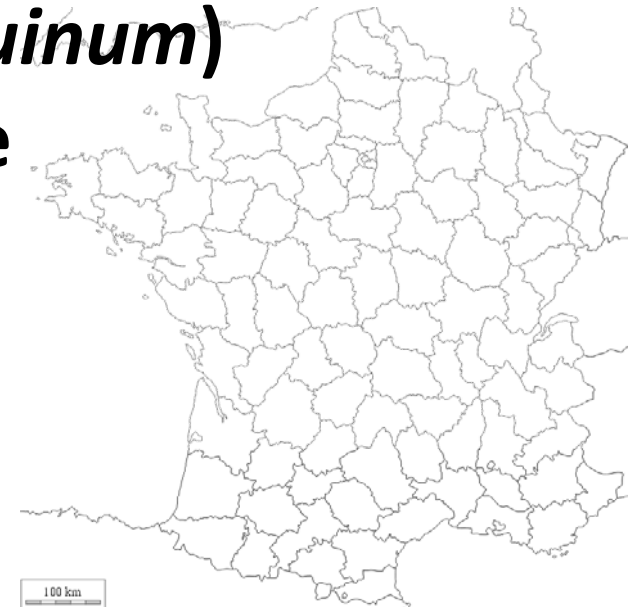


Population genetics of the greater horseshoe bat (*Rhinolophus ferrumequinum*) in Western France

Orianne Tournayre



orianne.tournayre@supagro.fr

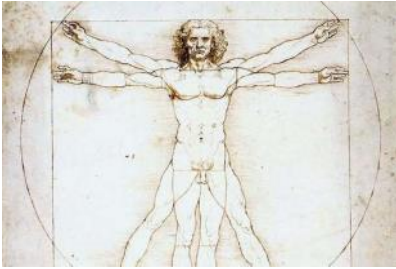




Severe decline at the North of Europe
(Harris et al. 1995)

→ By 90% in Great Britain





Mainly anthropogenic causes :

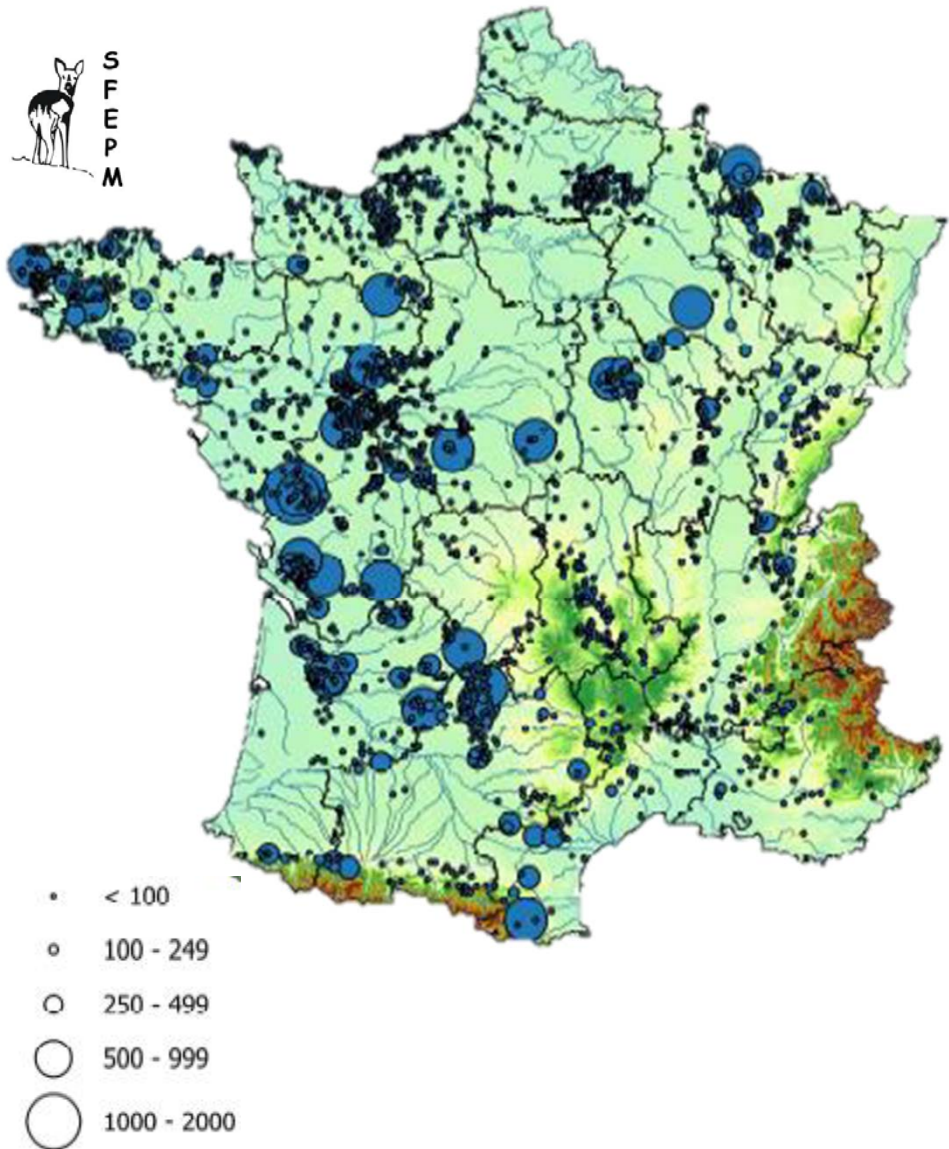
- ❖ Renovation of the buildings, closing of roosts :
——→ Disappearing of suitable roosts

- ❖ Increase of intensive agriculture & roads :
——→ Potential barriers to dispersal, increase of mortality

- ❖ Use of pesticides, antihelminthics
——→ Contaminations of bats, habitats & preys

Contexte

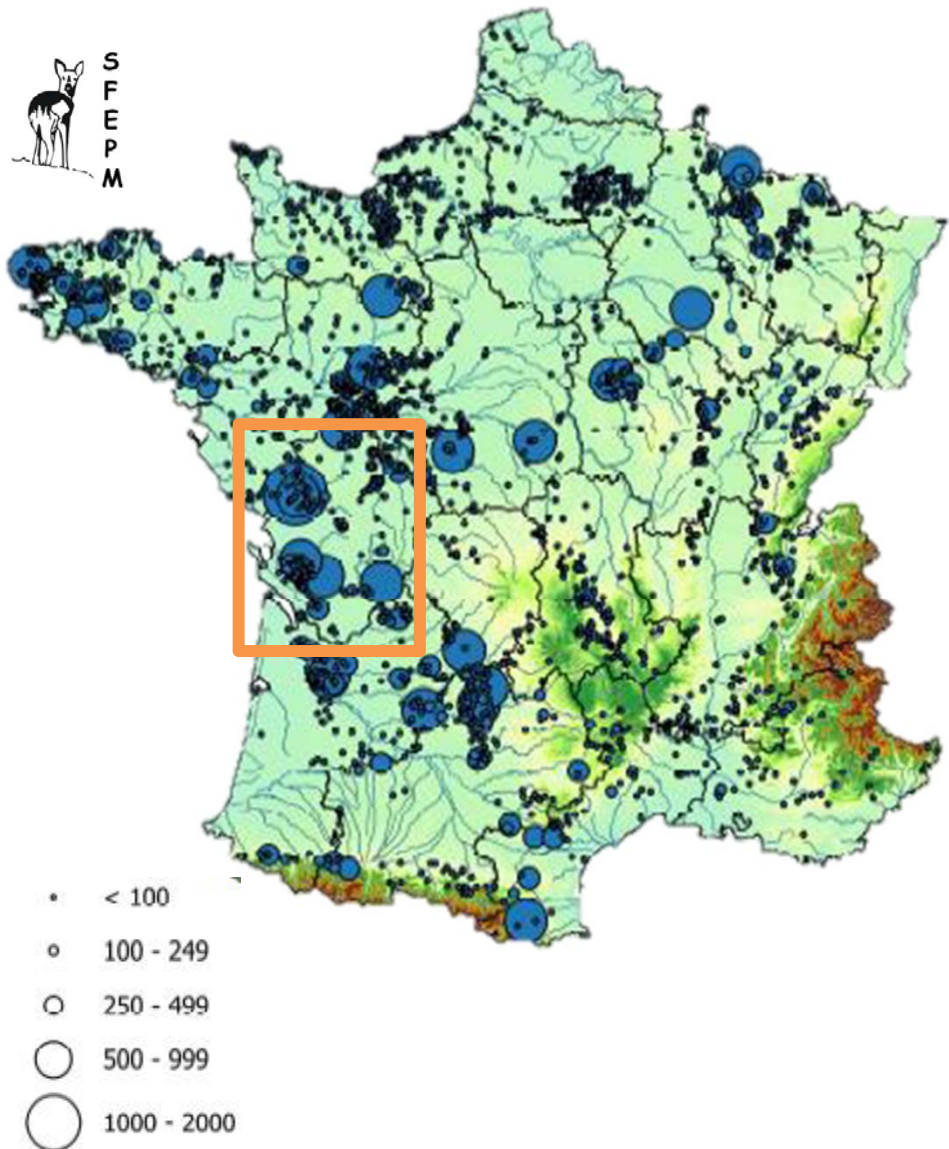
The greater horseshoe bat in France and Poitou-Charentes



