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Management of genetic variability in French small ruminants with and without pedigree information

Review and pratical lessons

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A large number of breeds with different objectives

- A significant number of breeds (more than 70 sheep and goat breeds)
- Different objectives depending on the genetic patterns :
  - Populations under selection
  - Populations in conservation
- Different organisation levels

with different constraints

- More or less important constraints :

  - Pedigree knowledge

  - Demographic parameters: limited population sizes , male rates

  - Breeding system : number of breeders, crossbreeding or not, etc.

Methods to answer to a common objective

- Avoid a fast increase of inbreeding

→ Development of methods based on:

- The standardization of sizes between breeding offspring
- Population sub-divisions into breeding groups

Simple rules confirmed by a pedigree analysis of rare French sheep breeds

(Pedigree analysis of seven small French sheep populations and lessons for the management of rare breeds – C. Danchin-Burge et al.)

Choice of a wide array of situations :

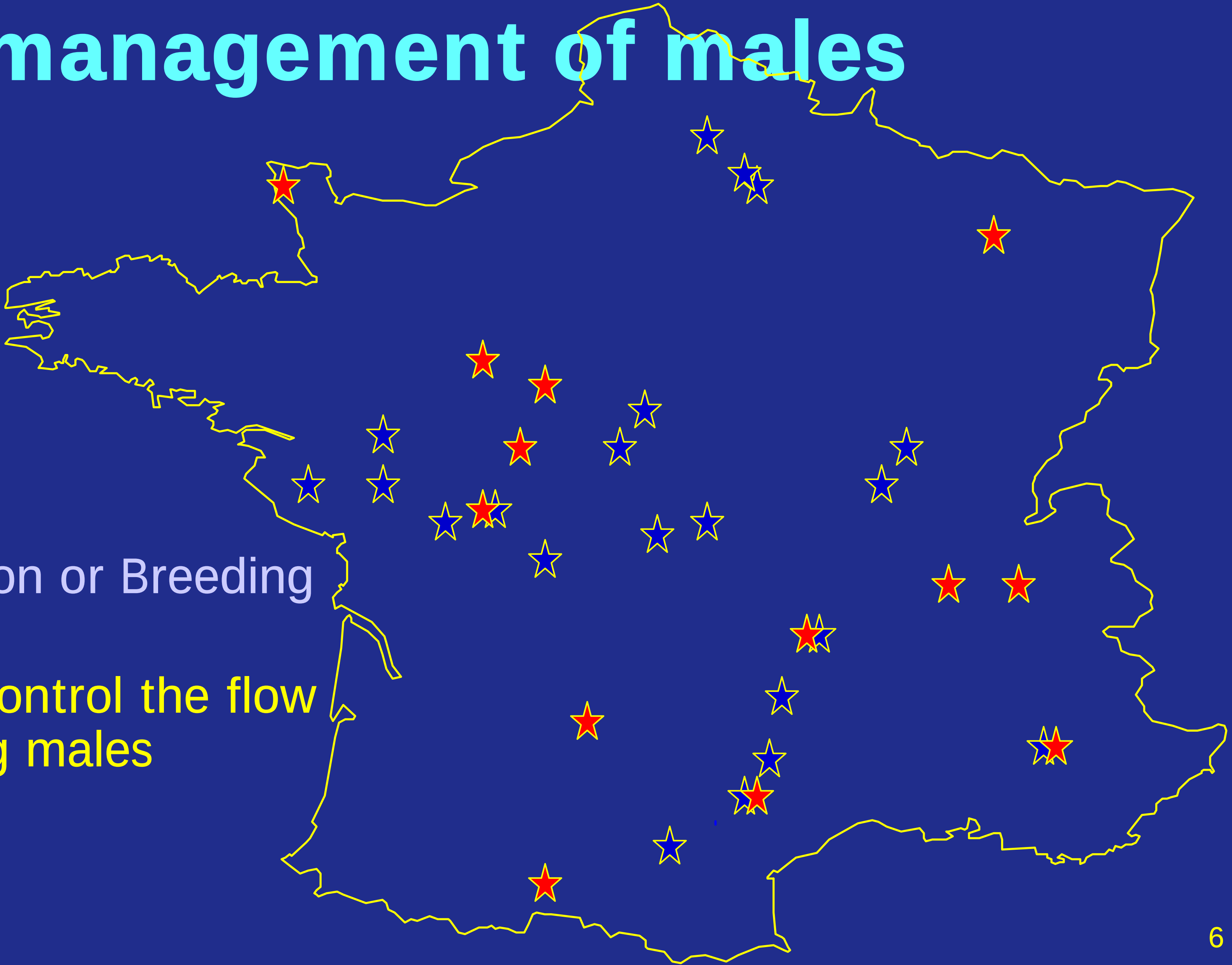
✓ Various demographic situations / Different methods of genetic variability management

