

# Evidence of a fine-scale genetic structure for the endangered Pyrenean desman

## (*Galemys pyrenaicus*) in the French Pyrenees

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### Introduction

The **Pyrenean desman** (*Galemys pyrenaicus*) is probably one of the most threatened European mammal species. This small insectivorous and semi-aquatic species is endemic to the Pyrenean Mountains and of the north of the Iberic Peninsula. It is currently considered as vulnerable in the IUCN Red List and has been suffering from habitat loss and fragmentation for decades, inevitably impacting its distribution.

A recent study, based on mitochondrial and intronic sequences, revealed that this species was characterized by very low levels of genetic diversity, especially in the Pyrenean Mountains where its populations seemed highly homogeneous genetically.

In the present study we focused on the French Pyrenean populations of *G.pyrenaicus* and conducted a thorough genetic study, based on microsatellites markers and an exhaustive sampling of faeces samples. Our aim was to obtain new information on the genetic structure of this species at a finer scale.



*Galemys pyrenaicus*

### Material and methods

#### Samples collection

355 feces and 38 tissue samples coming from the six French departments encompassed in the geographical range of this species, were used in this study.

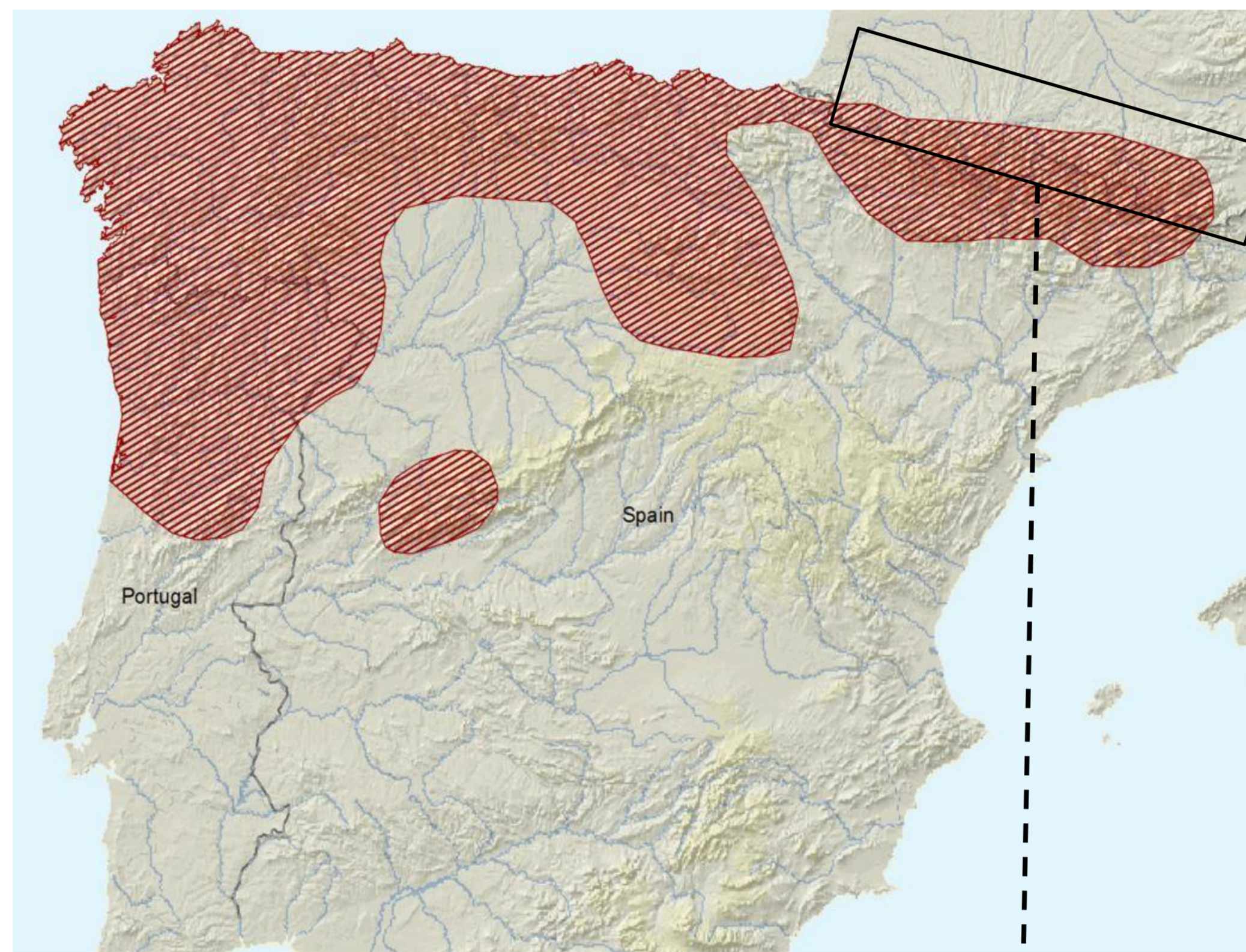
#### DNA amplification and sequencing

All samples were genotyped at 24 variable microsatellite loci, specifically designed for this species.

#### Statistical analyses

In addition to summary statistics, we used several population genetics softwares, notably to:

- Investigate the existence of a potential genetic structure among our data (STRUCTURE 2.3.1.)
- Infer the evolutionary history of *G.pyrenaicus* using approximate Bayesian computations (DIYABC1.0.4.45 beta software)