Disparate distribution of the known roosts

Contexte

The greater horseshoe bat in France and Poitou-Charentes



Poitou-Charentes

4th biggest hibernating population of France



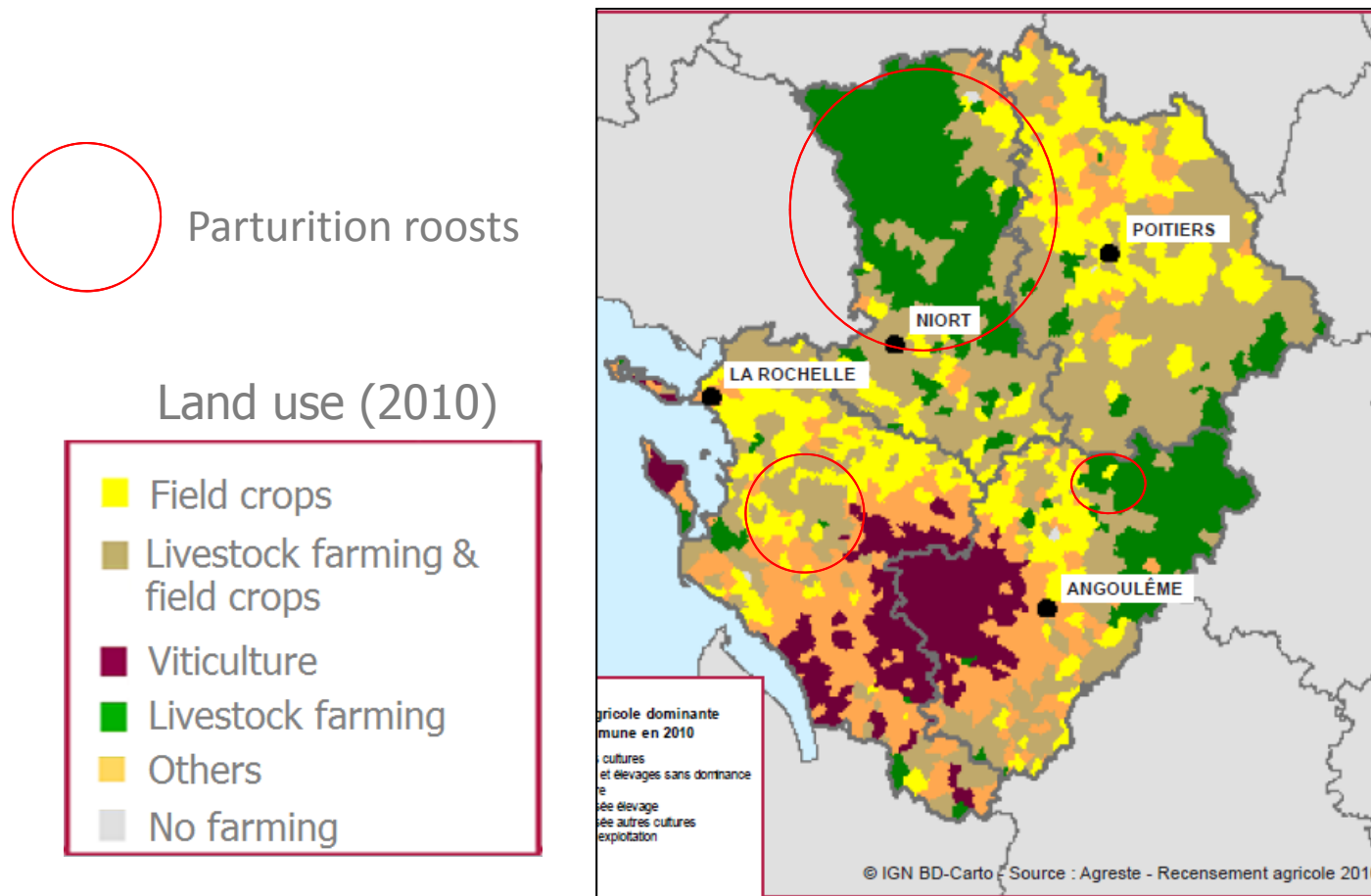
Counts of individuals in winter roosts



Decline by 30% over the last ten years

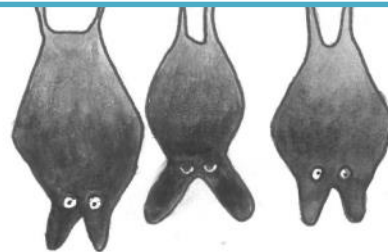
The greater horseshoe bat in France and Poitou-Charentes

A fragmented landscape with high anthropic pressure



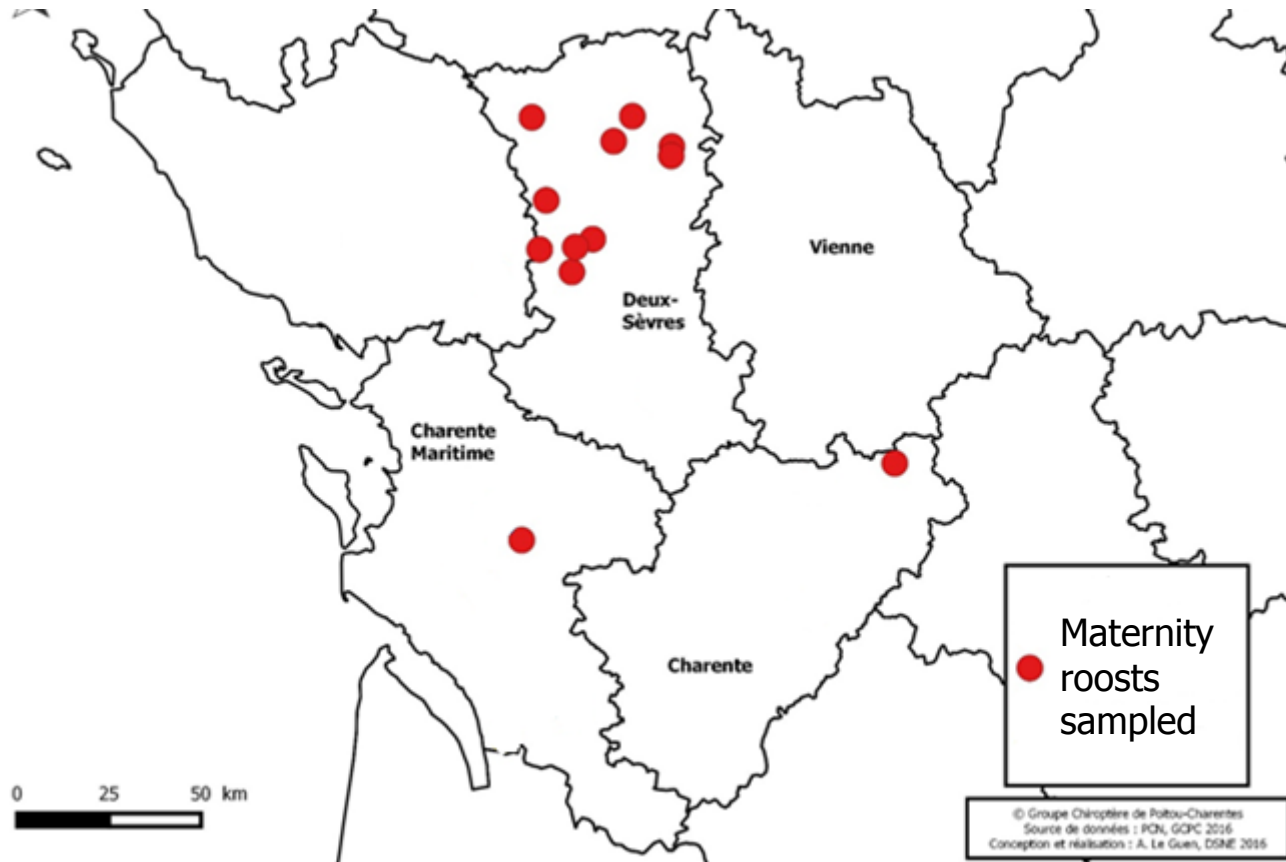
Possible isolation of the colonies from the North and the colonies of the South

- ❖ Describe the levels of genetic diversity
Variation between distant colonies ?
- ❖ Analyse the kinship inside the colonies
Can we detect matrilineal lines resulting from its philopatry behaviour ?
- ❖ Analyse the genetic differentiation between colonies
Are some colonies isolated ? Can we identify barriers to dispersal?
- ❖ Analyse signatures of population dynamics changes
Did these colonies experience recent bottlenecks ?