In a case of populations where AI is not used

The most importance is to help farmers to:

1. Keep a large number of males in their flock
2. Change their rams regularly

An advantage : the collective management of males



Insemination or Breeding centers

→ control the flow of breeding males

Different management methods

- Well Suited for specific situations and different needs
- Easily applied by managers and farmers
- In accordance with important rules for genetic variability
- Based on breeding male flow

In practice

A wide range of goat and sheep populations

Selection/ conservation

Pedigree knowledge

Demography

Organisation level

→ 30 breeds under selection
→ 40 breeds in conservation

A diversity of methods

More or less: - simple to apply
- efficient
- sophisticated

Different tools / softwares

Find a method adapted to each situation

Overview of the main management approaches applied in France

- Splitting the population into groups
- SAUVAGE : a software to optimize gene mixing in populations with no or few pedigrees
- Optimisation of genetic contributions

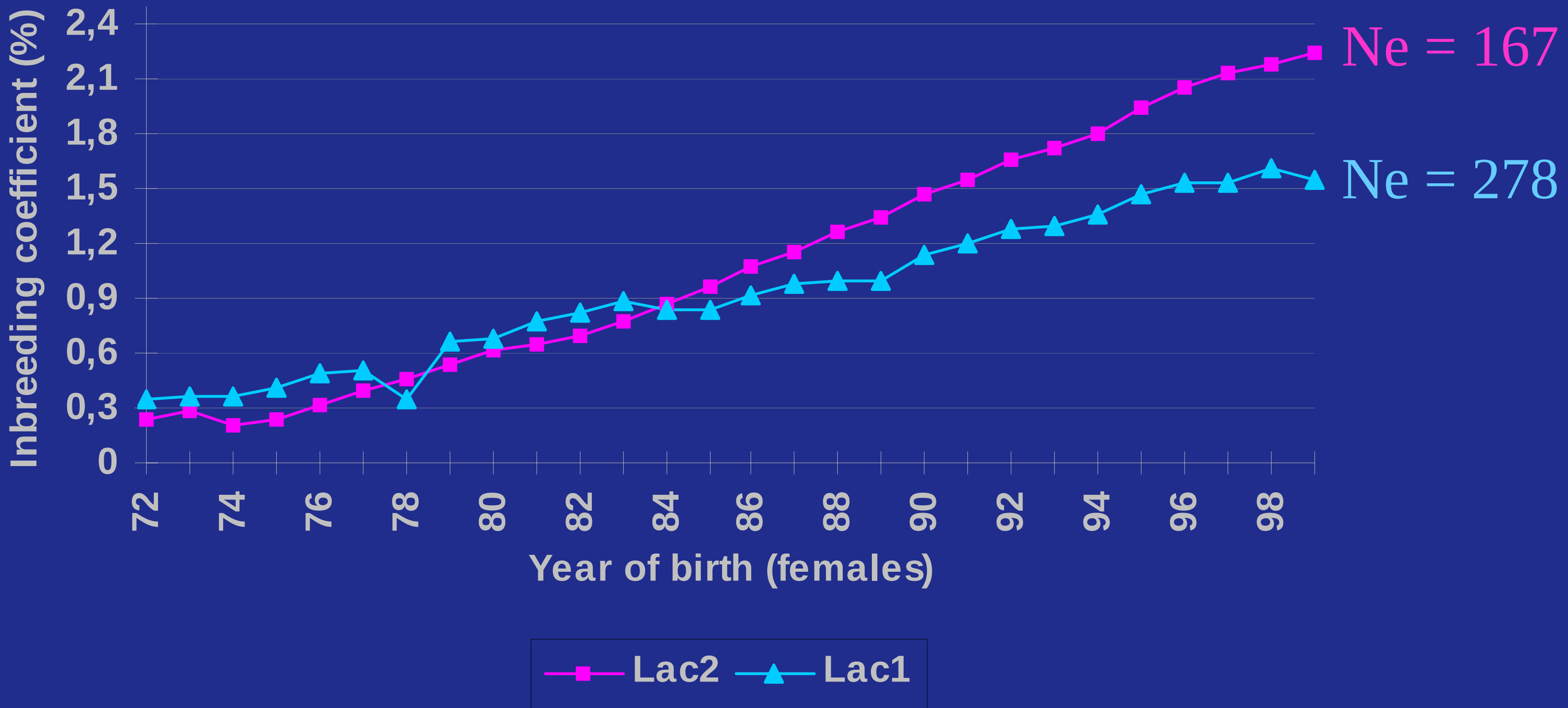
1. Splitting the population into groups

- Group = Flock OR Family → related animals
- Adapted to conservation or selection scheme
- Main rule: equalize the progeny size of each group
- Choice within group at each step of selection
- Simple to implement
- Very efficient if rules strictly applied

