

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* aka *Esox cisalpinus*) was identified as a distinct species from the **Northern pike** (*Esox lucius*) in 2011¹. It is endangered, because of habitat loss and degradation and hybridization with the exotic *E. lucius*. Limited ecological and genetic data make it challenging to define **Conservation Units (CU)** or **Evolutionary Significant Units (ESUs)** within the Italian pike.

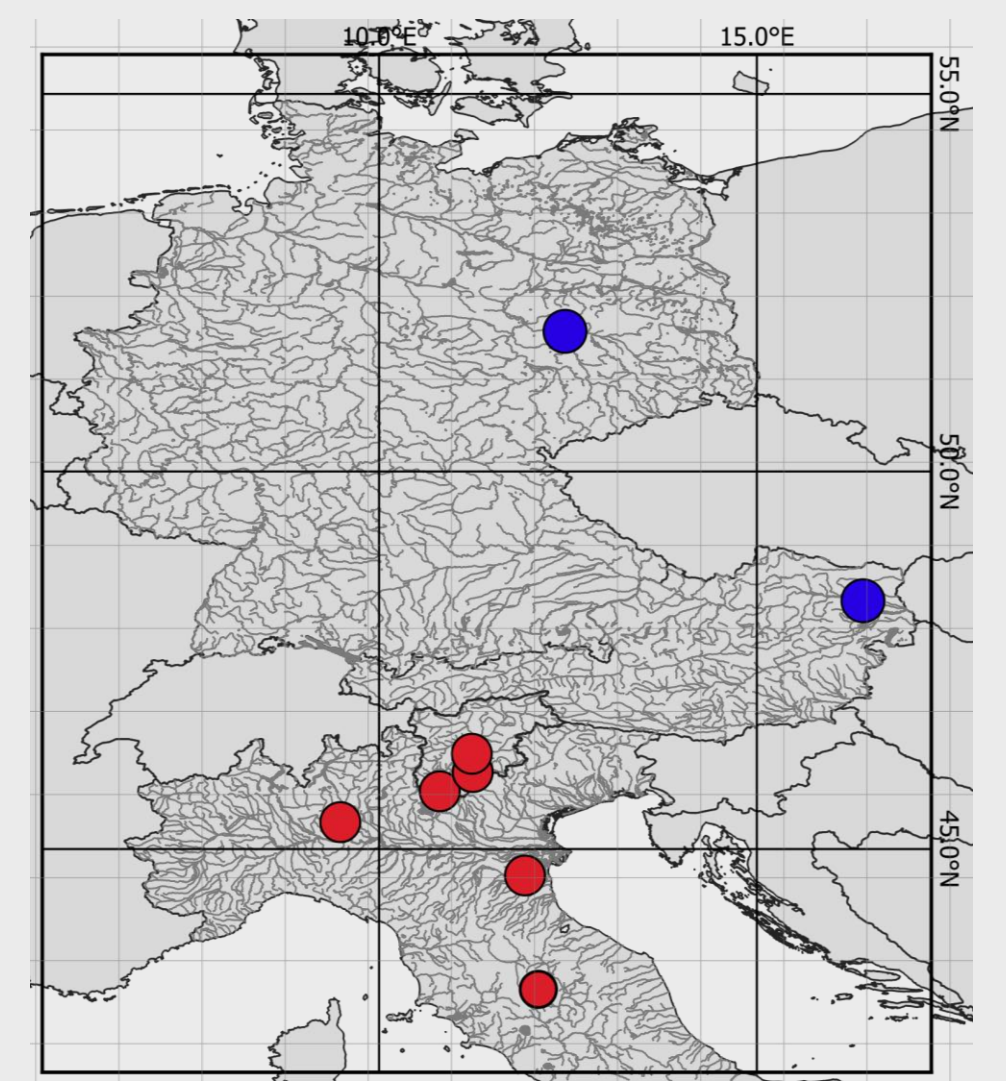
We aim to investigate the population structure and phylogenetic dynamics of five Italian populations using a **whole genome** approach, providing insight for **defining proper CUs**.

Methods

Samples and filtering: 62 pike individuals from 7 sites (*E. lucius*: blue dots, *E. flaviae*: red); **whole genome sequencing**, 10 million SNPs, 1 million SNPs after filtering.

