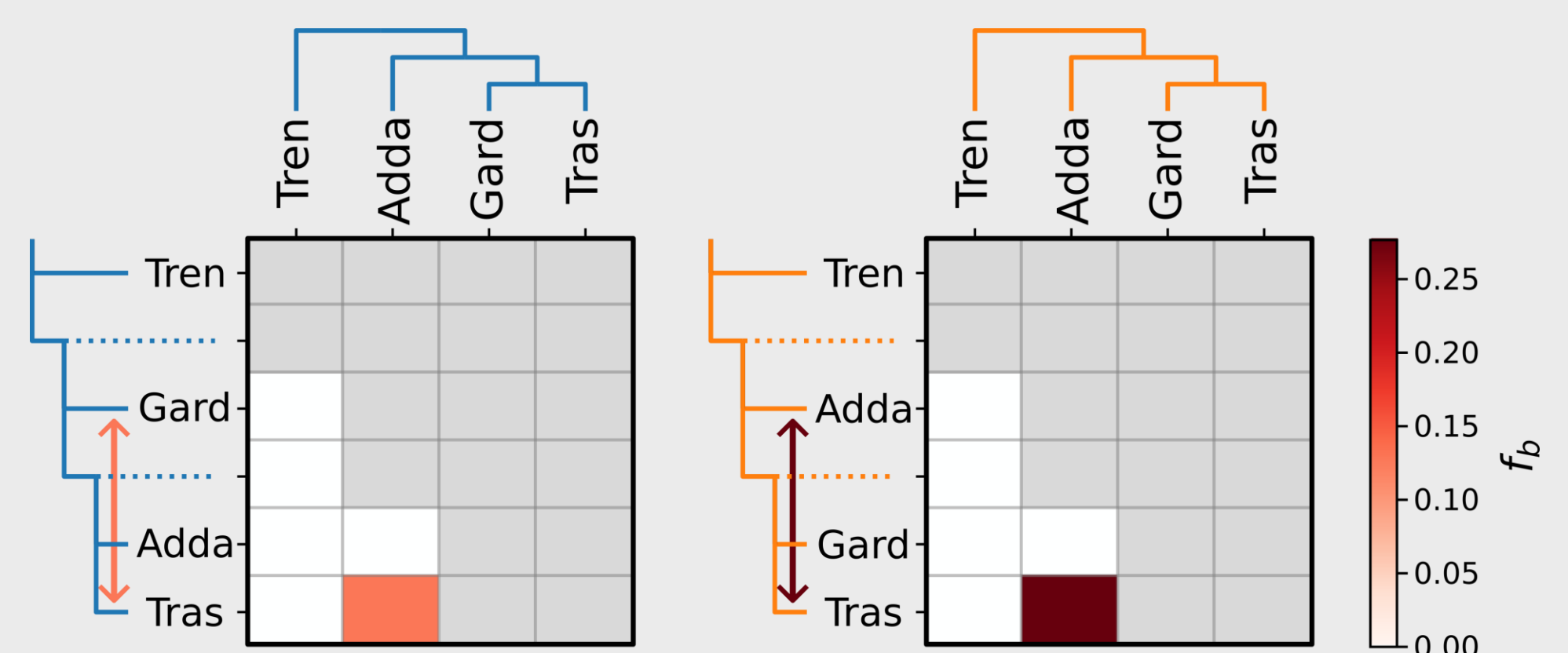


What's happening within the genome?



The **population tree** corresponds to the **topology A**. Regions with local topologies discordant from the population tree may have arisen through past admixture or ILS. **How can we tell ILS and admixture apart?**

Admixture among populations (D statistic)



Conclusions

The phylogenetic-based approach suggests:

- Population structure indicates admixture among Po population and mainly Trasimeno population.
- Varying relationships among *E. flaviae* populations across the chromosomes,
- D statistic reveals admixture events not initially evident in the structure analysis.
- Increased sampling size is needed for a comprehensive and deeper understanding of the conservation status of this new species
- The study will aid in determining CUs and developing well-informed management plans for *E. flaviae*.

Results