Sampling of 536 adult females in 11 known maternity roosts of Poitou-Charentes (2016)

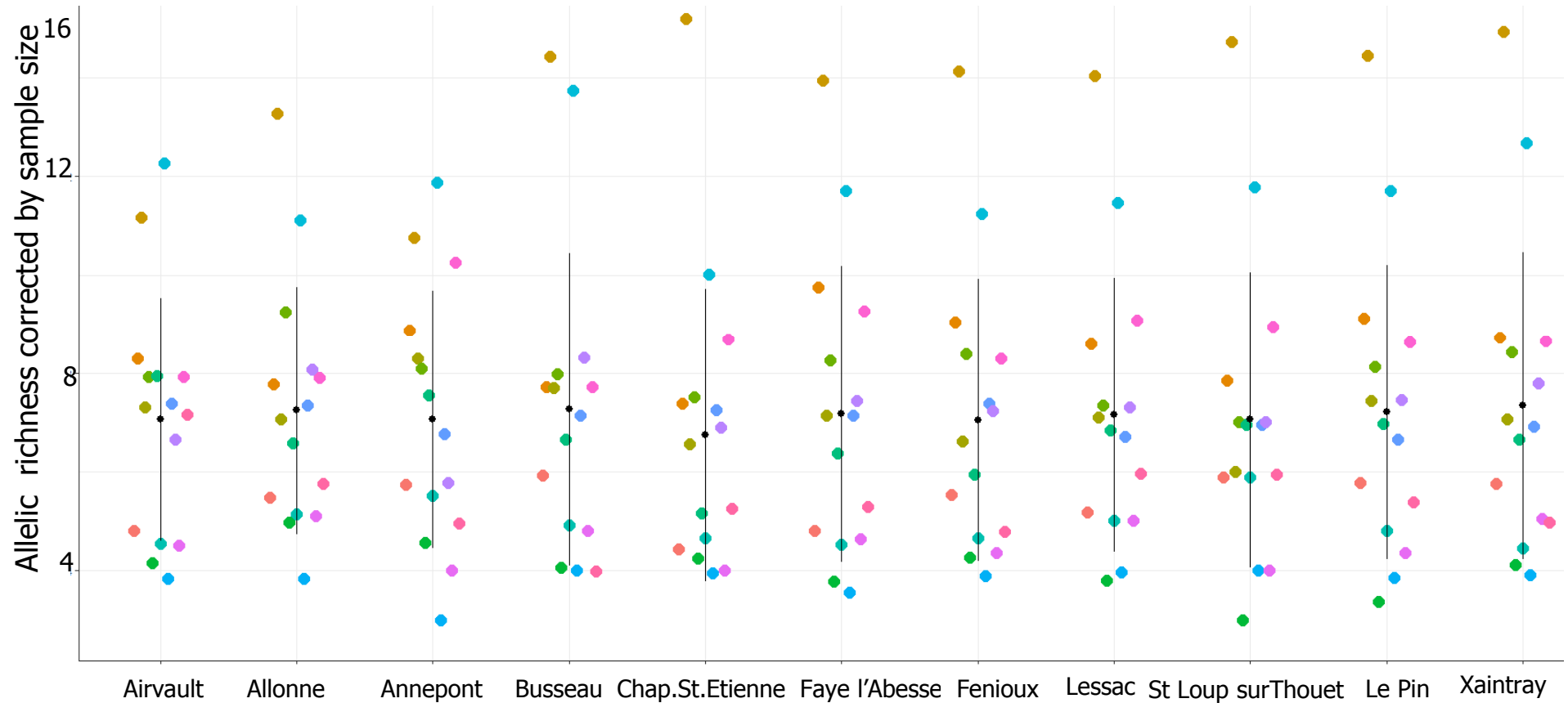


Capture/Mark/Recapture
Punch of patagium



Genotyping
18 microsatellites

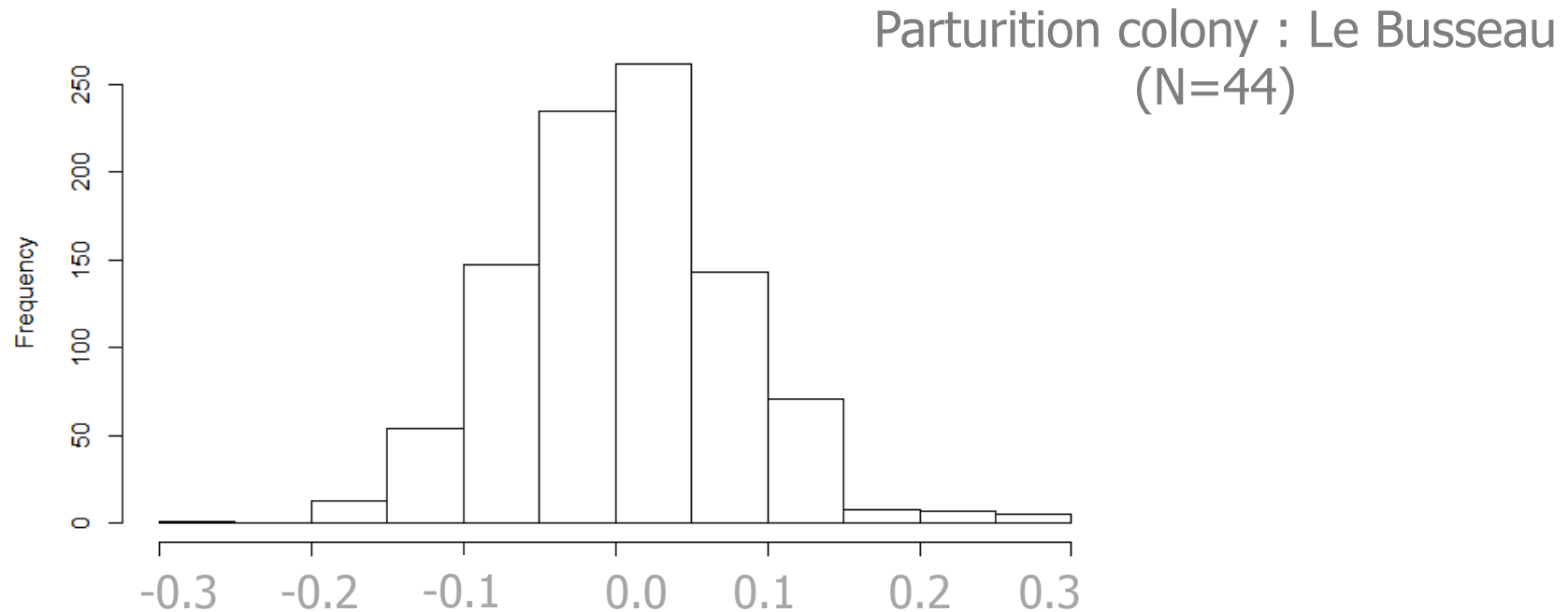




➡ High genetic diversity, homogeneous between loci and colonies

➡ High genetic diversity even within distant colonies of the South

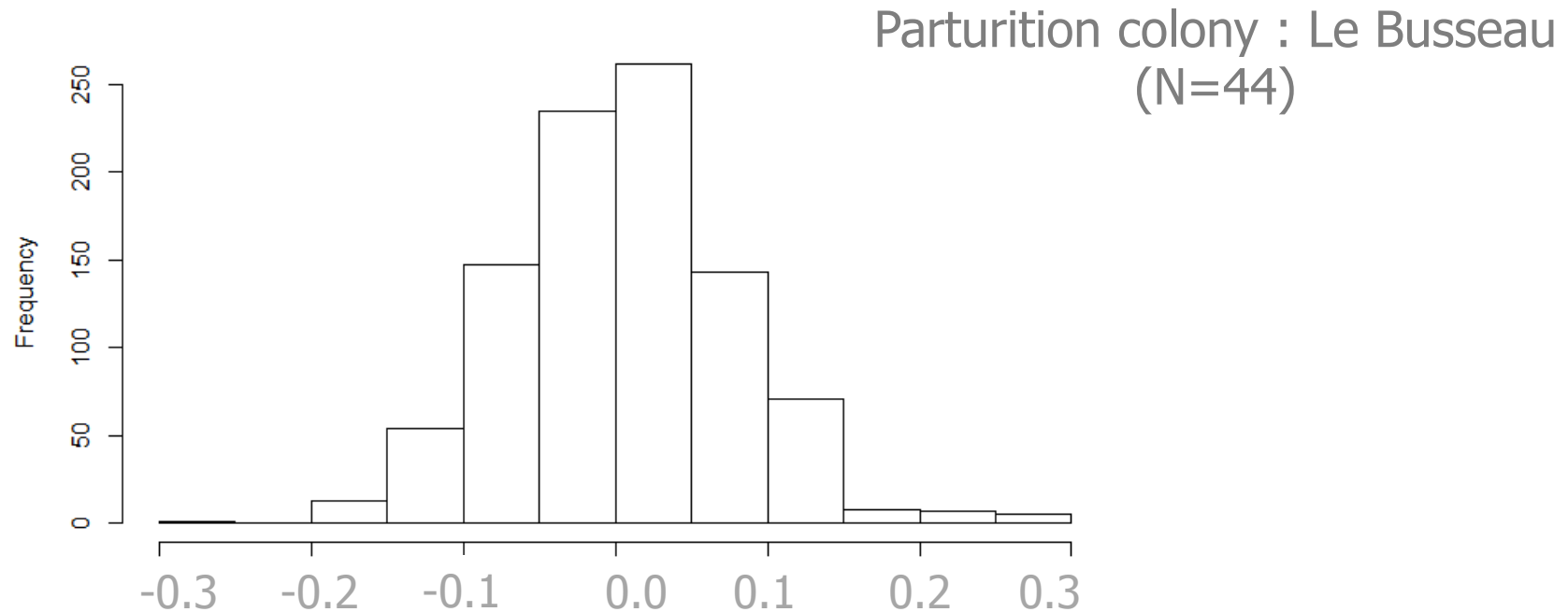
Distribution of the kinship coefficient (Loiselle et al. 1995) of adult females per colony



➡ Only very few strong kinship coefficient (≥ 0.2)

➡ Unimodal distribution, centered on zero

Distribution of the kinship coefficient (Loiselle et al. 1995) of adult females per colony