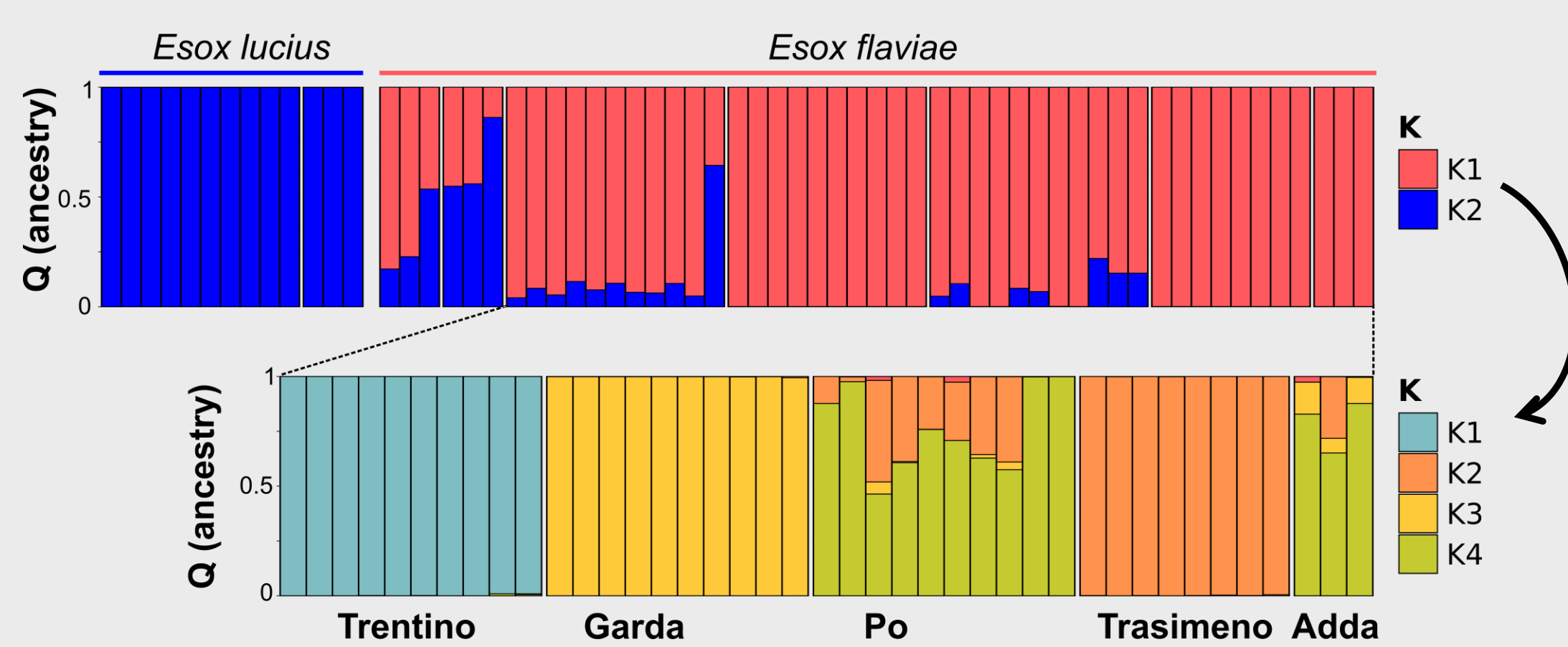
Population structure analysis: PCA, clustering using PopCluster².

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



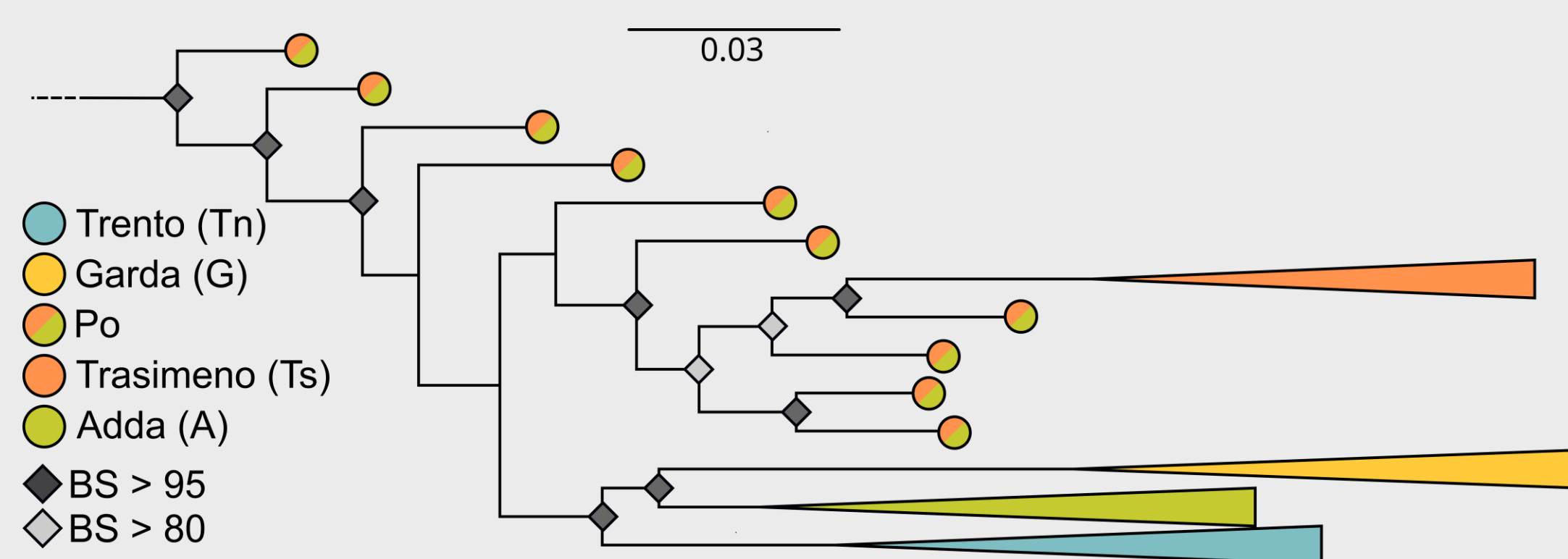
1. Introgression and Admixture in Southern Pike

