

# Rationalization and characterization of gene bank collections: a case study

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## Conservation programs in French rare goat breeds

- Most programs started in the nineties
- Goat species specificities
  - ✓ Breeds not historically documented / acknowledged
  - ✓ Wide variety of phenotypes in most breeds
- ⇒ Ex situ buck sampling based on:
  - Phenotypes
  - Birth place / bucks exchanges between farmers
  - Pedigree (nowadays)





### **Case study: rare French goat breeds**

Breed	Number of females	Number of bucks / Cryobank	Number of genotypes (incl. AI bucks)
Hedge Goat	1 200	15	34 - 9
Lorraine Goat	930	8	27 - 6
Poitou	3 700	30	52 - 9
Provençale	1 760	7	64 - 7
Pyrenean	4 270	13	32 - 7
Rove	9 000	3	13 - 2













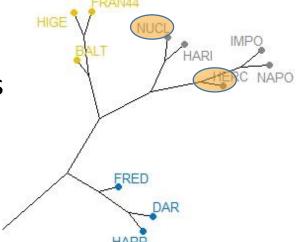
#### Real kinship level



Example:

Pedigree data => full sibs

SNP: half sibs?







#### Level of inbreeding *F*:

- Founders animals (pedigree analysis: F= 0)
- Recent animals without pedigrees









Animal	Molecular inbreeding	Pedigree inbreeding
H131 Sauze	0,150	11,0%
9028 Waroux	0,145	0 %
DALLIUS	0,123	0,5 %
9110 Sauze	0,120	11,0%
MARDI	0,114	1,2%
9009 Sauze	0,101	0 %
Luxembourg	0,093	3,7%
GROSOS	0,093	25,0%
GRELOT	0,083	6,4%
BOOSTER	0,083	0 %
ERMINIG	0,083	0,2%
CACAO_gamot	0,082	2,7%
8140	0,075	17,1%
JACOBIN	0,071	0 %





#### Genes introgression from other breeds?

Provençale "breed"





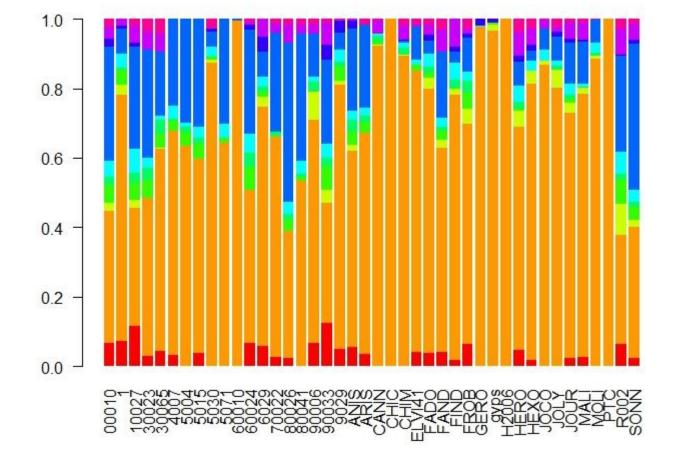




#### ... Not so easy to answer...

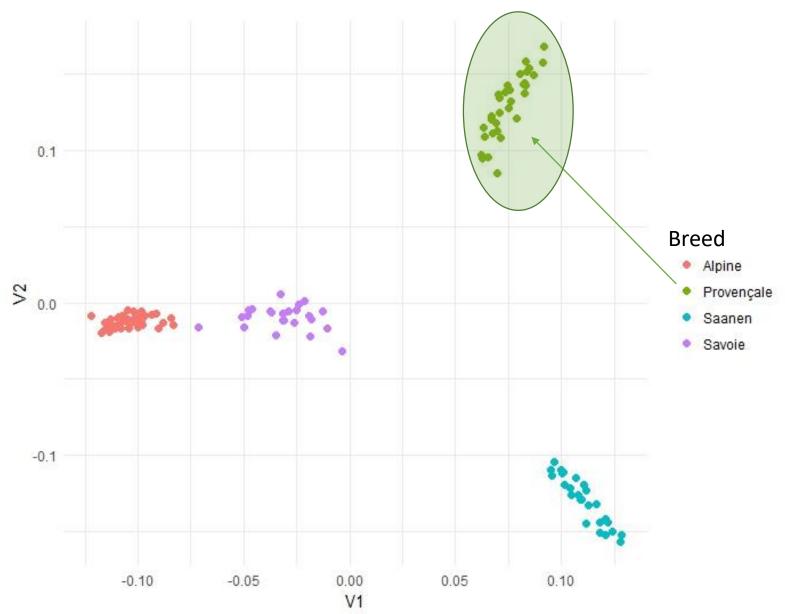
Provençale "breed"









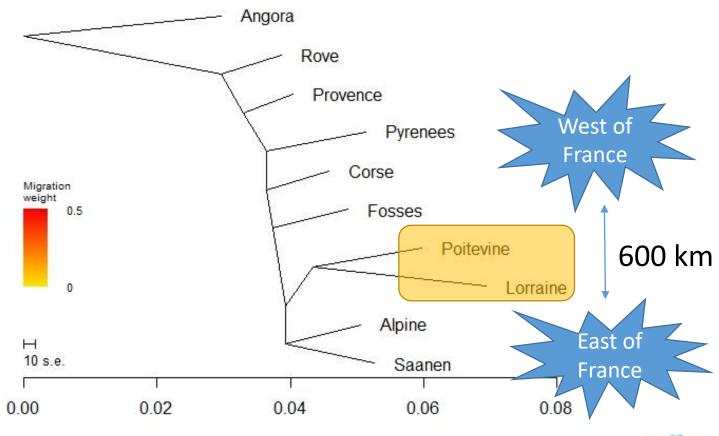






#### How breeds are related?

Treemix



Drift parameter





### SNP data analysis From research to "everyday" use

- MAF, Genotype rate, HWF: rates? Pruning?
- ROH (inbreeding): which length?
- Software well adapted to rare breeds (breeds size, recent bottlenecks)? Adaptation needed?

Sampling need to exclude animals with high:

- ✓ Kinship
- ✓ Inbreeding
- + Results can shift a great depending on the number of breeds / type of breeds included in the set





### SNP data analysis From research to everyday use

- Which indicators are:
  - the most relevant
  - most accurate and/or less sensitive to SNP bias?
  - the easiest to vulgarize

#### Examples of indicators that are difficult to explain:

- Negative inbreeding and kinships
- Kinship and inbreeding vary with the number of samples
- Numerous kinship and inbreeding indicators, different values
- Comparison between pedigree kinship/inbreeding (%) and molecular ones





#### Thank you for your attention

## Thanks to the breeders associations for their help









