# Reconstructing the demographic history of the adaptive radiation of silversides in the Malili lakes

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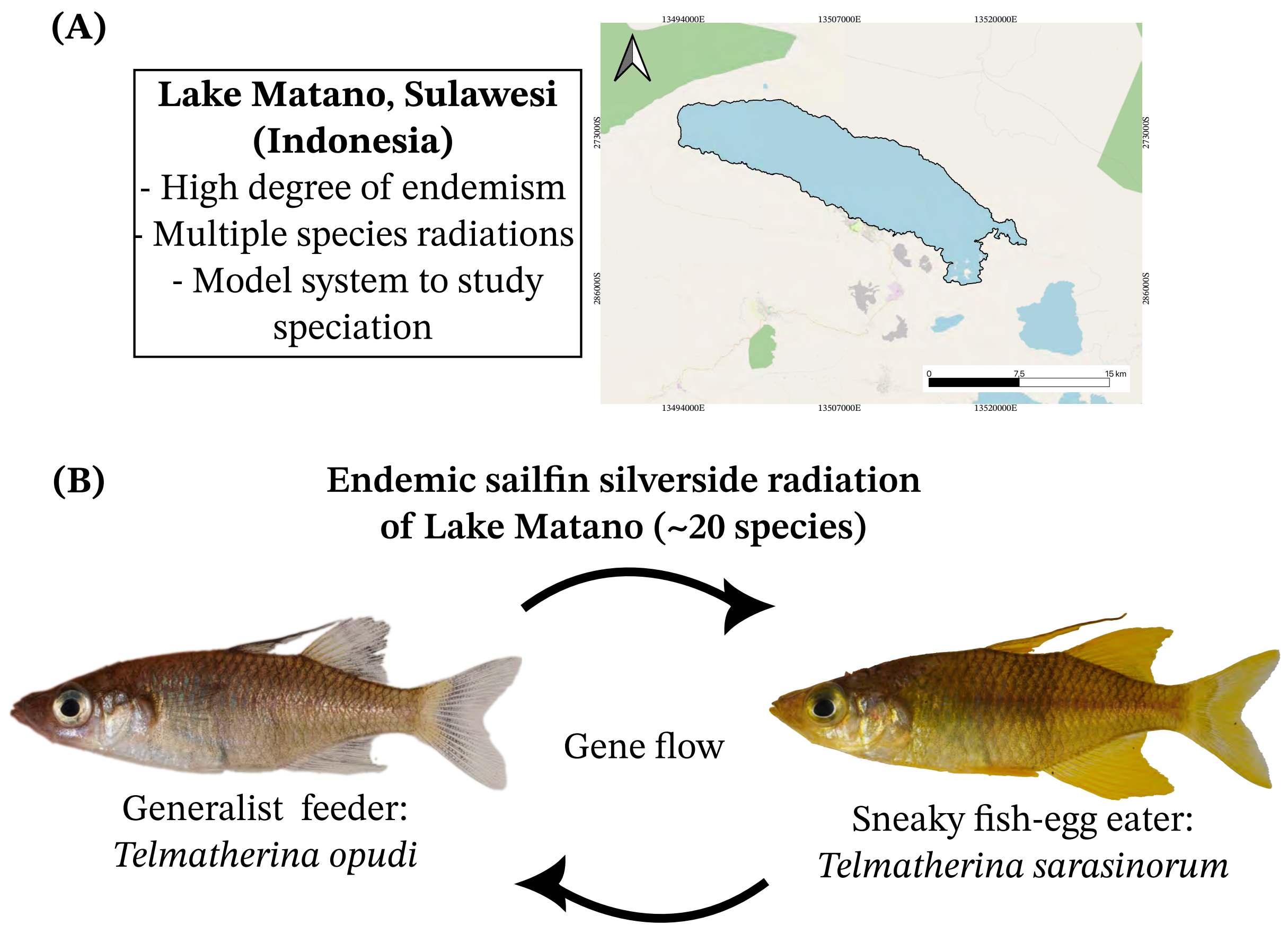
## Introduction

Our study focuses on modeling key demographic parameters of two closely related species, *Telmatherina opudi* and *Telmatherina sarasinorum*. Despite their classification and occupying different feeding niches, evidence of high ongoing gene flow raises questions about their speciation status. In this preliminary work, we attempted to reconstruct their evolutionary history from different perspectives and timescales using whole-genome sequencing data.



