

# Through the lynx's lens: Genetic insights from the Eurasian lynx (*Lynx lynx*) in France

[in /anaïs-beaumariage](#)  
Anaïs.Beaumariage@uliege.be



Anaïs Beaumariage<sup>1</sup>, Jonathan Drugmand<sup>1</sup>, Edeline Beïne<sup>1</sup>, Adrien André<sup>1</sup>, Rebecca Burlaud<sup>2</sup>, Juliette Caillé<sup>2</sup>, Marine Drouilly<sup>2</sup>, Johan Michaux<sup>1</sup>

## Introduction

The Eurasian lynx (*Lynx lynx*) was notably reintroduced in the Swiss Jura in the 1970s from a few Carpathian founders. It subsequently recolonized the **French Jura** naturally, after its extinction from the country in the early 20th century.

Today, the population remains **small, isolated**, and **endangered**, forming part of the Upper Rhine metapopulation. Founder effects and genetic drift likely threaten its long-term viability, yet its genetic status and connectivity remains poorly documented.

## Objectives

Evaluate  
**genetic  
structure**

Assess temporal  
**genetic diversity**  
and **inbreeding** levels

Investigate  
**gene flow**

## Material & Methods

177 lynx scats (2019–2024) & 20 microsatellites

- Individual identification and recapture detection
- Sex determination
- Genetic analysis :

## Results

### Individual identification and sex ratio

We identified **85** unique individuals between 2019–2024 (54 ♂, 31 ♀).

### Genetic structuring

Bayesian clustering (STRUCTURE) revealed **weak structuring** (Fig.1). Although  $K = 2$  was suggested, no clear spatial or temporal pattern emerged, indicating overall genetic homogeneity. This pattern likely reflects the common reintroduction origin rather than contemporary subdivision.

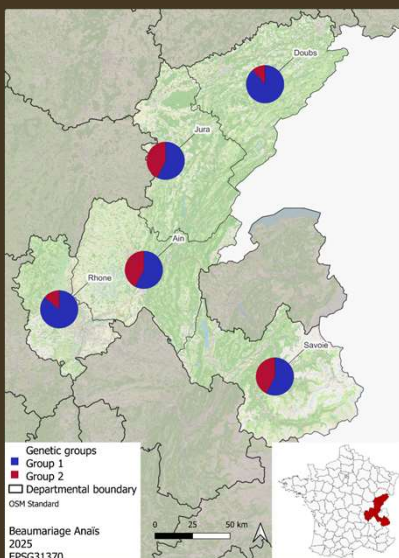


Fig. 1 : Representation of the proportion of samples belonging to each genetic cluster ( $K=2$ ) for each department.

## Temporal genetic diversity and inbreeding

The population exhibited **reduced diversity** ( $A_r = 3.79$ ;  $H_o = 0.365$ ;  $H_e = 0.405$ ) and a positive **inbreeding** coefficient ( $FIS = 0.10$ ). These values are lower than in the Carpathian population, highlighting the lasting impact of the founder effect and genetic drift.

Between 2019 and 2023, allelic richness remained **low but stable** (Fig.2).  $FIS$  fluctuated (0.063–0.37), but confidence intervals overlapped (Fig.3), suggesting **no significant temporal differentiation**.

However, these trends should be interpreted with caution, as they may partly reflect variation in annual sample size.

See Poster in  
collaboration with  
the **SFEPM** and the  
**LCE** for citizen  
science  
to collect lynx scats

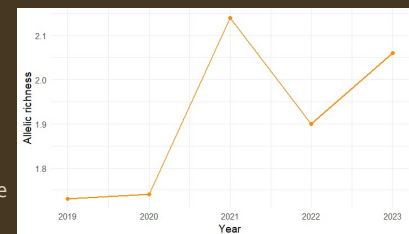


Fig. 2 : Changes in allelic richness values over the years.

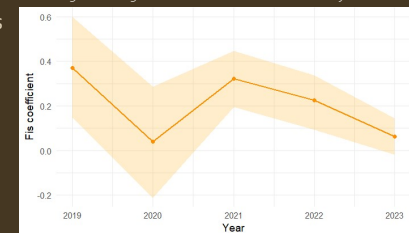


Fig. 3 : Changes in the values of the consanguinity index  $FIS$ , with its 95% confidence intervals, over the years.

## Gene flow in the studied zone

Pairwise **differentiation was minimal** ( $G'st \leq 0.033$ ;  $D_{jost} \leq 0.003$ ), with overlapping confidence intervals including zero. This either suggests sufficient ongoing gene flow to homogenize allele frequencies, or a uniform genetic background inherited from the shared reintroduction history.

## Synthesis

The lynx from the French Jura and northern Alps show **low but stable diversity**, **weak structuring**, and **limited differentiation across space and time** (2019–2023).

These findings likely emphasize the enduring genetic footprint of the reintroduction history and raise concerns about the extent of current functional connectivity with neighboring populations.

Improving ecological corridors, pursuing genetic reinforcement, and **maintaining long-term transboundary genetic monitoring** will be key to ensuring the long-term viability of lynx in France.