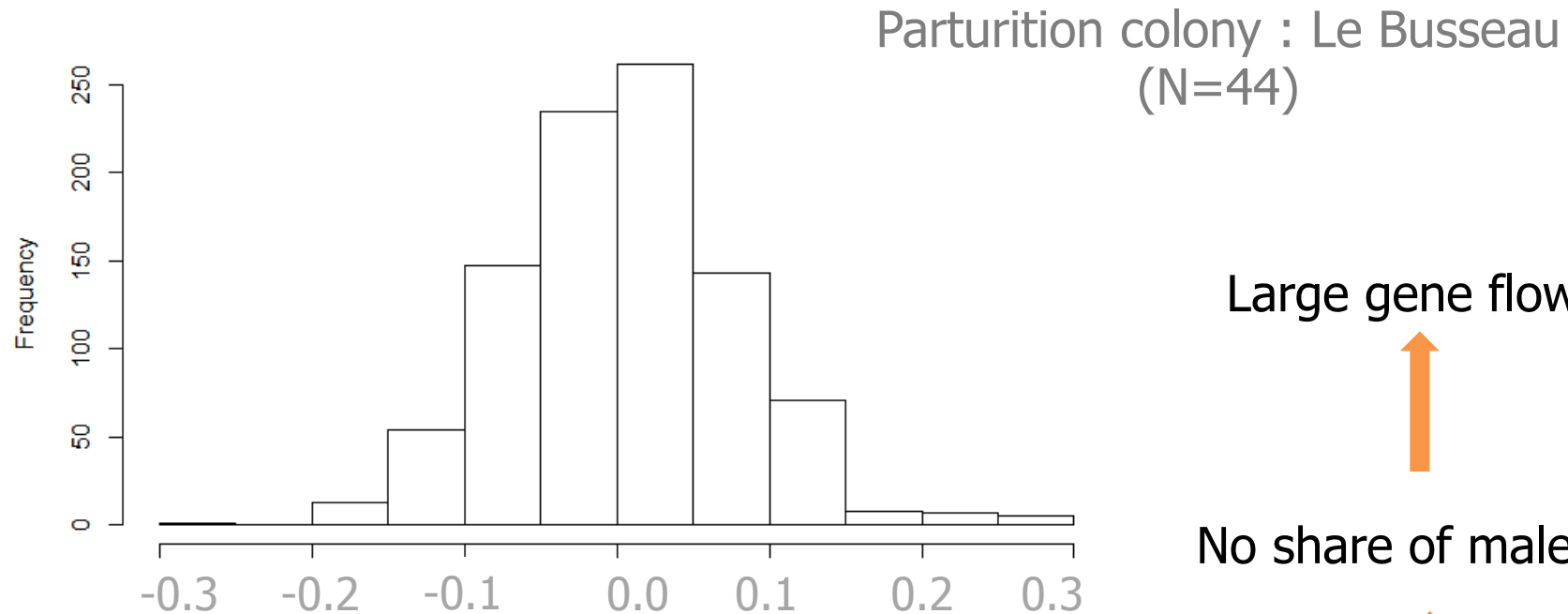


➡ Only very few strong kinship coefficient (≥ 0.2)

➡ Unimodal distribution, centered on zero

➡ No signature of
matrilines in the colonies

Distribution of the kinship coefficient (Loiselle et al. 1995) of adult females per colony



Large gene flow



No share of males



No signature of
matriline in the colonies

➡ Only very few strong kinship coefficient (≥ 0.2)

➡ Unimodal distribution, centered on zero





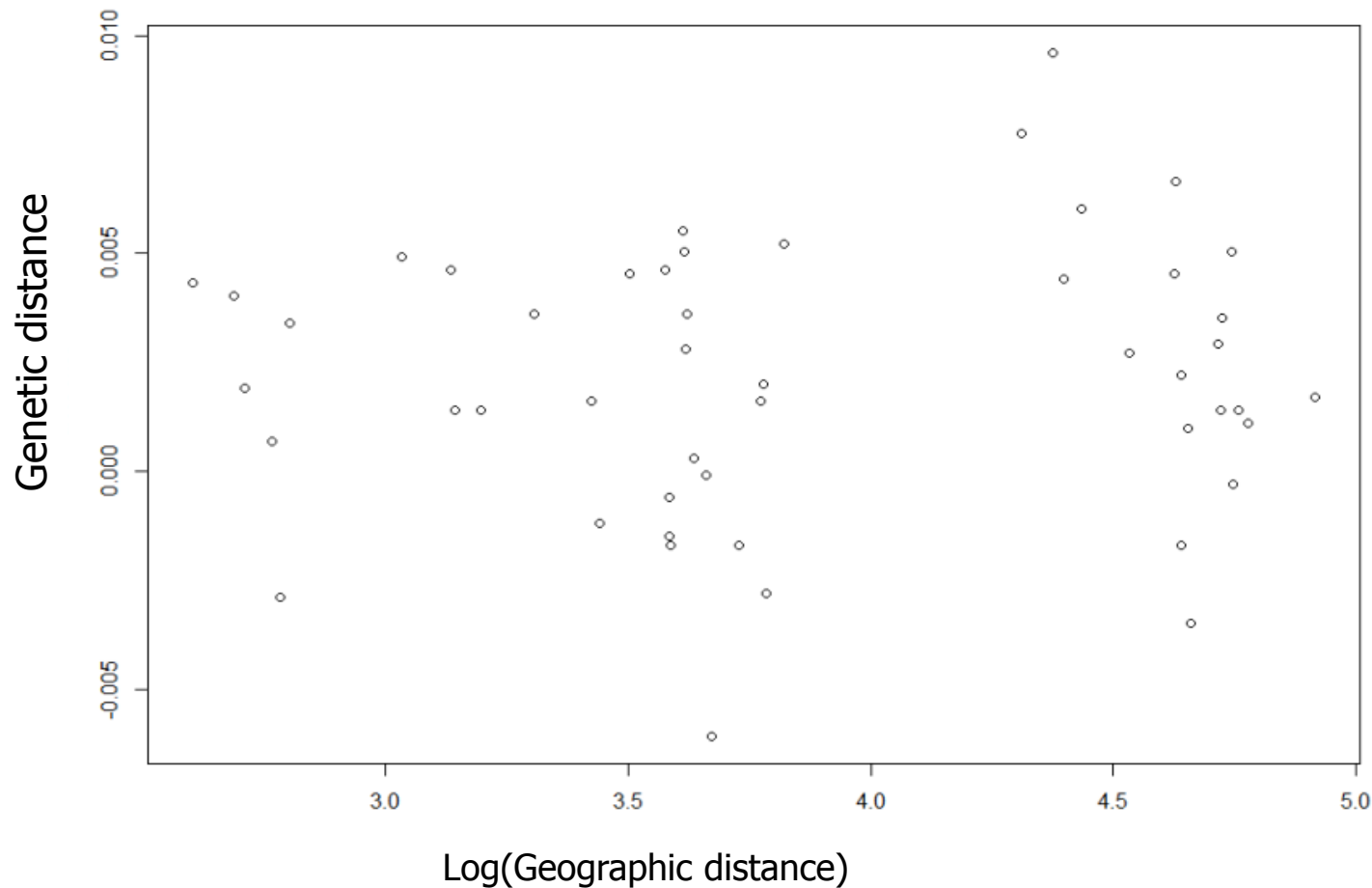
Results

Genetic structure between colonies

→ Genetic differentiation between colonies
Fst values very weak : from 0 to 0.009