(A)

**Lake Matano, Sulawesi (Indonesia)**
- High degree of endemism
- Multiple species radiations
- Model system to study speciation

(B)

**Endemic sailfin silverside radiation of Lake Matano (~20 species)**

Generalist feeder:
*Telmatherina opudi*

Gene flow

Sneaky fish-egg eater:
*Telmatherina sarasinorum*

Figure 1:

## Results

### Historical changes in effective population sizes

First, we used a sequentially Markov coalescent approach to infer the historical changes in effective population size.

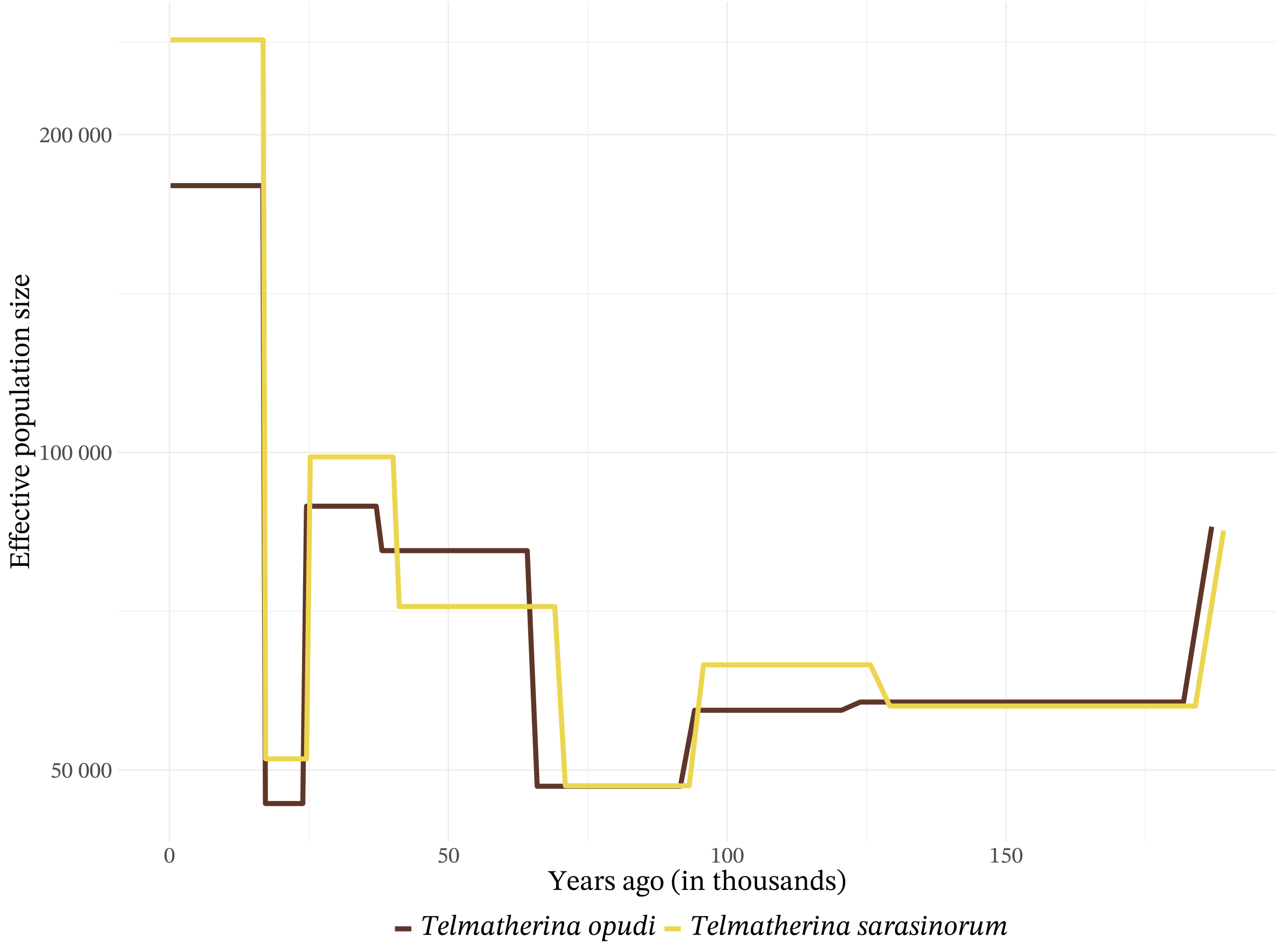


Figure 2: Effective population size estimated with SMC++ across all chromosomes. We assumed a mutation rate of $3.5 \times 10^{-9}$ and a generation time of one year.

- We observed a large effective population size after a large expansion 25 thousand years ago.
- *T. opudi* and *T. sarasinorum* showed highly similar demographic histories, which would be compatible with a low degree of separation between species.

### Recent effective population size estimates

The SMC++ analysis provides a broad evolutionary perspective. However, it is not informative about the recent past. We analyzed the observed linkage disequilibrium using GONE2 to infer the effective population size in the last 100-200 generations.