**Figure 1.** Theoretical distribution area of the Pyrenean Desman (IUCN, 2008).

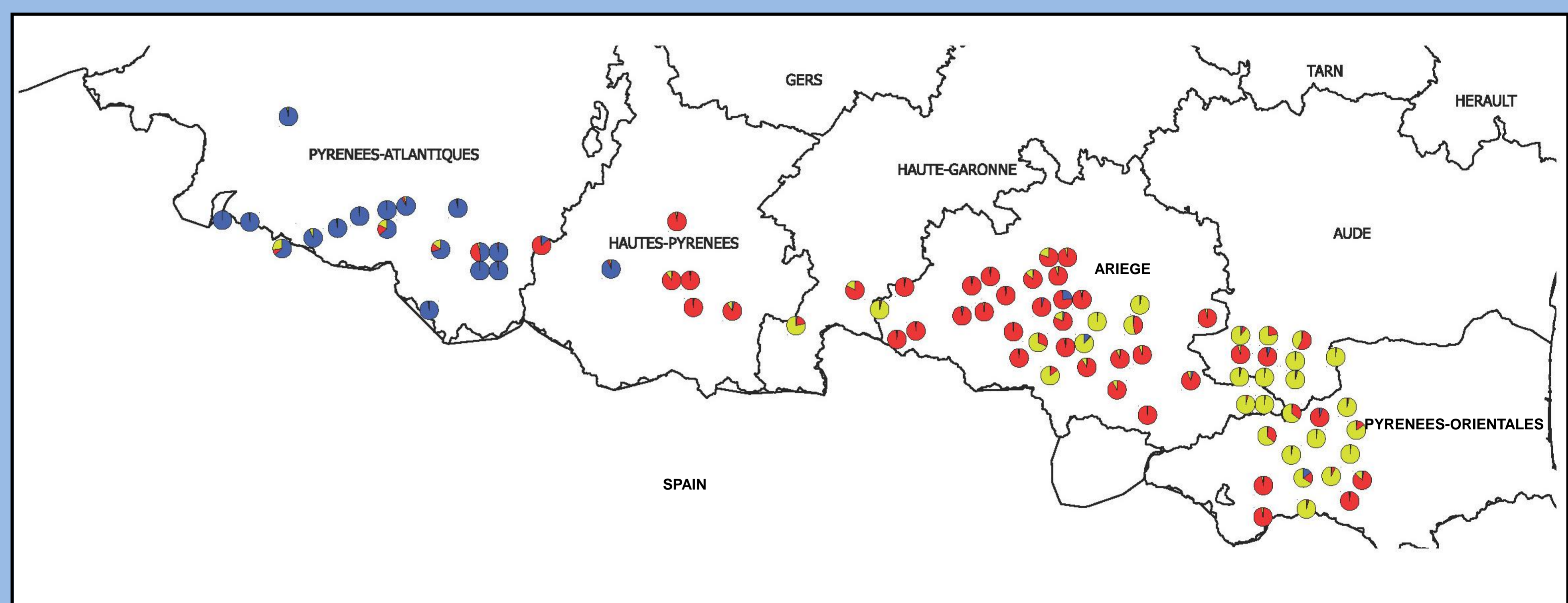
### Main Results

**Table 1.** Overview of the genetic parameters at each cluster. N : Number of samples, AR: Allelic richness, Ho: Observed heterozygosity, He: Expected heterozygosity, Fis: Inbreeding coefficient.

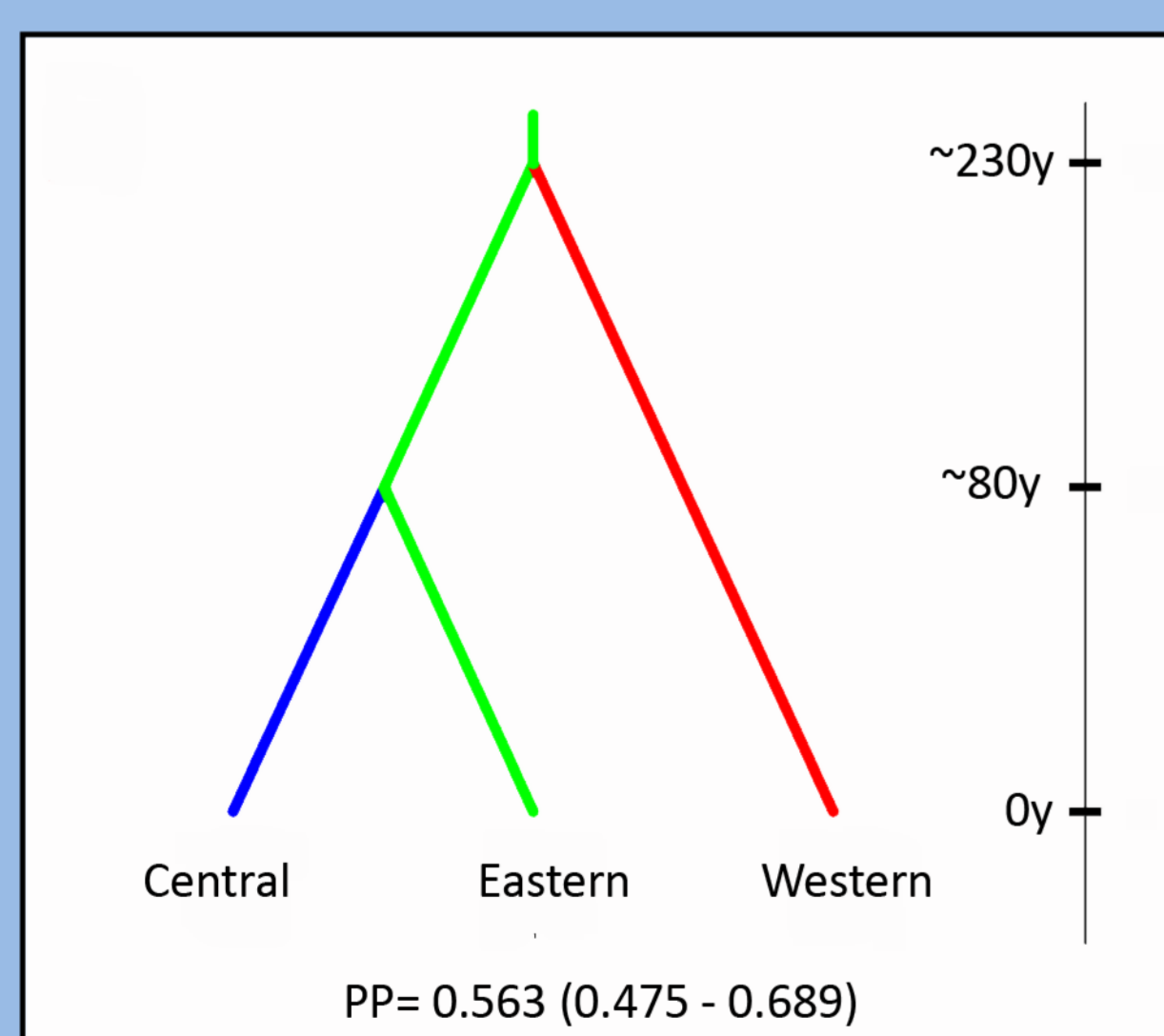
Clusters	N	Ho	He	AR	Fis
Central	42	0.226	0.274	1.405	0.179
Eastern	34	0.189	0.258	1.803	0.271
Western	25	0.216	0.368	1.703	0.434