Genetic structure between colonies

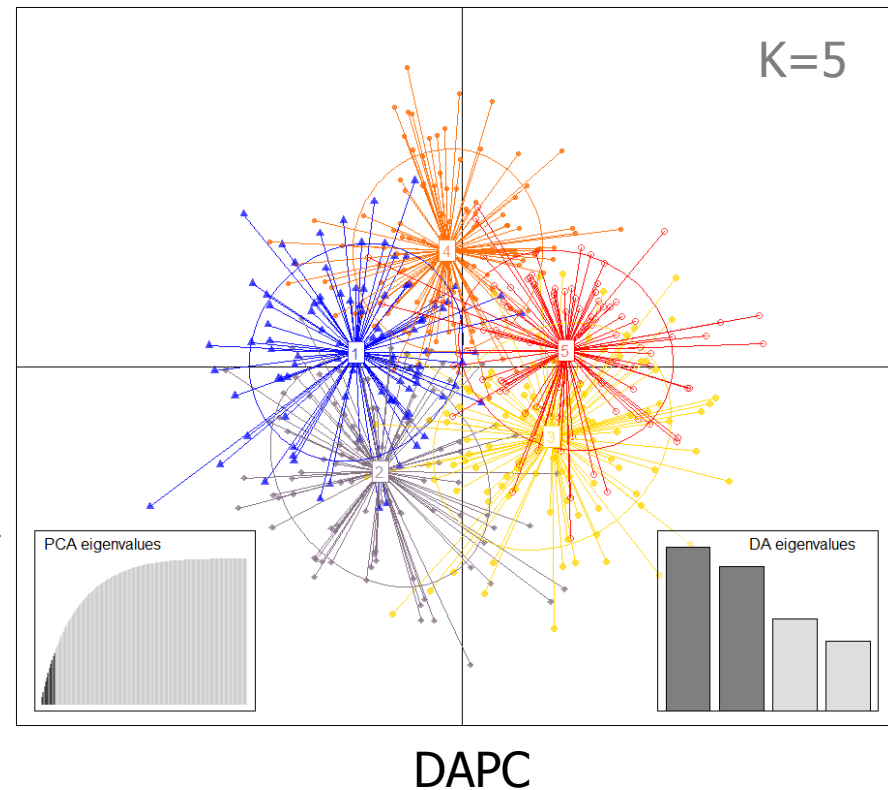
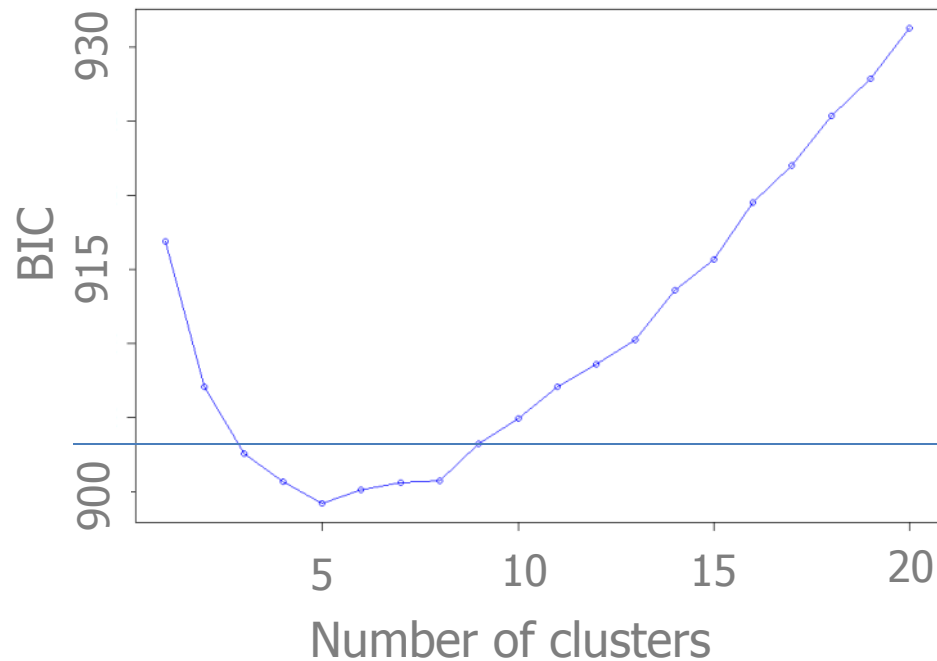
- ➔ Genetic differentiation between colonies
Fst values very weak : from 0 to 0.009
- ➔ No pattern of Isolation by distance (Mantel test: $p\text{-value} > 0.05$)



Results

Genetic structure between colonies

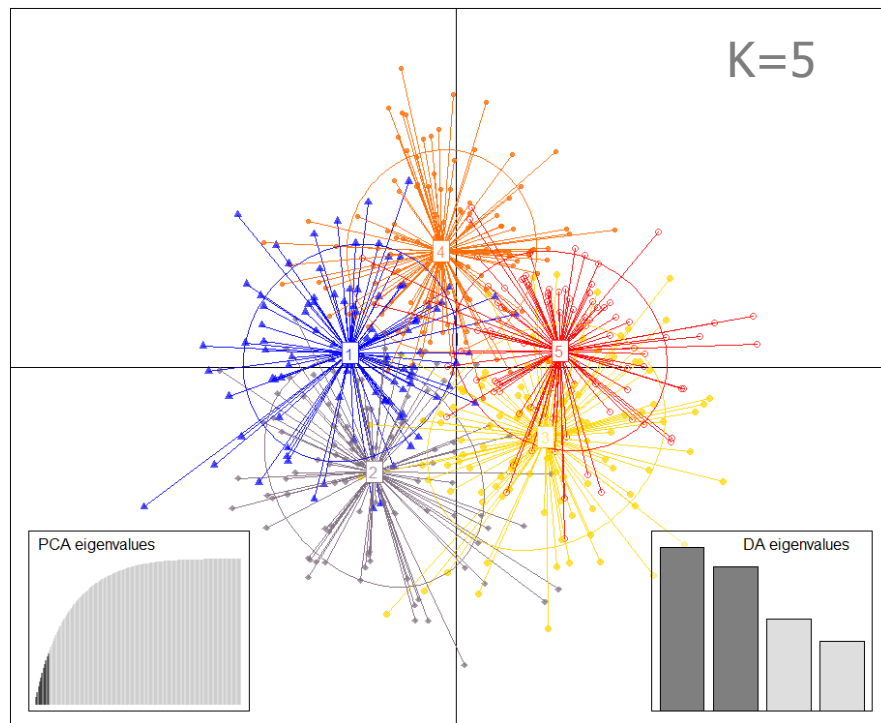
- ➔ Genetic differentiation between colonies
Fst values very weak : from 0 to 0.009
- ➔ No pattern of Isolation by distance
- ➔ No relevant clustering of colonies



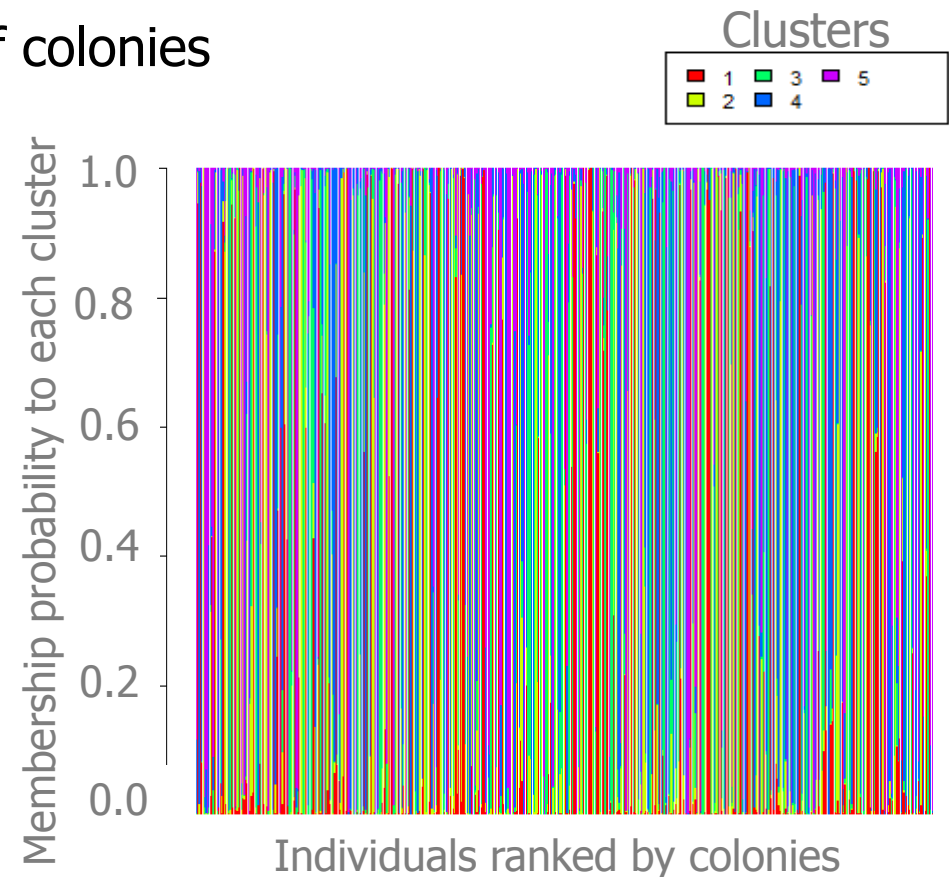
Results

Genetic structure between colonies

- ➔ Genetic differentiation between colonies
Fst values very weak : from 0 to 0.009
- ➔ No pattern of Isolation by distance
- ➔ No relevant clustering of colonies



DAPC



Individuals ranked by colonies

Results

Genetic structure between colonies

- ➡ Genetic differentiation between colonies
Fst values very weak : from 0 to 0.009
- ➡ No pattern of Isolation by distance
- ➡ No relevant clustering of colonies
 - ➡ Large gene flow at this regional scale
 - ➡ No barrier to dispersal (juvenile and reproduction)
 - ➡ Panmictic population in Poitou-Charentes?