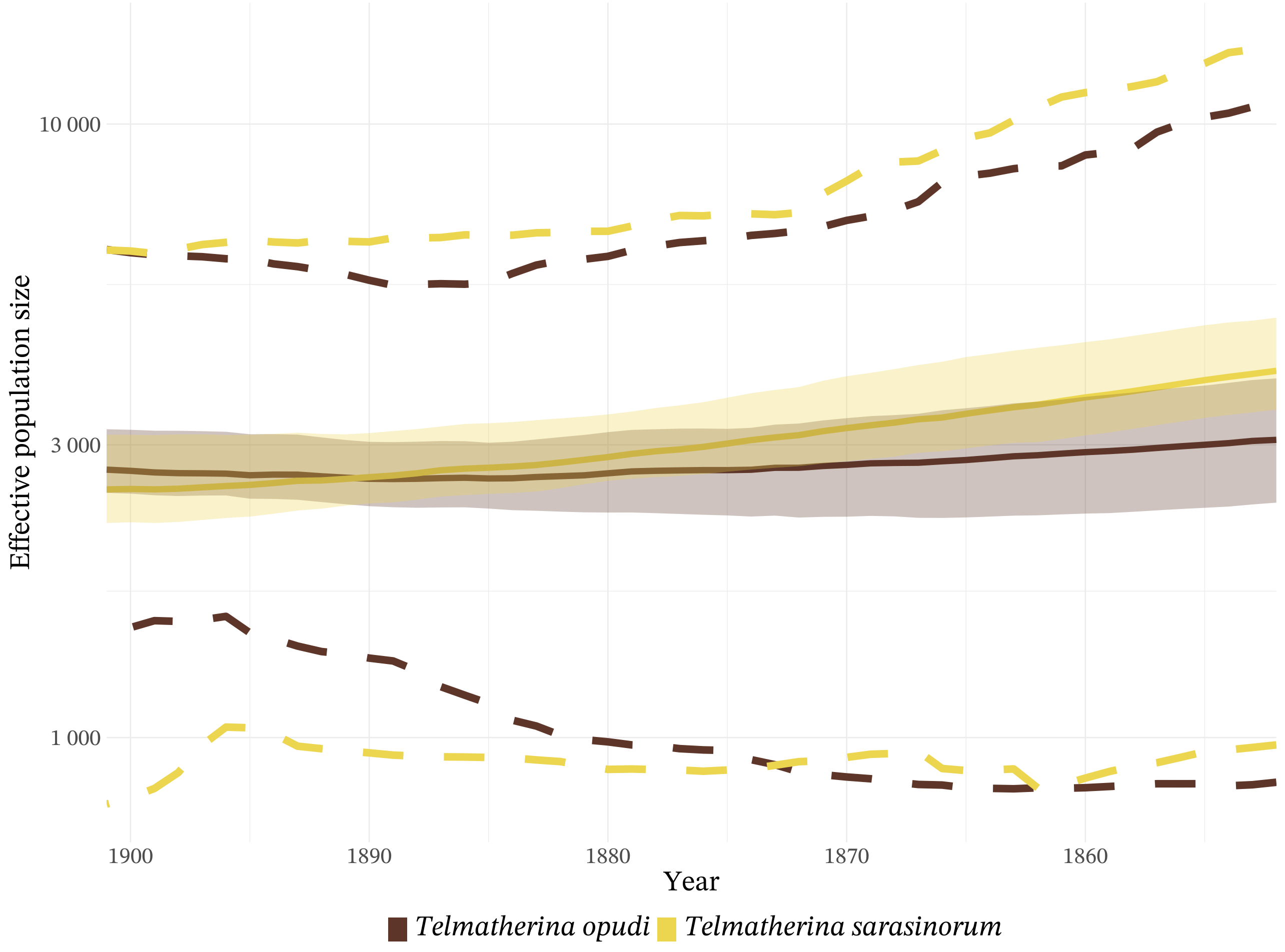


Figure 3: Recent effective population size inferred using GONE2 and averaged across all chromosomes. We used the recombination rate estimated from SMC++ and assumed a generation time of 1 year. Continuous lines represent the geometric mean. The 95% bootstrap confidence intervals are shown as shaded areas. The dashed lines show the maximum and minimum values of all chromosomes.

- We observed a slight decline in effective population size at the end of the 19th century. As before, *T. opudi* and *T. sarasinorum* showed similar identical demographic histories.
- Notably, the estimate is orders of magnitude lower than the historical effective population size, suggesting recent demographic changes.

### Posterior distribution of the mean effective dispersal rate[1]

Population genetic analysis is often based on a notion of discrete demes, rather than spatial continuum. Here, we acknowledge it and estimate the effective dispersal rate from shared identity-by-descent blocks[2]. We used a novel Bayesian inference approach based on the composite likelihood derived by Ringbauer, Coop and Barton (2017) to jointly estimate the effective density and dispersal rate.