The population structure suggests **hybridization** between *E. lucius* and *E. flaviae*. The analysis of *E. flaviae* individuals revealed strong structuring for **Trentino, Garda, and Trasimeno**. However, **Po** population is not assigned to a separate cluster, indicating an **admixture event** in the recent past.

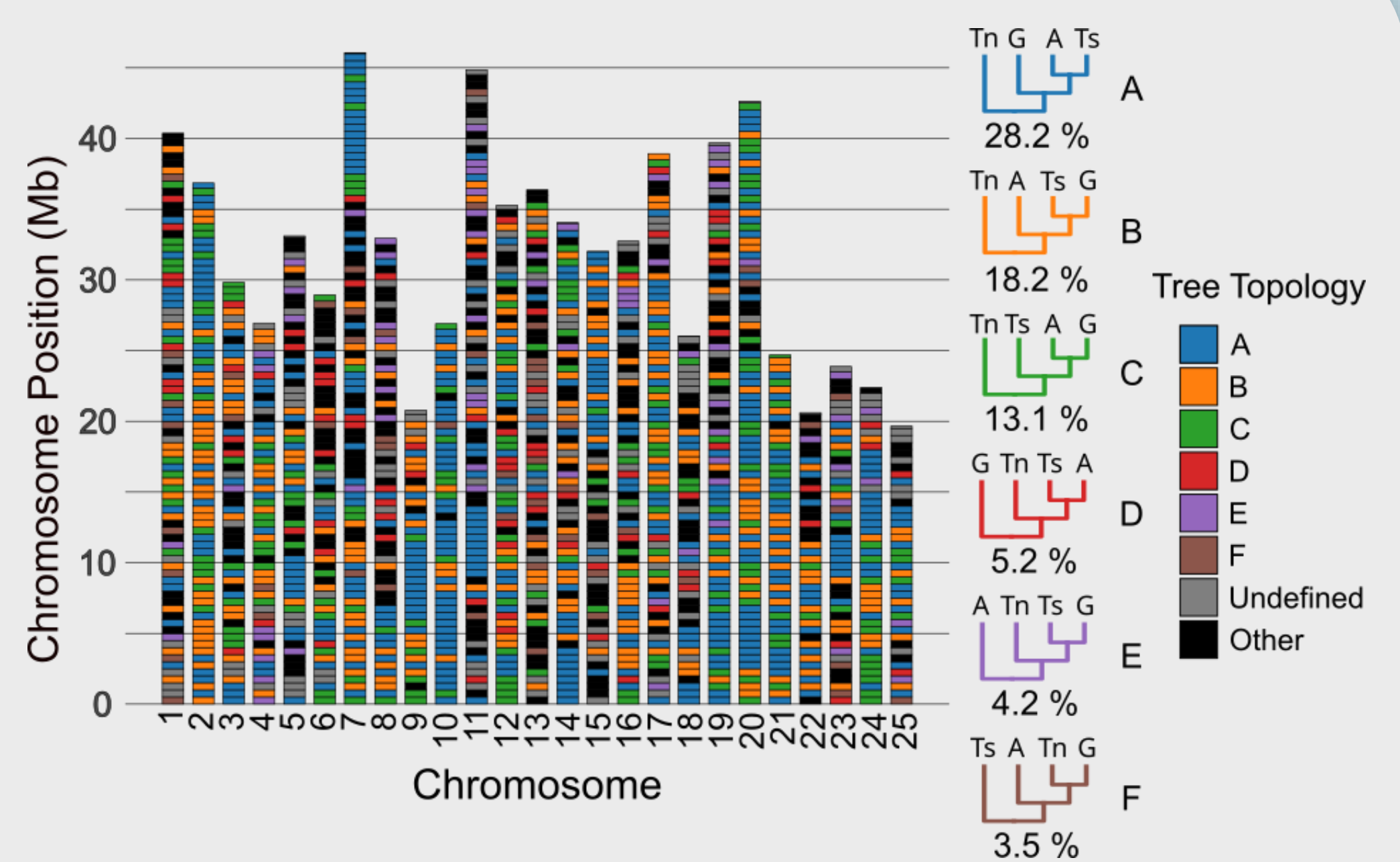


2. Are these populations monophyletic?

The populations' phylogeny can offer insight into past dynamics, such as admixture, incomplete lineage sorting (ILS), or rapid population differentiation. Po samples show a strong **polyphyletic** origin. The Adda, Trasimeno, Garda, and Trento populations' **monophyly** suggests isolation. The population name abbreviations used for the following figures are in brackets.