Ongoing analysis with the *Migrate* software (Leblois et al. 2014)

Maximum-Likelihood Inference of Population Size Contractions from Microsatellite Data

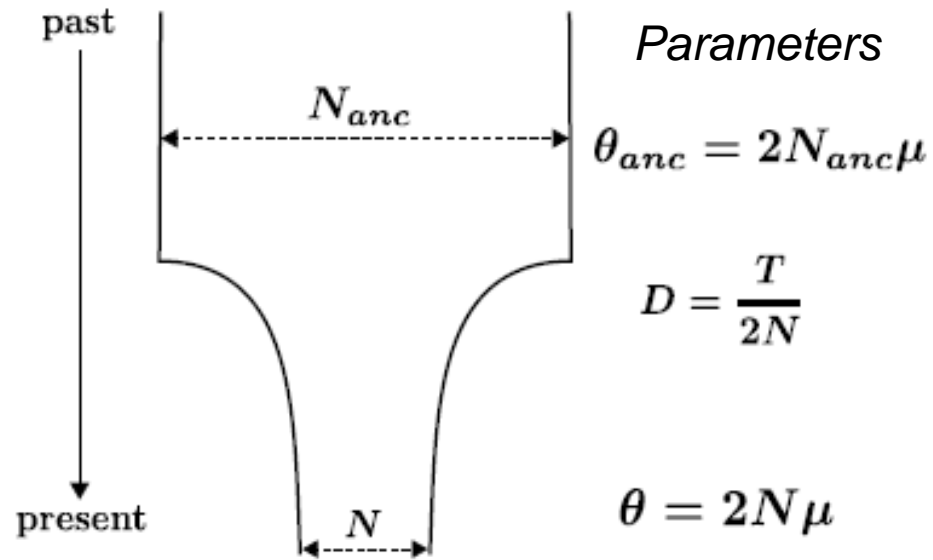
Raphaël Leblois,^{*1,2,3} Pierre Pudlo,^{1,3,4} Joseph Néron,² François Bertaux,^{2,5} Champak Reddy Beeravolu,¹ Renaud Vitalis,^{1,3} and François Rousset^{3,6}

MOLECULAR BIOLOGY AND EVOLUTION



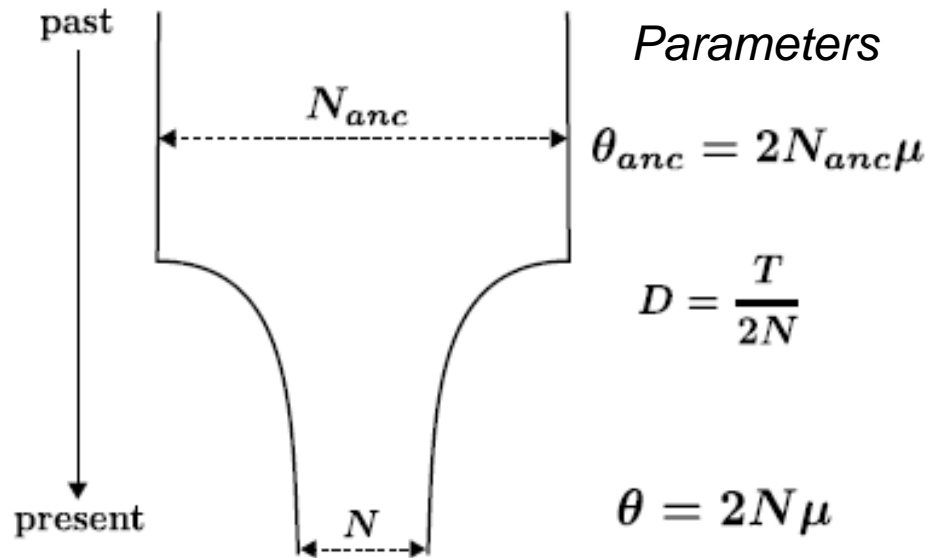
Analyse ancient or recent population size changes

Migraine software (Leblois et al. 2014)



'OnePopOneVar' model

Migraine software (Leblois et al. 2014)



'OnePopOneVar' model

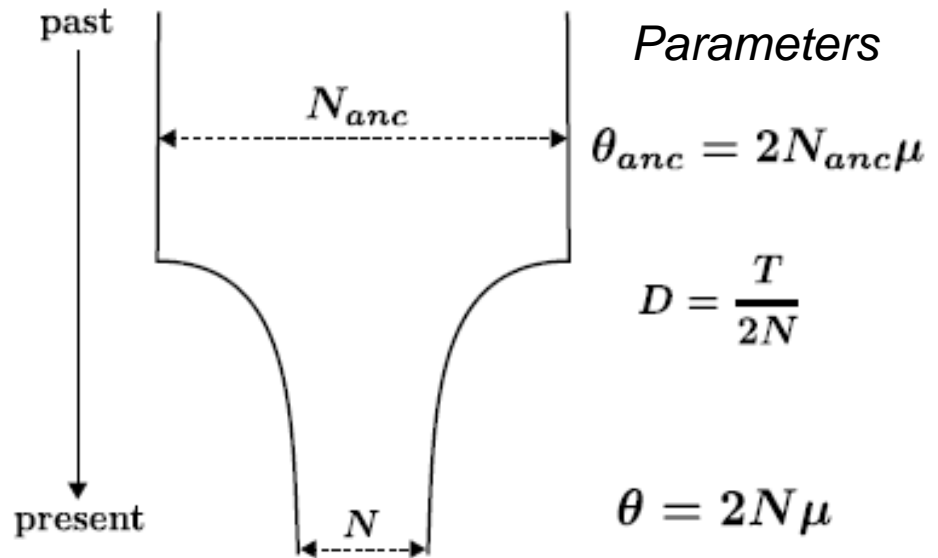


Simulations to explore the parameters space & maximum likelihood based on coalescence



Best estimations of the parameters

Migraine software (Leblois et al. 2014)



'OnePopOneVar' model



Simulations to explore the parameters space & maximum likelihood based on coalescence



Best estimations of the parameters



Ratio $\theta/\theta_{anc} < 1$: bottleneck
> 1 : expansion
 ≈ 1 : stable

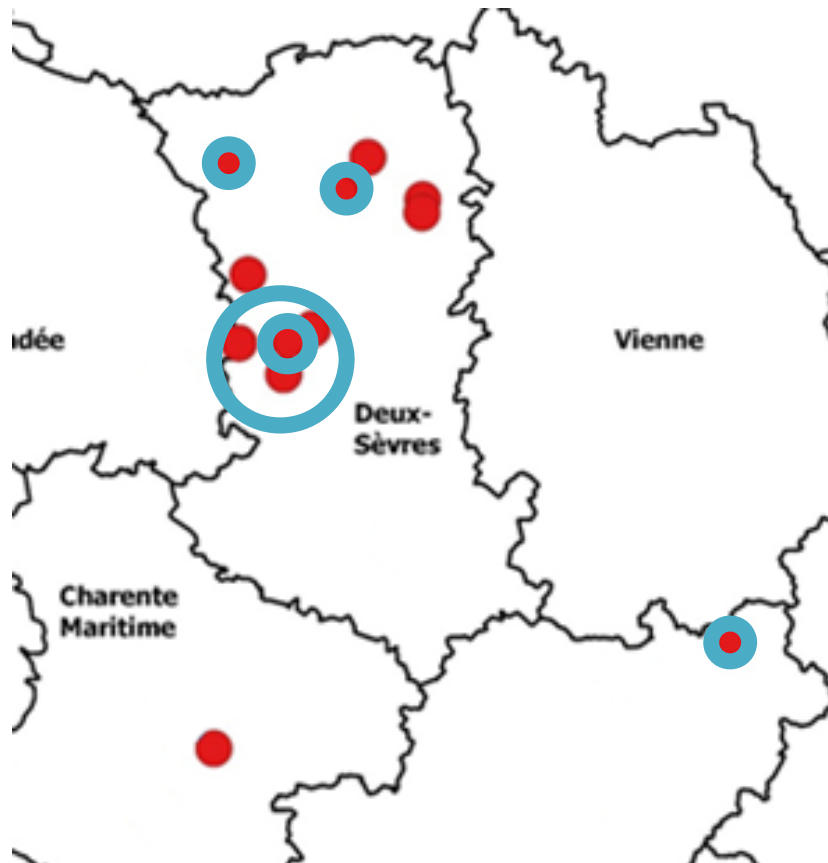
Migraine software



Analysis on :

- 4 colonies separately

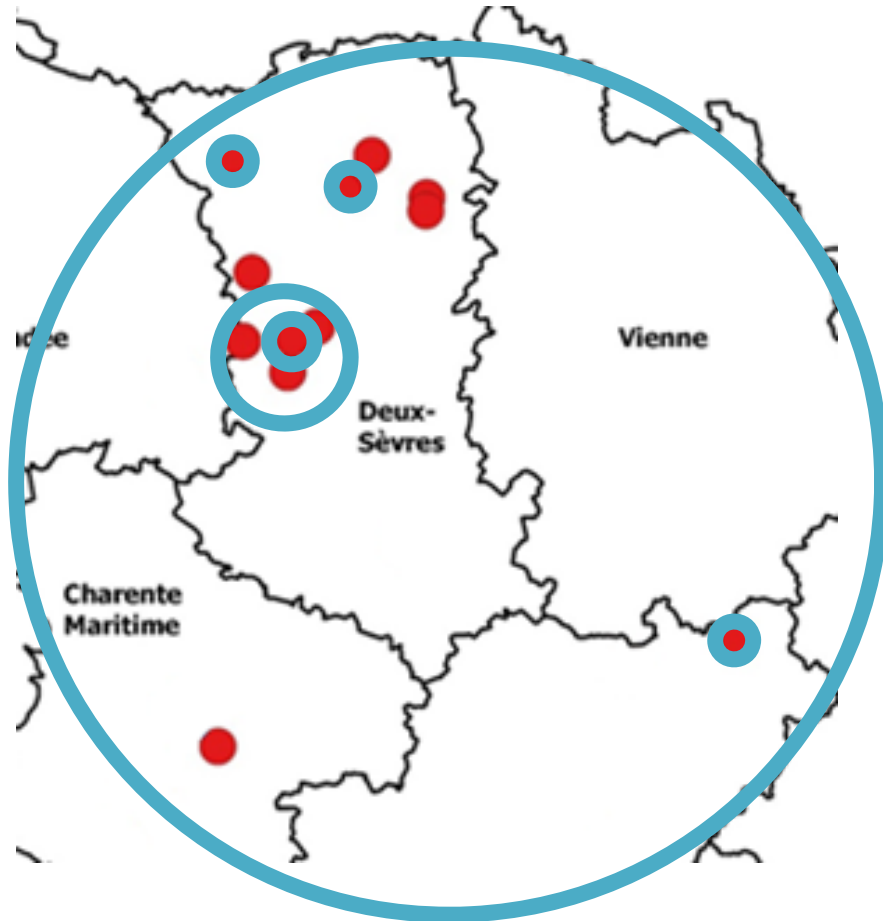
Migraine software



Analysis on :