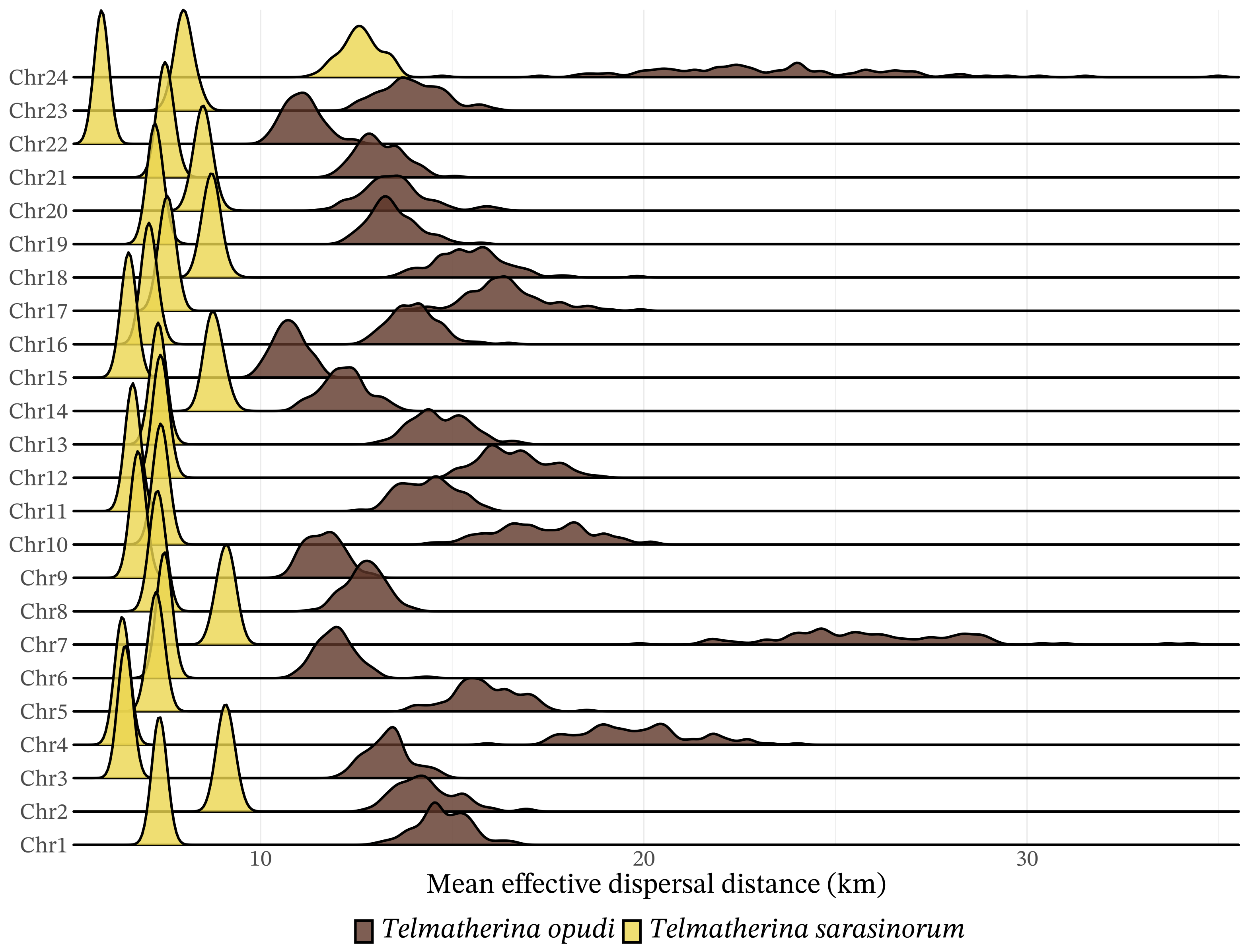


Figure 4: Estimated from shared identity-by-descent blocks using a composite likelihood Bayesian approach. We set a uniform prior to the dispersal of $U(0, 40)$ km. We jointly estimated the effective density (not shown).

- Based on specific forward-in-time simulations, we determined that we could accurately estimate the dispersal rate.
- We observed a lower dispersal rate in the specialist *T. sarasinorum* than in the generalist *T. opudi*. (95% HPD difference: $-0.9$-17 km).
- Although we do not discard this due to technical reasons, it could be caused by *T. sarasinorum* having fewer patches of suitable habitat.
- Taking into account that Lake Matano is roughly 30 x 5 km, our results indicate no evidence of isolation by distance.

## Methods

All analysis and simulations are available at https://github.com/currocam/benelux-zoology-conference

## Future work

Future work would benefit from more extensive sequencing of modern samples. Together, this would provide a better understanding of the evolutionary history of these species but can also lead to better conservation management strategies.

- More samples would allow us to estimate the historical effective population size further back in time (as more distant coalescent events would be observable).
- Modern samples would allow us to infer more recent demographic events and address the impact of human activities (nickel mining) and invasive species.

## Take-home message

1. We observed almost identical demographic histories in *T. opudi* and *T. sarasinorum*, whose species status is uncertain.
2. We inferred a large historical effective population size, but we estimated a much lower recent effective population size.
3. We found a higher dispersal rate in *T. opudi* than *T. sarasinorum*, but no evidence of isolation by distance. Different feeding niches might explain the lower dispersal rate in *T. sarasinorum*.

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[1] The mean effective dispersal rate is the average distance between an individual and its parents.

[2] Here, we define an identical-by-descent block as a contiguous segment of the genome inherited from a shared common ancestor without intervening recombination.

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