



How genetic structuring explains the national recovery of the Eurasian Otter

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Introduction

Otter populations in France fragmented in the 20th century due to persecution and pollution. Small **relict populations** persisted in Brittany, Massif Central, and the Atlantic coast. Since the 1980s, **legal protection** has led to a remarkable national **recolonization**.



Analyze the genetic **structure** and genetic **health** of the expanding French population.

1. Genetic structure

Refugial signatures: Six genetic clusters exhibit high geographic coherence, some mirroring historical refugia across France (**Breton**, **Central Massif**, **Atlantic**, **Pyrenees**, **Rhône-Alpes**, **South-East**). Further sampling would be valuable to refine and confirm the delimitation of the **South-East** cluster.

Recolonization footprint: The presence of "chimeric" (admixed) individuals and Atlantic genotypes in Central France (Limousin/Charente) marks the real-time footprint of expansion.

Active reconnection: 39% of individuals are admixed, showing that formerly isolated lineages are now merging, which reinforces national genetic health (Fig.1).

Material & methods

356

spraints and carcasses
collected across France and
Northern Spain.

9

highly variable
microsatellite loci

Analysis: Population **structuring** (STRUCTURE) and **diversity** indices (Ar, Fis, D_{jost})

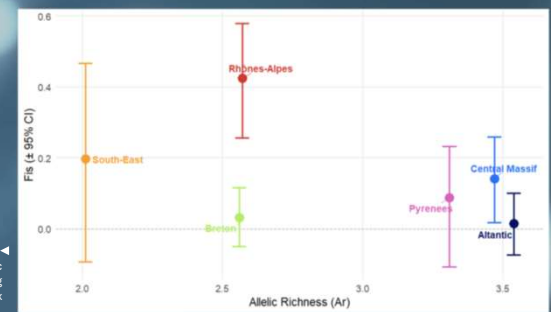


Fig.2: Genetic diversity. Relationship between Allelic Richness (Ar) and inbreeding indicator (Fis) across the six clusters (error bars: 95% CI).

3. Genetic differentiation

Historical fragmentation: The high differentiation between **Breton** and **Rhône-Alpes** lineages highlights the historical isolation across the national range.

Connectivity corridor: The low differentiation between **Atlantic** and **Central Massif** clusters identifies a connectivity corridor that facilitates gene flow and may contribute to the species' recovery (Fig.3).

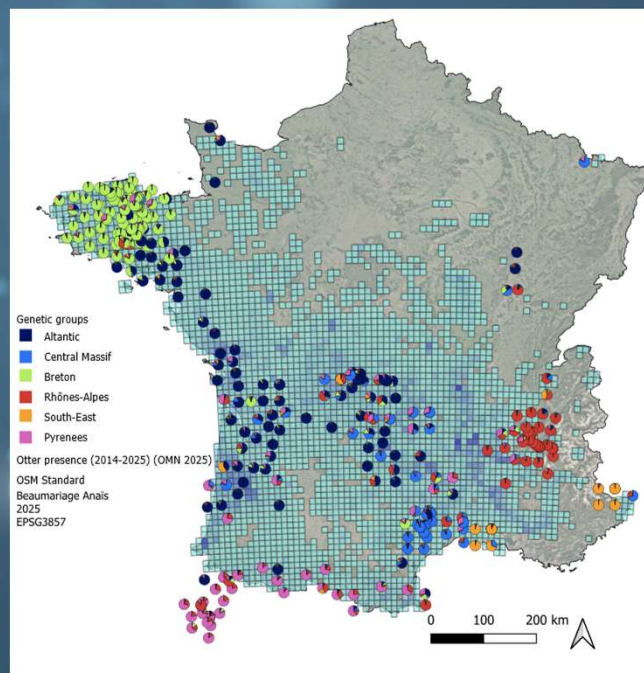


Fig.1: Spatial distribution of genetic groups. Pie charts represent membership probabilities to the K=6 clusters.

2. Genetic diversity

Main genetic reservoirs: **Atlantic** and **Central Massif** clusters host the highest allelic richness (Ar), driving the species' national recovery.

Heterozygote deficiency in the East: High Fis values in **Rhône-Alpes** and **South-East** suggest a Wahlund effect or restricted gene flow (Fig.2).

Adapted from Pigneur, L.M., et al. (2019). Current genetic admixture between relictual populations might enhance the recovery of an elusive carnivore. *Conserv. Genet.* 20, 1133-1148

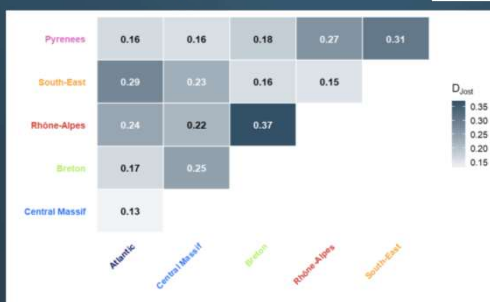


Fig.3: Pairwise genetic differentiation. Heatmap of D_{jost} values between the six genetic lineages.



While **refugial persistence** and **current admixture** fuel the species' recovery, persistent **genetic stress** in some clusters highlights that natural recolonization remains a fragile process, requiring continued **monitoring** and **habitat protection**.



A big thank you to all our collaborators and sample providers !