**Table 2.** Pairwise Fst values between clusters.

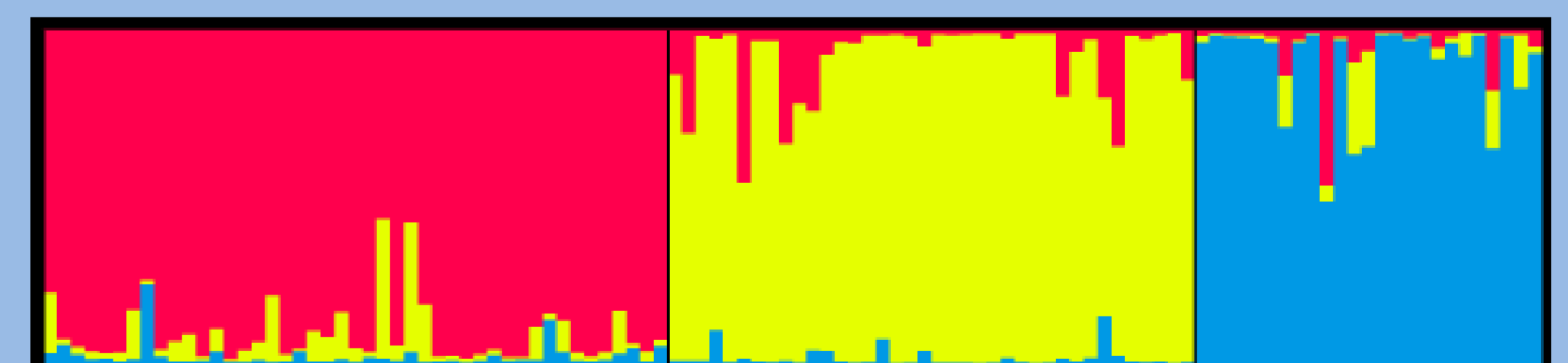
Clusters	Central	Eastern	Western
Central	-	0.288	0.203
Eastern	-	-	0.345
Western	-	-	-



**Figure 2.** Geographic distribution of the three genetic clusters that were discovered among our data. We can easily distinct an eastern, a central and a western cluster. Each diagram represents one individual with its respective clusters assignments.



**Figure 4.** Most likely evolutive scenario fitting to our data matrix, obtained with DIYABC. The estimated divergence times and posterior probabilities (PP) are displayed in the figure.



**Figure 3.** Clusters inferred with STRUCTURE, with Evanno correction (k=3). Cluster membership of each sample is shown by the colour composition of vertical lines. Spatial distribution is shown in Figure 2.

### Conclusion

The present study allowed to highlight a deep and fine scale genetic structure for the Pyrenean desman in the French Pyrenees. We evidenced three distinct clusters geographically spread across the French range of the species. This structure seems to have appeared more than 200 years ago, probably under the effect of concomitant human and environmental factors. Low levels of genetic diversity were found for all three clusters as well as a high inbreeding coefficient (Table 1) and high Fst values between clusters (Table 2). This is probably be the result of recent bottleneck events which could increase the risk of inbreeding depression for these populations, especially in the western one (Fis= 0.4). However, clusters are overlapping at some points and seem to have been exchanging alleles recently (Fig.2). This could lead to an improvement of the genetic diversity of the species in the future and would be an indication of a greater dispersal potential than previously accepted. Therefore connectivity between watersheds should not be discarded in order to ensure a certain level of genetic diversity and to improve the conservation of the Pyrenean desman in France.

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