Example of the two lines in Lacaune dairy breed

→ High genetic progress (same into both lines)
→ 90% AI (Artificial Insemination)
→ Selection within AI sires groups in both lines
→ Management more rigorous in Lac1

Evolution of inbreeding in both Lacaune lines (females)



Particular case of rotationnal scheme

- Very efficient
- But need very close monitoring
- Otherwise side effects are worse
- Ex. Solognote breed:
  - Bottleneck in the 90’s
  - Dramatic decrease of genetic variability

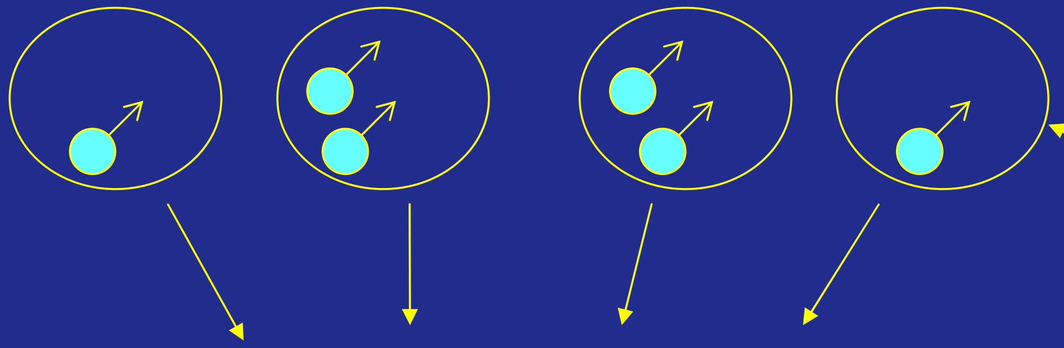
2. SAUVAGE

- Software based on a method from H. de Rochambeau, INRA
- Context: developp a management method:
  - For population with no/few pedigree and without selection programme
  - Easy to apply (less constraints than rotational scheme)
- Method :
  - Computation of flock genetic contributions
  - Probability of gene origin concept
  - Measure of similarity between a male and the females of a given flock

➡ **Optimize the gene mixing at the population level (exchange of males)**

2. SAUVAGE

Active sires



Flock = gene pool

New generation :
young males for replacement

Optimal dividing up
of males among flocks

Table of similarity measures

	flock1	flock2	flock3	flock4
Male1	0.25	0.03	0.01	0.07
Male2	0.18	0.08	0.07	0.22
Male3	0.03	0.02	0.06	0.20
Male4	0.09	0.05	0.12	0.04