- 4 colonies separately
- One cluster of 4 close colonies

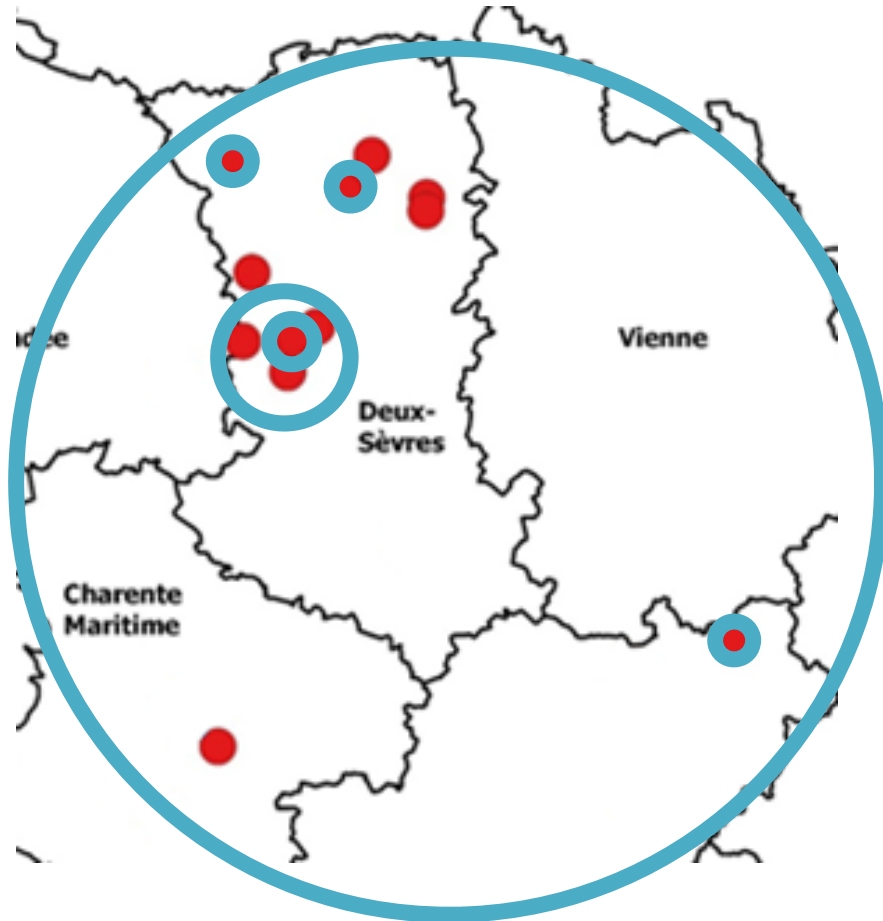
Migraine software



Analysis on :

- 4 colonies separately
- One cluster of 4 close colonies
- One cluster of all the colonies

Migraine software



Analysis on :

- 4 colonies separately
- One cluster of 4 close colonies
- One cluster of all the colonies

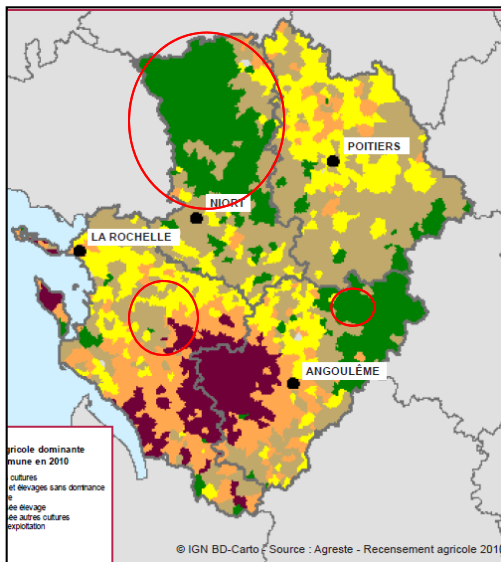


Signatures of stability

$$\text{Ratio } \theta / \theta_{\text{anc}} \approx 1$$

- ➔ No signal of matrines as expected under philopatric behaviour
 - ➔ Large genetic mixing during reproduction
 - ➔ Results contrasting with those of UK : because of methodology ?

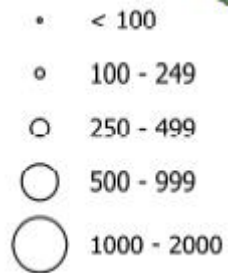
➔ No genetic structure : no landscape barrier at this scale



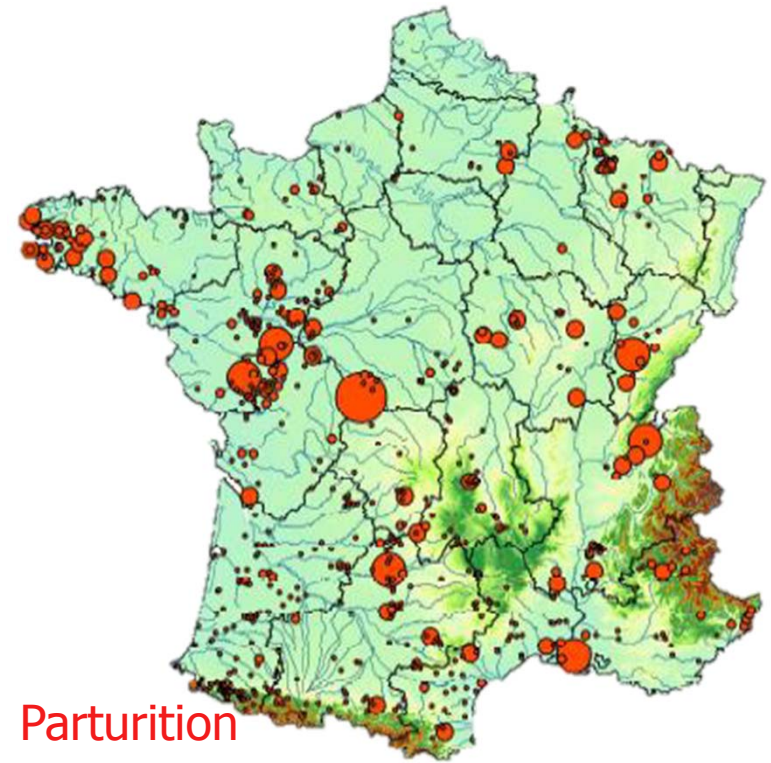
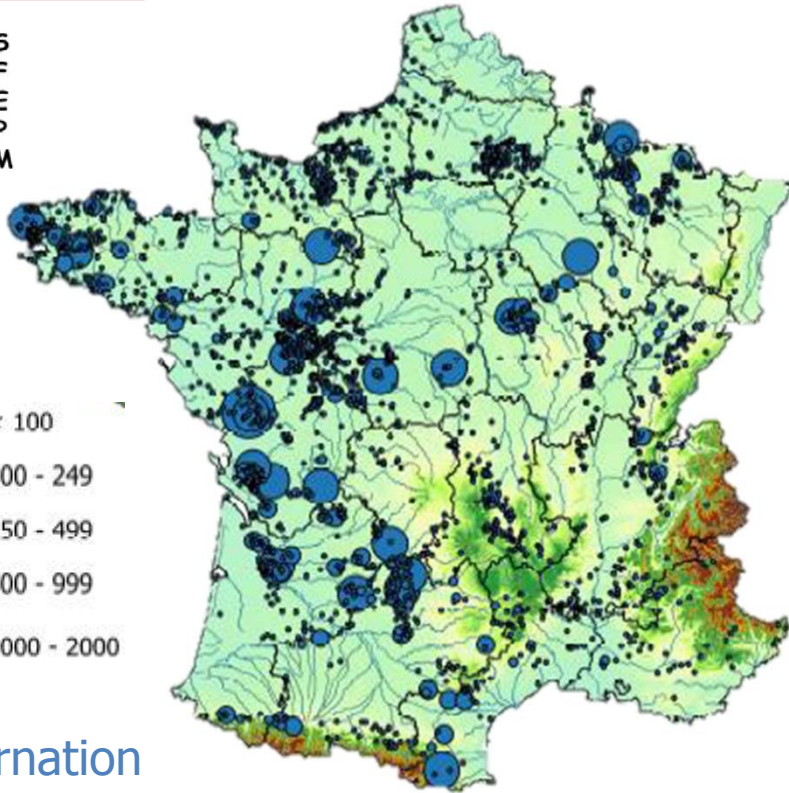
- ➔ Fragmentation and distance between colonies do not limit gene flow
 - ➔ Congruent with capture/recapture data
 - ➔ Need a bigger scale
- ➔ No risk of local extinction of Poitou-Charentes colonies due to genetic drift