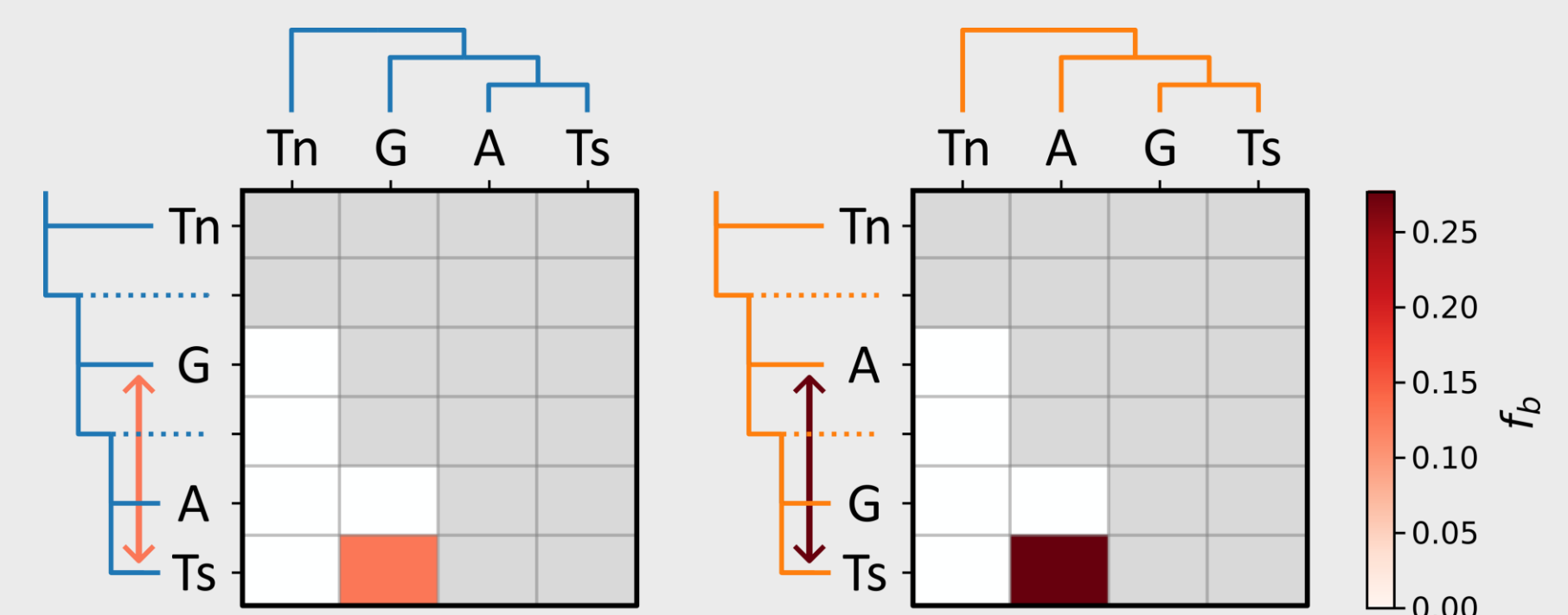
3. What's happening within the genome?



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?**

4. Admixture among populations (D statistic)

F-branch³ (f_b) statistics across our dataset highlight excess allele-sharing between tree tips. The tree topologies are the top two found in the previous analysis (using the same tree colour).



Results

Conclusions

The phylogenomic-based approach suggests:

- Population structure indicates admixture between Po and Trasimeno populations.
- 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*.

References

- ¹Lucentini, Livia, et al. "Molecular and phenotypic evidence of a new species of genus Esox (Esocidae, Esociformes, Actinopterygii): the southern pike, *Esox flaviae*." *PLoS One* 6.12 (2011): e25218.
²Gurinovich, Anastasia, et al. "PopCluster: an algorithm to identify genetic variants with ethnicity-dependent effects." *Bioinformatics* 35.17 (2019): 3046-3054.
³Malinsky, M., Matschner, M., & Svardal, H. (2021). Dsuite-Fast D-statistics and related admixture evidence from VCF files. *Molecular ecology resources*, 21(2), 584-595.