>0.10	**Forbidden**
0.05> x > 0.10	**Not advised**
<0.05	**Recommended**

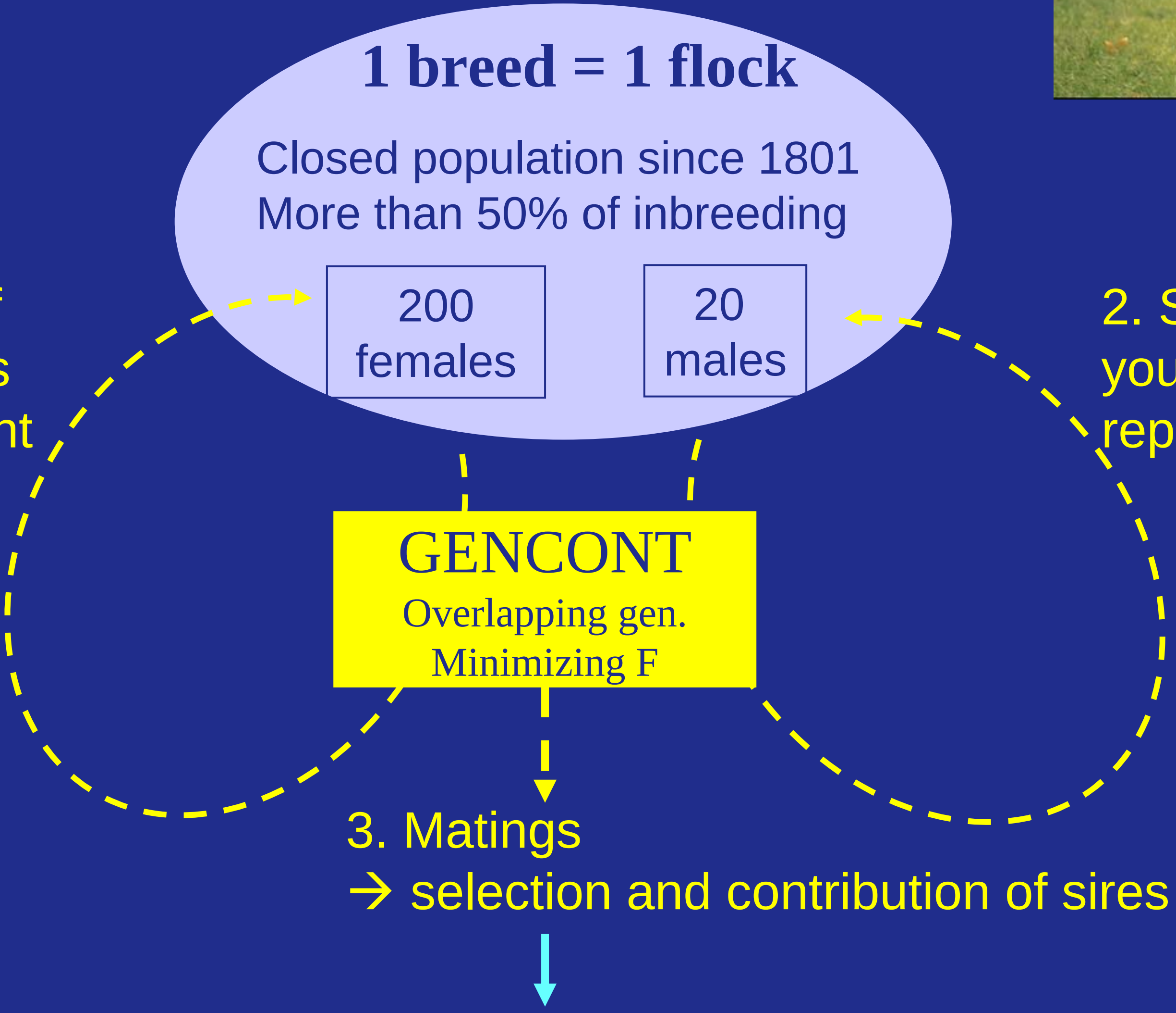
3. Optimisation of genetic contribution

- Only in populations with:
  - Good pedigree knowledge (based on relationship coefficient)
  - Well organized (to comply with the recommendations)

- Aim: Minimizing the rate of inbreeding
  - Populations in conservation → ex: GENCONT (ex. 1)
  - Populations under selection: with a predefined genetic gain → ex: method developped by Colleau et al. (2004) (ex. 2)

- Very efficient methods...but with some constraints

Example of Rambouillet Merino flock



1 breed = 1 flock

Closed population since 1801
More than 50% of inbreeding

200
females

20
males

1. Selection of
young females
for replacement

2. Selection of
young males for
replacement

GENCONT
Overlapping gen.
Minimizing F

3. Matings
→ selection and contribution of sires

Additionnal step to
minimize relationship
between sires and dams

Example of the French dairy goat breeding scheme

1. Method

- Developped by JJ. Colleau for dairy cattle since 2001
- Optimize inbreeding for a given expected genetic gain
- At each major step of selection:
  - Procreation of young bucks to be progeny tested
  - Selection of young bucks for service (after progeny testing)
  - Soon: use of service (AI) and progeny testing bucks

Example of the French dairy goat breeding scheme

2. Results : procreation of young bucks

Test of the method on real data

		Candidates	Realized	Optimized
Number of sires		131	14	37
Number of dams		695	470	470
Relationship coefficient	Mean	2.89	2.33	**1.07**
	Min	0.11	0.33	0.29
	Max	28.72	6.80	**1.91**

Same EBV
-54% of average relationship
Reduction of relationship max

Conclusion

- In practice the usual question is:
  which management method for a given population ?
- Pedigree analysis of different populations
  → confirm the relevancy of simple demographic rules
- Many methods exist, more or less complicated
  → successful if adapted to the population
- Key point : management of genetic variability at population level and collective

Thank you for your attention