Conclusion

Take home message



Hibernation



Parturition

➡ No evidence of a strong bottleneck in Western France

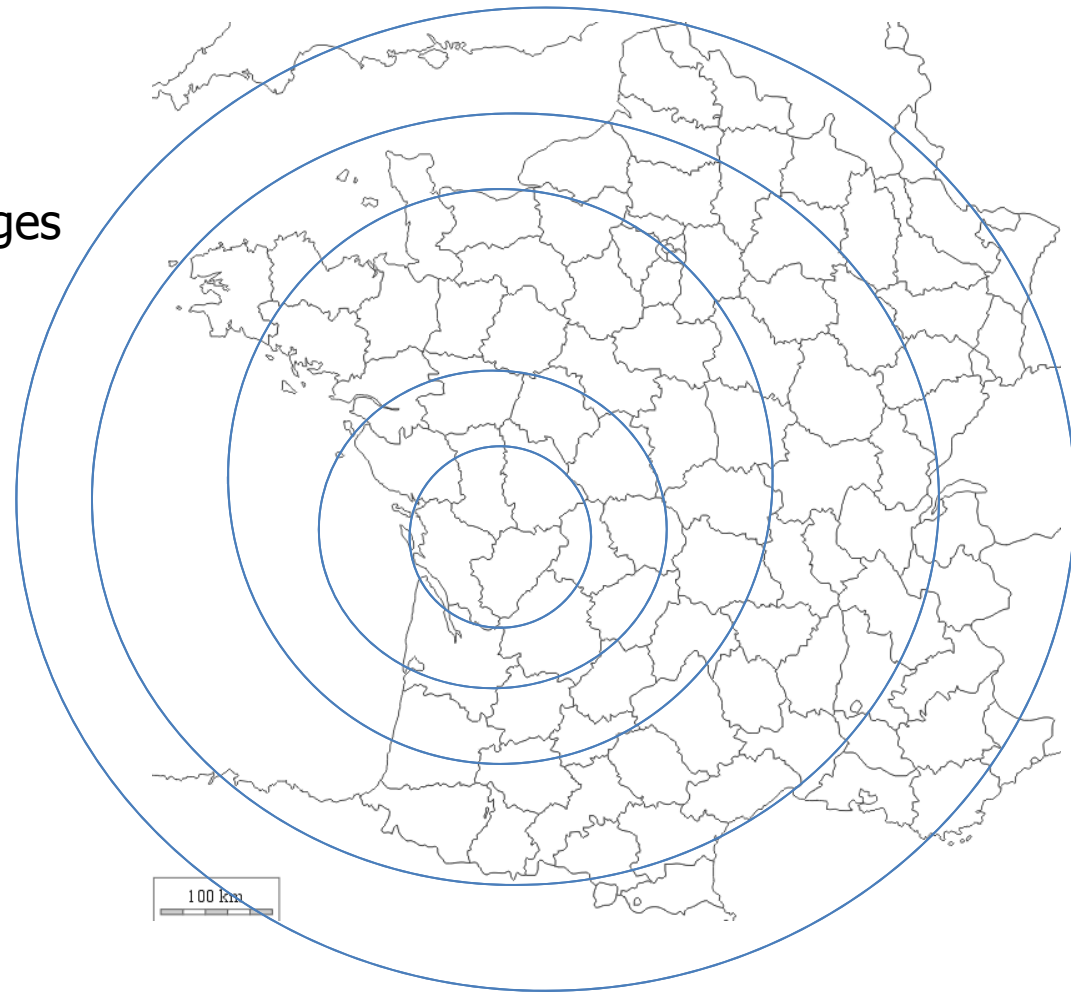
→ Not in contradiction to count data

→ Need a bigger scale

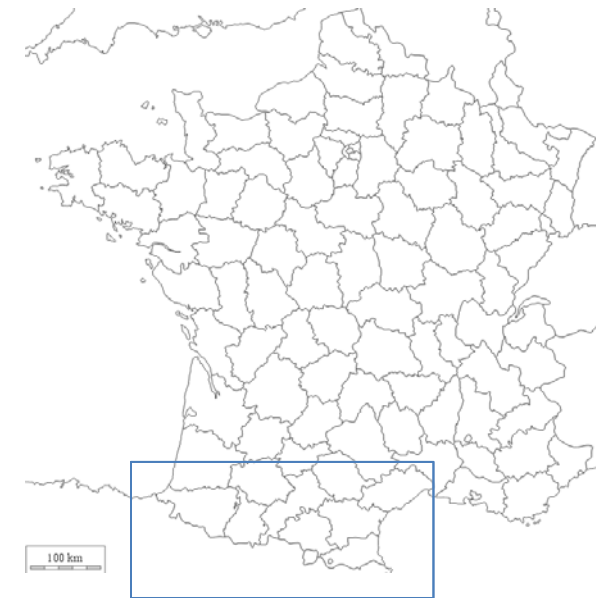
→ Limits of the model

★ Find the geographical scale at which the genetic differentiation occurs

- To define conservation units
- To estimate demographic changes



- ★ Find the geographical scale at which the genetic differentiation occurs
- ★ Test the impact of large landscape barriers: rivers & sea (Gironde, Channel), mountains (Pyrenees, Alps), *etc*



➔ Need samples from all over France and neighbouring countries !

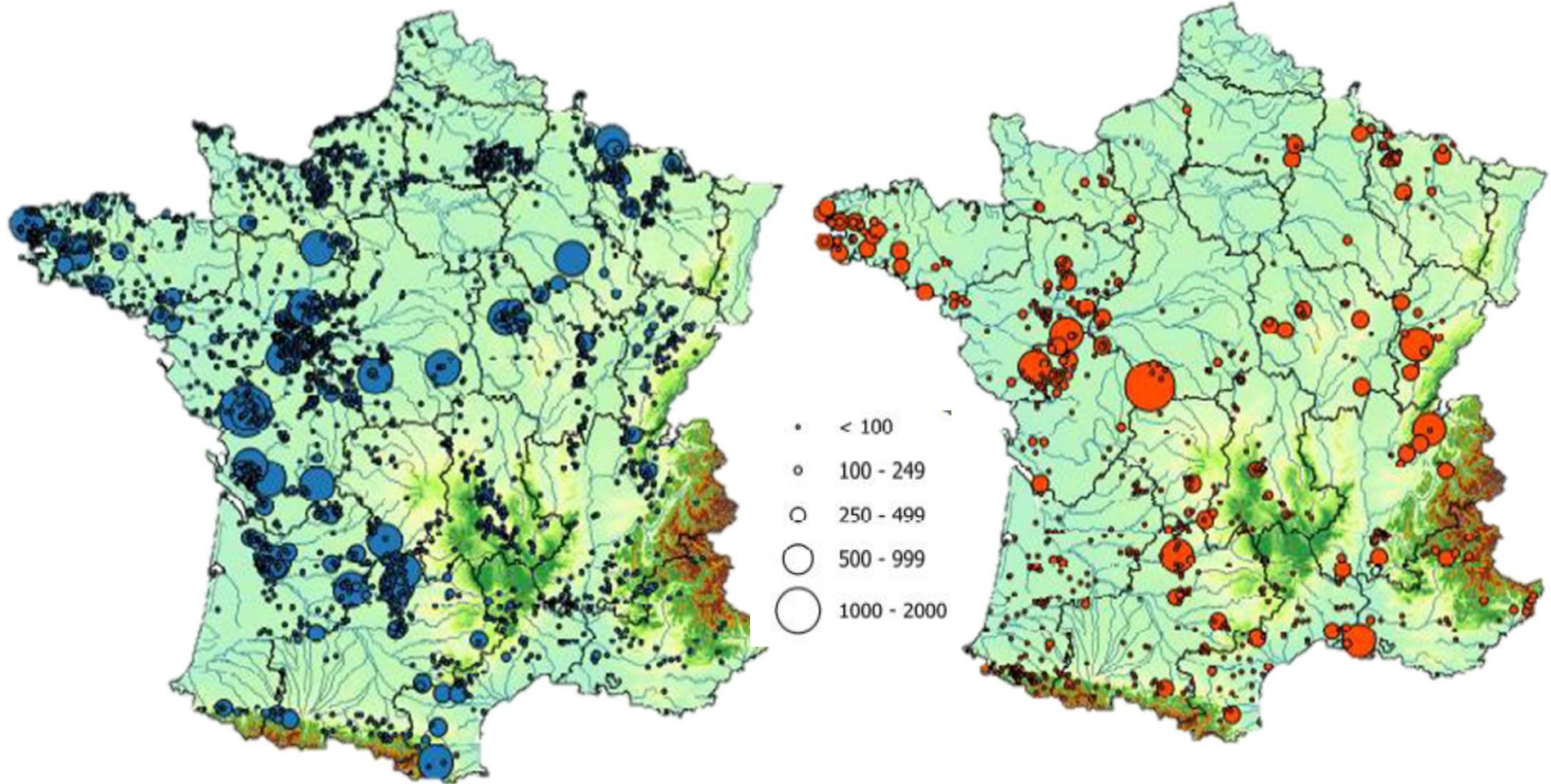


THANKS FOR YOUR ATTENTION

- Maxime Leuchtman and all our collaborators and volunteers that managed the field work (Nature-Environnement 17, Charente Nature, Deux-Sèvres Nature-Environnement, Vienne Nature, LPO France)
- All collaborators
 - LBBE (Lyon): Dominique Pontier & Jean-Baptiste Pons
 - CBGP (Montpellier) : Nathalie Charbonnel, Anne Loiseau, Raphael Leblois, Karine Berthier & Sylvain Piry



The greater horseshoe bat in France



Hibernation

Parturition